SHARED NEOANTIGENS

RELATED APPLICATIONS AND INCORPORATION BY REFERENCE

[0001] This application claims priority and benefit of U.S. Provisional application serial number 62/179,877 filed May 20, 2015 and U.S. Provisional application serial number 62/389,377 filed February 23, 2016.

[0002] The foregoing applications, and all documents cited therein or during their prosecution ("appln cited documents") and all documents cited or referenced in the appln cited documents, and all documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and may be employed in the practice of the invention. More specifically, all referenced documents are incorporated by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

FIELD OF THE INVENTION

[0003] The present invention relates to methods and compositions for treating neoplasias, e.g. tumors, particularly using at least one neoantigenic peptide which is suitable for treating a significant proportion of subjects in a population suffering from cancer.

BACKGROUND OF THE INVENTION

[0004] Approximately 1.6 million Americans are diagnosed with neoplasia every year, and approximately 580,000 people in the United States are expected to die of the disease in 2013. Over the past few decades there been significant improvements in the detection, diagnosis, and treatment of neoplasia, which have significantly increased the survival rate for many types of neoplasia. However, only about 60% of people diagnosed with neoplasia are still alive 5 years after the onset of treatment, which makes neoplasia the second leading cause of death in the United States.

[0005] Currently, there are a number of different existing cancer therapies, including ablation techniques (e.g., surgical procedures, cryogenic/heat treatment, ultrasound, radiofrequency, and radiation) and chemical techniques (e.g., pharmaceutical agents, cytotoxic/chemotherapeutic

agents, monoclonal antibodies, and various combinations thereof). Unfortunately, such therapies are frequently associated with serious risk, toxic side effects, and extremely high costs, as well as uncertain efficacy.

[0006] There is a growing interest in cancer therapies that seek to target cancerous cells with a patient's own immune system (e.g., cancer vaccines) because such therapies may mitigate/eliminate some of the herein-described disadvantages. Cancer vaccines are typically composed of tumor antigens and immunostimulatory molecules (e.g., cytokines or TLR ligands) that work together to induce antigen-specific cytotoxic T cells that target and destroy tumor cells. Current cancer vaccines may contain shared tumor antigens, which are native proteins (i.e. – proteins encoded by the DNA of all the normal cells in the individual) that are selectively expressed or over-expressed in tumors found in many individuals. While such shared tumor antigens are useful in identifying particular types of tumors, they are not ideal as immunogens for targeting a T-cell response to a particular tumor type because they are subject to the immune dampening effects of self-tolerance. Vaccines containing tumor-specific and patient-specific neoantigens can overcome some of the disadvantages of vaccines containing shared tumor antigens. However, the use of patient-specific neoantigens requires sequencing of individual subject's genomes, as well as the production of personalized compositions comprising a combination of neoantigens present in that individual subject. Accordingly, there is still a need for improved methods and compositions for delivering cancer vaccines.

[0007] Citation or identification of any document in this application is not an admission that such document is available as prior art to the present invention.

SUMMARY OF THE INVENTION

[0008] Preferred statements (features) and embodiments of this invention are set herein below. Each statements and embodiments of the invention so defined may be combined with any other statement and/or embodiments unless clearly indicated to the contrary. In particular, any feature indicated as being preferred or advantageous may be combined with any other feature or features or statements indicated as being preferred or advantageous. Hereto, the present invention is in particular captured by any one or any combination of one or more of the below statements and embodiments, with any other statement and/or embodiments.

[0009] It is an objective of the invention to provide methods and compositions for the treatment of a population of cancer patients by eliciting an immune response targeting the cancer. In one aspect, the present invention relates to a pharmaceutical composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor. The composition may include one neoantigenic peptide. In other embodiments, the composition may include more than 100 neoantigenic peptides. Preferably, the composition includes about 20 neoantigenic peptides. The at least one neoantigenic peptide may include a tumor-specific mutation. The mutation may be recurrent. Preferably, the mutation is present in a large proportion of a population. A recurrent mutation may be based on the mutation being present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer. The composition may include at least one neoantigenic peptide containing a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer. Additionally, the composition may contain at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer. The ability to elicit an immune response refers to the ability of the immune system to present an antigen to a lymphocyte. In order for the immune system to present an antigen, the antigen needs to be presented by a subjects HLA proteins. In order to elicit an immune response against a tumor, the tumor needs to contain the mutations leading to expression of the antigen. In order for the composition to provide a benefit to a population in need thereof, the population has to include subjects that express an HLA allele capable of binding the at least one neoantigenic peptide present in the composition and the population has to include subjects containing tumors with mutations that lead to neoantigenic epitopes present in the neoantigenic peptides.

[0010] The composition may be specific to a population of subjects suffering from cancer that share a characteristic. The population may have cancer or may have a specific cancer. The population may share a common set of HLA subtypes. They may share HLA subtypes based on ethnicity. Not being bound by a theory the percentage of HLA types in a population can be predicted based on ethnicity without testing. Not being bound by a theory, different populations express different HLA types capable of binding different neoantigenic peptides. Therefore a

composition can be formulated to provide a benefit to a large proportion of that population, whereas the composition would not provide a benefit to another population. Not being bound by a theory, different cancers contain different mutations and thus compositions tailored to specific cancers can be used to provide a greater benefit to a population with one type of cancer as compared to a population that includes more than one type. In one embodiment, the population is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS).

[0011] In one embodiment, the population of subjects is suffering from CLL; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of "CLL"; and at least one of a set of six of the at least one tumor-specific mutation will be found in 17.49% of subjects in the CLL population. The population of subjects may be suffering from BLCA, the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"BLCA"; and at least one of a set of six of the at least one tumor-specific mutation will be found in 26.92% of subjects in the population. The population of subjects may be suffering from BRCA; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"BRCA"; and at least one of a set of 18 of the at least one tumor-specific mutation will be found in 36.04% of subjects in the population. The population of subjects may be suffering from COAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"COAD"; and at least one of a set of three of the at least one tumor-specific mutation will be found in 27.14% of subjects in the population. The population of subjects may

be suffering from GBM; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"GBM"; and at least one of a set of 14 of the at least one tumor-specific mutation will be found in 34.36% of subjects in the population. The population of subjects may be suffering from HNSC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"HNSC"; and at least one of a set of 10 of the at least one tumor-specific mutation will be found in 21.61% of subjects in the population. The population of subjects may be suffering from KIRC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"KIRC"; and at least one of a set of four of the at least one tumor-specific mutation will be found in 6% of subjects in the population. The population of subjects may be suffering from LAML; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LAML"; and at least one of a set of 11 of the at least one tumor-specific mutation will be found in 47.45% of subjects in the population. The population of subjects may be suffering from LUAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LUAD"; and at least one of a set of 11 of the at least one tumor-specific mutation will be found in 33.42% of subjects in the population. The population of subjects may be suffering from LUSC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LUSC"; and at least one of a set of two of the at least one tumor-specific mutation will be found in 7.87% of subjects in the population. The population of subjects may be suffering from OV; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"OV"; and at least one of a set of ten of the at least one tumor-specific mutation will be found in 22.78% of subjects in the population. The population of subjects may be suffering from READ; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"READ"; and at least one of a set of two of the at least one tumor-specific mutation will be found in 20.51% of subjects in the population. The population of subjects may be suffering from SKCM; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"SKCM"; and at least one of a set 64 of the at least one tumor-specific mutation will be found in 90.91% of subjects in the population. The population of subjects may be suffering from UCEC; the at least one tumor-specific mutation comprises any combination of

mutations in Table 8 with an exemplary disease of"UCEC"; and at least one of a set of 30 of the at least one tumor-specific mutation will be found in 67.74% of subjects in the population. The population of subjects may be suffering from ACC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"ACC"; and at least one of a set of 161 of the at least one tumor-specific mutation will be found in 50% of subjects in the population. The population of subjects may be suffering from CESC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"CESC"; and at least one of a set of four of the at least one tumor-specific mutation will be found in 23.71% of subjects in the population. The population of subjects may be suffering from CRC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"CRC"; and at least one of a set of 15 of the at least one tumor-specific mutation will be found in 56.65% of subjects in the population. The population of subjects may be suffering from DLBCL; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"DLBCL"; and at least one of a set of 2 of the at least one tumor-specific mutation will be found in 13.79% of subjects in the population. The population of subjects may be suffering from KICH; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"KICH"; and at least one of a set of 24 of the at least one tumor-specific mutation will be found in 50% of subjects in the population. The population of subjects may be suffering from KIRP; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"KIRP"; and at least one of a set of nine of the at least one tumor-specific mutation will be found in 42.24% of subjects in the population. The population of subjects may be suffering from LIHC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LIHC"; and at least one of a set of 2 of the at least one tumor-specific mutation will be found in 6.57% of subjects in the population. The population of subjects may be suffering from MM; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"MM"; and at least one of a set of 6 of the at least one tumor-specific mutation will be found in 23.9% of subjects in the population. The population of subjects may be suffering from PRAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"PRAD"; and at least one of a set of 24 of the

at least one tumor-specific mutation will be found in 39.85% of subjects in the population. The population of subjects may be suffering from STAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"STAD"; and at least one of a set of 150 of the at least one tumor-specific mutation will be found in 48.79% of subjects in the population. The population of subjects may be suffering from TGCT; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"TGCT"; and at least one of a set of 14 of the at least one tumor-specific mutation will be found in 51.61% of subjects in the population. The population of subjects may be suffering from THCA; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"THCA"; and at least one of a set of five of the at least one tumor-specific mutation will be found in 69.88% of subjects in the population. The population of subjects may be suffering from UCS; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"UCS"; and at least one of a set of two of the at least one tumor-specific mutation will be found in 16.07% of subjects in the population. The population of subjects may be suffering from PAAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"PAAD"; and at least one of a set of 53 of the at least one tumor-specific mutation will be found in 50% of subjects in the population. The population of subjects may also be suffering from a solid tumor. The solid tumor may be clear cell Renal Cell Carcinoma (ccRCC), melanoma, sarcoma, or a cancer of the bladder, colon, brain, breast, head and neck, endometrium, lung, ovary, pancreas or prostate. The population of subjects may be suffering from a liquid tumor. The liquid tumor may be Non-Hodgkin's lymphoma or leukemia.

[0012] In another embodiment, the at least one tumor-specific mutation has an incidence of at least 500 patients a year in the population of subjects suffering from cancer, and wherein the at least one mutation may be a mutation listed for the population in Table 9. The at least one neoantigenic peptide may be at least one peptide listed in Table 9.

[0013] In another embodiment, the population suffering from cancer is being treated with a drug or therapy. The population suffering from cancer may have been previously treated with, is currently being treated with, or is selected to treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0014] In another embodiment, the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in a population of subjects suffering from cancer.

[0015] In another embodiment, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one tumor-specific mutation present in the composition; and at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one HLA protein which binds to a tumor-specific neoepitope present in the composition.

[0016] In one embodiment, the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations. In another embodiment, the tumor-specific mutations comprise drug resistance mutations. In one embodiment, the neoantigenic peptides include not only the resulting mutated neoantigen protein sequence, but a long peptide region surrounding and including the mutation and includes all contiguous segments within it (see Tables 1-4). In one embodiment, the tumor-specific mutations are present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1. In one embodiment, the tumor-specific mutations are present in one or more genes listed in any of the Tables presented herein. In one embodiment, the at least one tumor-specific mutation is derived from alternative splicing of PD-L1 or AR. In one embodiment, the at least one tumor-specific mutation is derived from splice variant sPD-L1, AR-V1 or AR-V7. In one embodiment, the least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L. In one embodiment, the drug

resistance mutation is induced by treatment with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy. In another embodiment, a subject has a drug resistance mutation before treatment.

[0017] In another embodiment, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 neoantigenic peptides. The composition may include 15 to 20 neoantigenic peptides. The composition may include greater than 100, 200, or 300 neoantigenic peptides. Each neoantigenic peptide may be from about 5 to about 50 amino acids in length.

[0018] In another embodiment, the pharmaceutical composition is an immunogenic or vaccine composition. The pharmaceutical composition may further comprise an immunomodulator or adjuvant. The immunodulator or adjuvant may be selected from the group consisting of poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, cyclic di-nucleotides such as STING, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryllipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel®, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon.

[0019] In another embodiment, the pharmaceutical composition comprises one or more neoantigenic peptides as defined in Table 1, 2, 3 or 4.

[0020] In one embodiment, each tumor-specific neoepitope binds to HLA-A, -B or –C or to HLADRB, HLADBM XXXXX with a K_D of less than 500 nM.

[0021] In another aspect, the present invention relates to a method of treating or preventing a tumor in a subject in need thereof by administering to the subject any pharmaceutical composition as described herein.

[0022] In one embodiment, a method of treating or preventing a tumor in a patient in need thereof is provided, comprising administering to a patient a composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein the composition comprises at least one neoantigenic peptide comprising a tumor-

specific mutation present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer; the composition comprises at least one neoantigenic peptide comprising a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer; and the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

[0023] In one embodiment, the population of subjects is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS). In one embodiment, the population of subjects is suffering from a solid tumor. The solid tumor may be clear cell Renal Cell Carcinoma (ccRCC), melanoma, sarcoma, or a cancer of the bladder, colon, brain, breast, head and neck, endometrium, lung, ovary, pancreas or prostate. In one embodiment, the population of subjects is suffering from a liquid tumor. The liquid tumor may be Non-Hodgkin's lymphoma or leukemia.

[0024] In one embodiment, the population suffering from cancer was treated with, is being treated with, or is selected to treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0025] In one embodiment, the at least one neoantigenic peptide is capable of eliciting an immune response against a tumor present in at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population of subjects suffering from cancer. In one embodiment, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one tumor-specific mutation present in the composition

and, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one HLA protein which binds to a tumor-specific neoepitope present in the composition.

[0026] In another embodiment, the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations. The tumor-specific mutations may be drug resistance mutations. The tumor-specific mutations may be present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1. The tumor-specific mutations may be present in one or more genes listed in any of the Tables. The at least one tumor-specific mutation may be derived from alternative splicing of PD-L1 or AR. The at least one tumor-specific mutation may be derived from splice variant sPD-L1, AR-V1 or AR-V7.

[0027] In one embodiment, the at least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L. The drug resistance mutation may be induced by treatment with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0028] In another embodiment, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 neoantigenic peptides. In a preferred embodiment, the composition comprises 15 to 20 neoantigenic peptides.

[0029] In another embodiment, each neoantigenic peptide is from about 5 to about 50 amino acids in length.

[0030] In another embodiment, the composition is an immunogenic or vaccine composition. For instance, the immunogenic or vaccine composition may comprise an immunomodulator or

adjuvant. The immunodulator or adjuvant may be selected from the group consisting of poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, cyclic di-nucleotides such as STING, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryllipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel®, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon.

[0031] In one embodiment, the composition comprises one or more neoantigenic peptides as defined in Table 1, 2, 3 or 4.

[0032] In one embodiment, each tumor-specific neoepitope binds to HLA-A, -B or –C or to HLADRB, HLADBM XXXXX with a K_D of less than 500 nM.

[0033] In another aspect, the present invention provides a method of prophylactic cancer treatment comprising selecting a cancer drug for a patient in need thereof, the drug selected from the group consisting of ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK and antiestrogen therapy; and administering prophylactically to the subject, before drug resistant mutations can be detected, a pharmaceutical composition comprising neoantigenic peptides derived from drug resistant mutations associated with the selected cancer drug.

[0034] The shared neoantigen immunogenic composition can be administered via subcompositions, each containing a portion of the neoantigens, and sub-compositions can be administered to different places on the subject or patient; for instance, a composition comprising 20 different neoantigens, can be administered in four (4) subcompositions, each containing 5 of the 20 different neoantigens, and the four (4) subcompositions can be administered so as to endeavor to deliver each subcomposition to a separate set of draining lymph nodes of the patient, e.g., to each of the arms and legs (e.g., thigh or upper thigh or near buttocks or lower back on each side of the patient) so as to endeavor to deliver fewer neoantigens to each set of draining lymph nodes of the patient or subject and thereby limit competition between neoantigens. Of course, the number of locations and hence number of subcompositions can vary, e.g., the skilled practitioner could consider administration at or near the spleen to have a fifth point of administration, and the skilled practitioner can vary the locations such that only one, two

or three are used (e.g., each arm and a leg, each of legs and one arm, each of the legs and no arms, or only both arms). The shared neoantigen immunogenic composition administered at the aforementioned various intervals can be different formulations, and the subcompositions administered at different places on the subject or patient during a single administration can be different compositions. For instance, a first administration can be of a whole shared neoantigen immunogenic composition and a next or later administration can be of a vector (e.g., viral vector or plasmid) that has expression of antigen(s) in vivo. Likewise, in the administration of different subcompositions to different locations on the patient or subject, some of the subcompositions can comprise a whole antigen and some of the subcompositions can comprise a vector (e.g., viral vector or plasmid) that has expression of antigen(s) in vivo. And some compositions and subcompositions can comprise both vector(s) (e.g., viral vector or plasmid) that has / have expression of antigen(s) in vivo and whole antigens. Some vectors (e.g., poxvirus) that have expression of antigen(s) in vivo can have an immunostimulatory or adjuvanting effect, and hence compositions or subcompositions that contain such vectors can be self-adjuvanting. Also, by changing up the nature of how the antigens are presented to the immune system, the administrations can "prime" and then "boost" the immune system. And in this text, when there is mention of a "vaccine" it is intended that the invention comprehends immunogenic compositions, and when there is mention of a patient or subject it is intended that such an individual is a patient or subject in need of the herein disclosed treatments, administrations, compositions, and generally the subject invention.

[0035] Moreover, the invention applies to the use of any type of expression vector, such as a viral expression vector, e.g., poxvirus (e.g., orthopoxvirus or avipoxvirus such as vaccinia virus, including Modified Vaccinia Ankara or MVA, MVA-BN, NYVAC according to WO-A-92/15672, fowlpox, e.g., TROVAX, canarypox, e.g., ALVAC (WO-A-95/27780 and WO-A-92/15672) pigeonpox, swinepox and the like), adenovirus, AAV, herpesvirus, and lentivirus; or a plasmid or DNA or nucleic acid molecule vector. Some vectors that are cytoplasmic, such as poxvirus vectors, may be advantageous. However adenovirus, AAV and lentivirus can also be advantageous to use in the practice of the invention.

[0036] In a ready-for-use, especially reconstituted, shared neoantigen immunogenic composition, the vector, e.g., viral vector, is present in the quantities within the ambit of the

skilled person from this disclosure and the knowledge in the art (such as in patent and scientific literature cited herein).

[0037] Whole antigen or vector, e.g., recombinant live vaccines may exist in a freeze-dried form allowing their storage and are reconstituted immediately before use in a solvent or excipient, which can include an adjuvant as herein discussed.

[0038] The subject of the invention is therefore also a vaccination or immunization set or kit comprising, packaged separately, freeze-dried vaccine and a solution, advantageously including an adjuvant compound as herein discussed for the reconstitution of the freeze-dried vaccine.

[0039] The subject of the invention is also a method of vaccination or immunization comprising or consisting essentially of or consisting of administering, e.g., by the parenteral, preferably subcutaneous, intramuscular or intradermal, route or by the mucosal route a vaccine or immunogenic composition in accordance with the invention at the rate of one or more administrations. Optionally this method includes a preliminary step of reconstituting the freeze-dried shared neoantigen immunogenic composition (e.g., if lyophilized whole antigen or vector) in a solution, advantageously also including an adjuvant.

[0040] In one embodiment, the shared neoantigen immunogenic composition is administered at a dose of about 10 μg to 1 mg per 70 kg individual as to each neoantigenic peptide. In another embodiment, the shared neoantigen immunogenic composition is administered at an average weekly dose level of about 10 μg to 2000 μg per 70 kg individual as to each neoantigenic peptide. In another related embodiment, the administration is intravenous. In one embodiment, the shared neoantigen immunogenic composition is administered intravenously or subcutaneously.

[0041] In another embodiment, the method further comprises (a) obtaining a sample of tumor tissue from each subject; (b) detecting one or more of the tumor-specific mutations in the sample; and (c) selecting a subject from the population of subjects for treatment with the at least one neoantigenic peptides if at least one of the tumor-specific mutations are detected in the sample from the subject.

[0042] In another embodiment, the method further comprises (a) determining HLA allotypes present in each subject; and (b) selecting a subject from the population of subjects for treatment with the at least one neoantigenic peptides if one or more HLA allotypes present in the subject

binds to one or more of the tumor-specific neoepitopes present in the at least one neoantigenic peptides.

[0043] Embodiments of the present invention relate to compositions and methods using shared neoantigens, which (unlike shared native (non-mutated) antigens derived from genes differentially expressed in tumors) have desirable properties such as not being subject to the immune-dampening effects of central tolerance and high tumor specificity. This is because the neoantigens are expressed only in tumor tissue, e.g. are generated by tumor-specific mutations or splicing defects. Such splice variants or mutations may generate immunogenic epitopes across a variety of HLA alleles, thus covering a significant proportion of the population. Moreover, because these mutations may be present in a significant proportion of subjects suffering from cancer, the compositions described herein do not require sequencing of whole genomes of subjects and may be used as an "off-the-shelf" product to treat multiple subjects. For instance, the method may simply involve detecting in a tumor sample from the subject one or more of the specific mutations present in the composition, and administering the composition to subjects in which at least one mutation is present. This is in contrast to methods using patient-specific neoantigen mixtures, which require whole genome or whole exome sequencing of each subject and the production of personalized treatment compositions.

[0044] Other embodiments relate to a combination therapy wherein the methods of treatment using a shared neoantigen composition of the present invention are used in concert with a current drug regimen. The shared neoantigen composition may be administered prophylactically. In one embodiment, a patient in need thereof is treated with chemotherapy and/or a targeted therapy in combination with a shared neoantigen immunogenic composition before a drug resistance mutation can be detected. The shared neoantigen immunogenic composition can be tailored to include neoantigen peptides specific to the resistance mutations associated with a chosen therapy. In another embodiment, the shared neoantigen composition is administered before the subject is treated with a chemotherapy and/or a targeted therapy, to generate an immune response to cells harboring a drug resistance mutation before such cells develop. The administering can be serially or sequentially or at substantially the same time or substantially simultaneously. For example, the administering of the shared neoantigen immunogenic composition and the administering of a cancer therapy can be at about the same time or substantially simultaneously. Alternatively, the administering of the shared neoantigen immunogenic composition can be on

one time schedule, e.g., weekly, biweekly, every three weeks, monthly, bimonthly, every quarter year (every three months), every third of a year (every four months), every five months, twice yearly (every six months), every seven months, every eight months, every nine months, every ten months, every eleven months, annually or the like, and the administering of the cancer therapy can be on a different schedule that is typical for the therapy such that the subject or patient has two different treatment schedules running concomitantly and the administering of the shared neoantigen immunogenic composition and the administering of the cancer therapy can be sequentially or serially. In preferred embodiments the subject may be treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0045] In another aspect the present invention provides a diagnostic method for early detection and tracking of cancer progression by determining the presence of at least one neoantigenic peptide of the present invention in a patient sample. The patient sample may be derived from blood, sputum, saliva, urine, tumor tissue, lymphatic fluid, semen or feces.

[0046] In one embodiment, the diagnostic method is used before administering the shared neoantigen composition as described herein. The diagnostic method may include comparing the amount of shared neoantigen mutations in a series of at least two samples taken during treatment with a cancer therapy and/or shared neoantigen composition. Not being bound by a theory, an increase or decrease in shared neoantigen mutations can be used to determine treatment efficacy.

[0047] In one embodiment, the mutated genes can be detected using PCR based methods or sequencing. Reverse transcription PCR (RT-PCR) can be used to detect mutations in transcribed neoantigen genes. Additionally, any sequencing technique can be used to determine the presence of a mutation. In a preferred embodiment, pyrosequencing is used. The present invention also provides for a kit that includes primers that are specific to sequences encompassing the neoantigen mutations.

[0048] In another embodiment the mutated genes are detected by immunological detection methods. Antibodies specific to the shared neoantigen mutations can be used to detect the muations. The antibodies may be bound to an array. The array may include antibodies to detect more than one of the shared neoantigen mutations of the present invention. The antibodies can be configured for use in an ELISA assay. Therefore, a composition or kit may be provided that includes antibodies specifically recognizing the shared neoantigens of the present invention.

[0049] In another aspect the present invention provides a method of treating or preventing a tumor in a population of subjects in need thereof, comprising administering to a subject an agent comprising an extracellular ligand-binding domain recognizing a tumor-specific neoepitope comprising a tumor-specific mutation having an incidence of at least 1% of subjects in the population. The agent may be an antibody, antibody fragment, antibody drug conjugate, aptamer, CAR, or T cell receptor. The antibody or antibody fragment may be humanized, fully humanized, or chimeric. The antibody fragment may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment. The tumor-specific mutation may be a mutation listed for any population in Table 9. The tumor-specific mutation may be within a gene containing an extracellular domain. The tumor-specific mutation may be FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P. The tumor-specific mutation may be within the extracellular domain. The tumor-specific mutation comprises FGFR3 S249C or ERBB3 V104M. Not being bound by a theory, the presence of a neoepitope in a protein with an extracellular domain allows the neoepitope to be presented on the surface of a cell. Not being bound by a theory, the presence of a neoepitope in the extracellular domain allows the neoepitope to be presented on the surface of a cell.

[0050] The invention is further described by the following numbered paragraphs:

1. An isolated neoantigenic peptide comprising a tumor-specific neoepitope defined in Tables 1-9, wherein the isolated neoantigenic peptide is not a native polypeptide.

2. An isolated neoantigenic peptide 100 amino acids or less in length which comprises a tumor-specific neoepitope defined in Tables 1-9.

3. The isolated neoantigenic peptide of paragraph 1 or 2, which is between about 5 to about 50 amino acids in length.

4. The isolated neoantigenic peptide of any of paragraphs 1-3, which is between about 15 to about 35 amino acids in length.

5. The isolated neoantigenic peptide of paragraph 4, which is about 15 amino acids or less in length.

6. The isolated neoantigenic peptide of paragraph 5, which is between about 8 and about 11 amino acids in length.

7. The isolated neoantigenic peptide of paragraph 6, which is 9 or 10 amino acids in length.

8. The isolated neoantigenic peptide of any of paragraphs 1-7, which binds major histocompatibility complex (MHC) class I.

9. The isolated neoantigenic peptide of paragraph 8, which binds MHC class I with a binding affinity of less than about 500 nM.

10. The isolated neoantigenic peptide of any of paragraphs 1-3, which is about 30 amino acids or less in length.

11. The isolated neoantigenic peptide of paragraph 10, which is between about 6 and about 25 amino acids in length.

12. The isolated neoantigenic peptide of paragraph 11, which is between about 15 and about 24 amino acids in length.

13. The isolated neoantigenic peptide of paragraph 11, which is between about 9 and about 15 amino acids in length.

14. The isolated neoantigenic peptide of any of paragraphs 1-3 and 10-13, which binds MHC class II.

15. The isolated neoantigenic peptide of paragraph 14, which binds MHC class II with a binding affinity of less than about 1000 nM.

16. The isolated neoantigenic peptide of any of paragraphs 1-15, further comprising flanking amino acids.

17. The isolated neoantigenic peptide of paragraph 16, wherein the flanking amino acids are not native flanking amino acids.

18. The isolated neoantigenic peptide of any of paragraphs 1-17, which is linked to at least a second neoantigenic peptide.

19. The isolated neoantigenic peptide of paragraph 18, wherein peptides are linked using a poly-glycine or poly-serine linker.

20. The isolated neoantigenic peptide of paragraph 18 or 19, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 1000 nM.

21. The isolated neoantigenic peptide of paragraph 20, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 500 nM.

22. The isolated neoantigenic peptide of paragraph 20 or 21, wherein both of the neoepitopes bind to human leukocyte antigen (HLA) -A, -B, -C, -DP, -DQ, or -DR.

23. The isolated neoantigenic peptide of any of paragraphs 20-22, wherein the isolated neoantigenic peptide and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide and the second neoantigenic peptide binds a class II HLA.

24. The isolated neoantigenic peptide of any of paragraphs 20-22, wherein the isolated neoantigenic peptide binds a class II HLA and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide binds a class I HLA and the second neoantigenic peptide binds a class II HLA.

25. The isolated neoantigenic peptide of any of paragraphs 1-24, further comprising modifications which increase in vivo half-life, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation.

26. The isolated neoantigenic peptide of paragraph 25, wherein the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids.

27. The isolated neoantigenic peptide of paragraph 25, wherein the cells that are targeted are antigen presenting cells.

28. The isolated neoantigenic peptide of paragraph 27, wherein the antigen presenting cells are dendritic cells.

29. The isolated neoantigenic peptide of paragraph 29, wherein the dendritic cells are targeted using the CD141, DEC205, or XCR1 marker.

30. A pharmaceutical composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein:

(a) the composition comprises at least one neoantigenic peptide comprising a tumor-specific mutation present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer;

(b) the composition comprises at least one neoantigenic peptide comprising a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer; or

(c) the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

31. The pharmaceutical composition of paragraph 30, wherein the population of subjects is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS).

32. The pharmaceutical composition of paragraph 30 or 31, wherein the population suffering from cancer was treated with, is being treated with, or is selected to be treated with a cancer therapeutic, optionally ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitor or antiestrogen therapy..

33. The pharmaceutical composition of any of paragraphs 30-33, wherein the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations.

34. The pharmaceutical composition of any of paragraphs 30-33, wherein the at least one neoantigenic peptide comprises at least one neoantigenic peptide derived from a long peptide

region flanking and including the tumor specific mutation, and wherein all contiguous segments within the long peptide are included.

35. The pharmaceutical composition of any of paragraphs 30-34, wherein the tumor-specific mutations are present in one or more genes listed in Tables 1-9.

36. The pharmaceutical composition of any of paragraphs 30-35, wherein the composition comprises at least one neoantigenic peptide as defined in any of Tables 1-9.

37. The pharmaceutical composition of any of paragraphs 30-36, wherein the tumor-specific mutations are present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1.

38. The pharmaceutical composition of paragraph 37, wherein at least one tumor-specific mutation is derived from alternative splicing of PD-L1 or AR.

39. The pharmaceutical composition of paragraph 38, wherein at least one tumor-specific mutation is derived from splice variant sPD-L1, AR-V1 or AR-V7.

40. The pharmaceutical composition of any of paragraphs 30-39, wherein the tumor-specific mutations comprise drug resistance mutations.

41. The pharmaceutical composition of paragraph 40, wherein at least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L.

42. The pharmaceutical composition of any of paragraphs 30-41, wherein the at least one tumor-specific mutation has an incidence of at least 500 patients a year in the population of subjects suffering from cancer, and wherein the at least one mutation comprises a mutation listed for the population in Table 9.

43. The pharmaceutical composition of paragraph 42, wherein the at least one neoantigenic peptide comprises at least one peptide listed in Table 9.

44. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from CLL; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of SF3B1:p.K700E, MYD88:p.L273P, NOTCH1:p.P2514fs, ABCA11P:p.E901D, AHNAK:p.D3823E, ZNF814:p.E348D, AHNAK:p.V1220I, AHNAK:p.H1203N, ANKRD30A:p.A232V, APOOL:p.I138L, EGR2:p.H397N, MKI67:p.H2213D, NRAS:p.Q61R, PLIN4:p.M691V, XPO1:p.E571K, ZCRB1:p.L76F, ZNF700:p.N652H, ZNF700:p.Q654R, ZNF844:p.D458H, AHNAK:p.A4046V, ANKRD36:p.P337R, C1orf170:p.T203I, CAST:p.D639E, EGR2:p.E369K, GPR123:p.L630P, IKZF3:p.L162R, MUC4:p.P4224R, OR9Q1:p.M34L, PKD2:p.Y486F, PRAMEF11:p.R104Q, SYNJ1:p.I681F, TP53:p.R248Q, TP53:p.R248W, TRPV2:p.L627del, ZNF254:p.S498A, ZNF732:p.A459T, ZNF749:p.E530Q, ZNF845:p.M423I, ABCA11P:p.G900E, ACRC:p.E243D, ACRC:p.A244V, ACSL3:p.T188S, ADAMTS2:p.D948N, AGAP6:p.S127I, AHNAK:p.A2114G, ANKRD36:p.D1014Y, ARID3A:p.G550fs, ARID4A:p.D1154E, ATP2B4:p.R183H, ATRNL1:p.L1244F, BNC1:p.Y937N, BRAF:p.K601N, BTLA:p.Q86K, C14orf177:p.G90V, C2orf44:p.N456K, C3orf15:p.R552Q, CACNA2D1:p.Y376N, CALD1:p.E340K, CCDC15:p.P488H, CCDC79:p.N440T, CCNB3:p.A932T, CD109:p.L470Q, CD209:p.Q189L, CKAP2:p.*684K, CMA1:p.I81K, CMIP:p.A230T, CNTNAP4:p.I12F, CRYM:p.*315K, DICER1:p.E1705K, DPCR1:p.L716P, EIF3A:p.M1093L, EIF4G3:p.R8H, ETFDH:p.I281F, EWSR1:p.Y656C, F5:p.L1332P, F5:p.L1253F, FAM50A:p.H317R, FBXL13:p.S102R, FBXW7:p.R465H, FHL1:p.D184E, FILIP1:p.I522K, FRG1B:p.Q39K, GNB1:p.I80T, GPR110:p.R443G, GPR98:p.Y6152F, HDGFL1:p.188_189insA, IGF2BP2:p.T186S, IL1R2:p.L364fs, KIAA1109:p.L4680P, KRAS:p.G13D, KRTAP19-1:p.G61S, MAF:p.G53fs, MAGEC1:p.L609H, MAP2K1:p.K57N, MED12:p.L36R, MED12:p.G44S, METAP2:p.Y137N, METTL9:p.Y57F, MGP:p.V15L, MKI67:p.R2222K, MUC16:p.T11005I, MUC4:p.S3941N, MUC4:p.S3941G, MUC4:p.V3091L, MUC4:p.S2951Y, MUC4:p.A2841S, MUC4:p.S2760A, MUC4:p.T2335M, MUC4:p.T1627K, MUC4:p.T1547S, MUC4:p.H1133Q, MYD88:p.M240T, NEDD4L:p.P194del, NEFH:p.S704T, NRG4:p.G21fs, OR2A25:p.S105C, OR4C16:p.Y63F, OR4N4:p.L150fs, PABPC1:p.K254fs, PIWIL1:p.P372fs,

PLCD3:p.E499fs, PLEKHB1:p.S146P, PPIL4:p.S382R, PRDM4:p.*802K, PRG4:p.N675H, PRKAB1:p.P104H, R3HDM2:p.S592G, R3HDM2:p.S588N, R3HDM2:p.R206W, RPS2:p.R200G, RPTN:p.G364S, SF3B1:p.K666E, SF3B1:p.N626Y, SF3B1:p.Y623C, SIX3:p.I27L, SLC39A7:p.L456fs, SLC6A9:p.R94K, TFG:p.A382V, TGOLN2:p.K83R, TGOLN2:p.T80S, TLR2:p.D327V, TNKS2:p.T619fs, TP53:p.R273H, TP53:p.C242F, TP53:p.R175H, TWISTNB:p.H306Q, UBXN7:p.A276V, WDR78:p.N110K, XIRP2:p.V3008E, ZNF382:p.H186Q, ZNF578:p.R306H, ZNF578:p.G311S, ZNF578:p.H334R, ZNF700:p.S649C, ZNF705A:p.D298N, ZNF836:p.K608Q, and ZNF836:p.I571N; and

45. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from BLCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, FGFR3:p.S249C, TP53:p.R248Q, PIK3CA:p.E542K, RXRA:p.S427F, ZNF814:p.D404E, FBXW7:p.R505G, NOTCH2:p.P6fs, TP53:p.E285K, ANKRD30A:p.A353P, C3orf70:p.S6L, EFCAB6:p.R379K, ERCC2:p.N238S, FAM47C:p.Q225E, FOXQ1:p.S135L, HLA-A:p.Q78R, MUC4:p.H4205Q, OTUD4:p.T909I, SLAMF1:p.S277fs, SPRED3:p.S128del, TMCO2:p.S15fs, TP53:p.R280T, TP53:p.E271K, TP53:p.A159V, ZNF706:p.I8N, ZNF706:p.R3P, ACACB:p.E2318Q, ACPP:p.E321K, ACRC:p.A264V, ADAMTS2:p.23_24insL, AFF3:p.E919K, AHNAK:p.S4150F, AHNAK:p.D2889H, AHNAK:p.V1940A, ALX4:p.R126Q, ANKRD12:p.E627K, ANKRD32:p.T999N, ARID1A:p.S614L, ASXL2:p.117_118SS>S, ATP12A:p.R858C, ATP9A:p.R519Q, BCAS3:p.T214M, BPI:p.M255I, CACNG8:p.V146G, CAMSAP1:p.T466fs, CDC27:p.I91fs, CDKN1A:p.E44fs, CEP192:p.S2058L, CGB8:p.T18A, CHRNA3:p.L23del, CHST4:p.D352N, CLIP1:p.S1018fs, COX6A1:p.S8L, CREBBP:p.D1435H, CRIPAK:p.M48fs, CSPG5:p.D119N, CUL1:p.E485K, DLC1:p.S741T, DLL3:p.D318H, DOPEY2:p.E1196K, ECM1:p.E266K, EEF1A2:p.Y418S, EEF2K:p.E673K, EMILIN1:p.R27G, ERBB2:p.S310F, ERBB3:p.M91I, ERBB3:p.V104L, ERBB3:p.D297Y, ERCC2:p.Y14C, FAM155A:p.Q86del, FAM43B:p.E272del, FASTKD3:p.Q625E, FBXW7:p.S546L, FGFR3:p.R248C, FGFR3:p.G380R, FGFRL1:p.H479fs, GBE1:p.M587I, GIMAP1-GIMAP5:p.S311C, GNA13:p.R200G, H1FOO:p.A214fs, HEATR7B2:p.E1109K, HIST1H1D:p.I81M, HRAS:p.G12D, HRCT1:p.H92P, ILF3:p.E484K, KCNK2:p.S6W, KIAA0907:p.Q446P, KIF23:p.E350K, KLF5:p.S118L, KLHL15:p.D185G, LAMA4:p.E639K,

LILRA1:p.H410Y, LILRB1:p.L479del, LLGL2:p.P955fs, LPIN1:p.S974L, LRRC16A:p.D227N, LRTM2:p.S139L, LURAP1L:p.55_56insGGG, MAGEC1:p.P553del, MCL1:p.E171del, MN1:p.S472L, MUC7:p.A191V, MVP:p.E412K, NBPF10:p.E3455K, NFE2L2:p.E79K, NFE2L2:p.R34G, NOS1AP:p.Q306del, OR2T35:p.V319fs, OR4N2:p.L150fs, PABPC3:p.K333fs, PAX3:p.S197L, PBX2:p.E70K, PBXIP1:p.H729del, PCDP1:p.E537K, PEX1:p.I370fs, PHLDA3:p.E82K, PLEKHM2:p.S459L, PLVAP:p.A321V, POLR3B:p.L372F, POTEC:p.R477Q, PPL:p.H326Y, PPP1R15A:p.E196K, PRDM16:p.E271Q, PRIC285:p.E1289Q, PRMT8:p.S31P, PUF60:p.S396L, RAB11FIP4:p.S596L, RAD51C:p.D167N, RAD51C:p.Y224H, RALGPS1:p.R381Q, RARS2:p.R6C, RBM26:p.P644A, RERE:p.K176N, RXRA:p.S427Y, SERPINA12:p.R211G, SF3B1:p.E902K, SLC6A9:p.R243W, SLC9A5:p.L447F, SPESP1:p.F121L, SRPRB:p.G14S, SYN2:p.A34del, SYTL2:p.I440M, TAB3:p.R211T, TAF1B:p.R292C, TAOK2:p.L981del, TAS1R3:p.E525K, TAS2R9:p.E163Q, TBC1D1:p.S71F, TBC1D2B:p.R920Q, TFPI2:p.R222C, TM6SF1:p.S15W, TMEM131:p.K640fs, TMEM19:p.G331fs, TP53:p.R273C, TP53:p.R248W, TP53:p.R175H, TP53:p.K132N, TRAM1:p.E41Q, TSKS:p.E513K, TTN:p.C20935G, UBOX5:p.S417L, UGP2:p.D262H, VGF:p.E433K, XAB2:p.E782K, XYLB:p.S87F, ZC3H4:p.E798K, ZNF208:p.K852E, ZNF208:p.I647S, ZNF626:p.G198E, ZNF749:p.Q457E, ZNF761:p.H373R, ZNF799:p.T43A, ZNF799:p.W41G, ZNF799:p.E589G, ZNF844:p.P503R, ZNF845:p.M423T, ZNF845:p.T479M, ZNF860:p.H464R, ZNF878:p.S181R, ZNF91:p.R333H, and ZNF91:p.H305R.

46. The pharmaceutical composition of any of paragraphs 30-43, wherein:

(a) the population of subjects is suffering from BRCA; and

(b) the at least one tumor-specific mutation comprises any combination of frameshift mutations selected from the group consisting of GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, and GATA3:p.S408fs.

47. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from BRCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.H1047R, PIK3CA:p.E545K, PIK3CA:p.E542K, AKT1:p.E17K, TP53:p.R175H, PIK3CA:p.N345K, PIK3CA:p.H1047L,

SF3B1:p.K700E, GATA3:p.S408fs, PIK3CA:p.E726K, TP53:p.Y220C, TP53:p.H193R, PIK3CA:p.Q546R, TP53:p.R273C, TP53:p.R248W, TP53:p.R273H, TP53:p.I195T, TP53:p.H179R, FGFR2:p.N549K, NUP93:p.E14K, PIK3CA:p.C420R, PIK3CA:p.E453K, PIK3CA:p.Q546K, TP53:p.V216M, TP53:p.C176F, CDH1:p.E243K, ERBB2:p.L755S, KRAS:p.G12V, PIK3CA:p.E545A, TBL1XR1:p.I141fs, TP53:p.G266E, TP53:p.R248Q, TP53:p.Y163C, TP53:p.C141Y, TP53:p.G108fs, ACPP:p.R43W, AKT2:p.I289M, ARHGAP9:p.R137C, C9orf174:p.R136W, CDC42BPA:p.P675T, COL12A1:p.S395L, CRISPLD1:p.R222W, CT47B1:p.234_243EKLTEEATEE>E, CYP1A2:p.V483M, DAB2IP:p.E161K, DGKB:p.S13L, DMD:p.K1772N, DPEP1:p.V11L, ERBB2:p.S310F, ERBB2:p.D769Y, ERBB3:p.E928G, ESYT1:p.R816W, FAM179A:p.A831T, FAM58BP:p.A70T, FMN2:p.S751F, GALNTL6:p.K567del, GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, GDAP1:p.T307A, GRB14:p.A300T, GUCY2C:p.G549C, IL17B:p.R34W, KCNB2:p.R231H, KIF1B:p.R1320W, KIF26B:p.V1113M, KLF4:p.K434Q, LY9:p.I69L, MAP2K4:p.S184L, MAP2K4:p.S251I, MAP2K4:p.T261fs, MAP3K1:p.L318fs, MAP3K1:p.I761fs, MAP3K1:p.V1346del, MAP3K1:p.L1384fs, MAPK13:p.E315K, MAPK4:p.V100M, MARCH5:p.R170C, MBP:p.E120K, MEFV:p.R377H, METTL15:p.Q53E, MS4A4A:p.V99M, MUC17:p.R4415H, MYH6:p.T847M, MYO5B:p.A405V, NARS2:p.P240R, NLGN4X:p.D382N, NLRC4:p.R288W, OR13G1:p.R258H, OR2AK2:p.V45I, OTOF:p.T388M, PACSIN2:p.Q331H, PALM2-AKAP2:p.A299T, PCDH19:p.R286C, PCDHGC5:p.D664N, PIK3CA:p.R88Q, PIK3CA:p.E110del, PIK3CA:p.K111del, PIK3CA:p.PVPHGLEDL447del, PIK3CA:p.L455fs, PIK3CA:p.M1004I, PIK3CA:p.M1043I, PIK3CA:p.N1044Y, PIK3R1:p.KPDL567del, PREX2:p.R363Q, PRRX1:p.A196V, PTEN:p.V317fs, RGSL1:p.V222I, RUNX1:p.R142fs, RUNX1:p.D96fs, SCN2A:p.R36K, SLC25A32:p.Q83E, SLC25A45:p.G106C, STRA6:p.Q68R, STX6:p.H153D, TBX3:p.H187Y, TFPT:p.S252C, TINAG:p.R332W, TMEM71:p.R63Q, TP53:p.E286K, TP53:p.R282W, TP53:p.V272M, TP53:p.S241fs, TP53:p.C238fs, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.Y220S, TP53:p.R209fs, TP53:p.G199V, TP53:p.L194R, TP53:p.H193L, TP53:p.H193Y, TP53:p.V173L, TP53:p.V173M, TP53:p.K132N, TP53:p.R110fs, TUBD1:p.A200V, VLDLR:p.R231H, VWA3A:p.V955I, VWF:p.K1720N, XPO1:p.E571K, and ZNF268:p.F901del.

48. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from COAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofKRAS:p.G12D, BRAF:p.V600E, KRAS:p.G12V, ACVR2A:p.K435fs, GRB14:p.KKK295del, SEC63:p.L532fs, TGFBR2:p.E125fs, ATR:p.K771fs, ICA1:p.N204fs, KRAS:p.G12C, TP53:p.R175H, ABCA8:p.R842Q, ACTL7B:p.R354H, ACVR2A:p.K435fs, AIM2:p.K340fs, ALG2:p.S302Y, ANKIB1:p.K144fs, ARSG:p.V131I, ATP10D:p.R311H, AXIN2:p.W663fs, C5orf30:p.D4N, CACNG3:p.V134I, CASP5:p.K78fs, CC2D2A:p.R1284C, CDH10:p.E349K, DNMT1:p.E432K, DOCK2:p.G170R, DOCK5:p.E177K, EGR2:p.R390H, ERBB3:p.V104M, FAM135B:p.R884H, FBXW7:p.R505C, FBXW7:p.R465H, FHDC1:p.R254W, FOXL1:p.N89K, HCN4:p.R525H, HLA-DMA:p.E84K, HTR3B:p.R236C, ITGA4:p.T673M, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KRAS:p.A146T, KRAS:p.G13D, LPHN3:p.R1183Q, MAP2K4:p.R287H, MAPK8IP1:p.L217fs, MFSD5:p.R280Q, MUC16:p.R8606H, MYO6:p.D1180N, NAA25:p.S807Y, NBPF14:p.V44L, NRAS:p.Q61K, NRAS:p.G13R, PAX3:p.T424M, PGAM1:p.R240H, PHF3:p.R1410I, PIK3CA:p.R88Q, PIK3CA:p.E545K, PIK3CA:p.H1047R, PLXNA3:p.V14fs, POSTN:p.R508C, PTPRU:p.D1434N, PYGO2:p.Q150fs, RBBP7:p.E274K, SFPQ:p.R611Q, SGSM1:p.F1117L, SLC25A40:p.R96Q, SLC8A1:p.R431H, SLITRK3:p.S298L, SPATA22:p.S150L, SUN3:p.E128K, TGFBR1:p.S241L, TP53:p.R273H, TP53:p.R273C, TP53:p.R248W, TRPV5:p.R492H, USP40:p.S851L, VPS13C:p.D1359Y, ZBTB24:p.L607I, ZNF434:p.R306C, ZNF443:p.R301I, ZNF484:p.R138C, and ZNF770:p.S441P.

49. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from GBM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, IDH1:p.R132H, EGFR:p.A289V, EGFR:p.G598V, WASH3P:p.G175S, ZNF814:p.D404E, RPSA:p.Q111E, NBPF10:p.E3455K, TP53:p.R248Q, BRAF:p.V600E, EGFR:p.A289T, PRB2:p.N230del, RGPD5:p.P1760A, TP53:p.R175H, CHEK2:p.K373E, EGFR:p.R108K, EGFR:p.R222C, PIK3CA:p.E545K, PIK3R1:p.G376R, POTEC:p.K507E, SDHAP2:p.V195E, SLC6A10P:p.K88N, TP53:p.R282W, TP53:p.R273H, CD3EAP:p.K219del, DST:p.R146C,

EGFR:p.A289D, EGFR:p.H304Y, FRG1B:p.S71N, GOLGA8DP:p.A116E, KRTAP4-11:p.R121K, KRTAP4-11:p.S48R, MAP3K1:p.P324L, OGDH:p.I78fs, PODXL:p.S162fs, PSPH:p.V145I, SPINT1:p.A316V, TP53:p.R248W, TP53:p.G245S, TP53:p.Y220C, TP53:p.R158H, TSHZ2:p.A222T, UBC:p.L149R, ZDHHC4:p.R300H, ZNF844:p.R447P, AASS:p.T878fs, ABCC10:p.R570W, ADAM29:p.V205I, ADAMTS8:p.V524M, AGAP3:p.R766W, AICDA:p.Y144F, AK7:p.A159V, AK8:p.D243A, ANO2:p.R334C, AOX1:p.A507V, ARHGAP5:p.M691L, CALN1:p.V231I, CARM1:p.A202V, CD163L1:p.V721M, CD1D:p.L25fs, CD209:p.A283T, CDH18:p.A195T, CILP2:p.V553M, CIZ1:p.L89P, CLOCK:p.L123fs, COL6A5:p.T2224M, CSF2RB:p.G298S, CSMD3:p.E171K, CYP2D6:p.H352R, DCAF12L1:p.R335H, DCAF12L2:p.R246H, DPP10:p.V183I, DPY19L2P1:p.R378Q, DQX1:p.R505H, DRD5:p.S275R, DVL2:p.V66G, EFCAB6:p.R379K, EGFR:p.L62R, EGFR:p.R252C, EGFR:p.P596S, EGFR:p.P596L, EGFR:p.G598A, EGFR:p.E709K, EPHA1:p.A184T, ERC2:p.R20H, ESPNP:p.R627Q, FAM126B:p.R382H, FBN3:p.V886I, FGF14:p.T229M, FLG2:p.H1901fs, FLG:p.R2886H, FLNA:p.V1240M, FOXG1:p.H57del, FPR2:p.R54Q, FRG1B:p.K13N, FRG1B:p.A53T, GABRA6:p.V314I, GJB3:p.R160H, GLT8D2:p.A178V, GRM3:p.R183C, HERC1:p.R2330H, HNF1B:p.T417M, HTRA3:p.Q403R, IDH1:p.R132G, IFNA10:p.L80F, IFNA10:p.V79A, JHDM1D:p.R313H, JPH1:p.A395T, KEL:p.V411M, KIAA0907:p.R516fs, KIAA1704:p.D88del, KLK6:p.R120H, KRAS:p.G12D, KRTAP4-7:p.L121V, KRTAP4-7:p.L148V, KRTAP5-4:p.S131C, LAT2:p.L18W, LIMK2:p.R203H, LUM:p.R330C, MCOLN3:p.V141I, MGAT4B:p.T444P, MUC17:p.V77M, MUC17:p.3204_3205insP, MYO1D:p.T109M, MYO6:p.Q914fs, NAP1L5:p.140_141EE>E, NF1:p.F1658fs, NHP2L1:p.R84C, NLRP5:p.R737W, NPTX1:p.A263T, NUFIP2:p.Q29del, ODF4:p.R61C, OR11H12:p.H154P, OR2A7:p.V18I, OR2H1:p.V287I, OR2T12:p.R184H, OR5D13:p.R236C, OR5P2:p.A100V, OR6N2:p.R293C, PASD1:p.A236del, PCDH11X:p.T486M, PCDHB13:p.P221L, PDGFRA:p.E229K, PDGFRB:p.S650L, PHC3:p.T35del, PIK3C2B:p.R287fs, PIK3CA:p.M1V, PIK3CA:p.R88Q, PIK3CA:p.M1043V, PIK3CA:p.H1047R, PIK3R1:p.K379N, PODNL1:p.A150V, POTEE:p.V166M, POTEG:p.R136H, PRKCD:p.G432fs, PROKR2:p.V297I, PTEN:p.C136Y, PTEN:p.S170N, PTEN:p.R173H, PTEN:p.T277I, PTEN:p.V317fs, PTPN14:p.E716del, R3HDM2:p.412_413QQ>Q, RAB11FIP5:p.R170H, RASAL3:p.R82H, RB1:p.N316fs, RDH8:p.A198V, REN:p.15_16LL>L, RIMBP2:p.R830H, SCAF11:p.E926fs,

SCN7A:p.R1358H, SCNN1G:p.R564H, SDHAP2:p.R31C, SDHAP3:p.A66T, SEMG2:p.R292C, SH3RF2:p.R318C, SHB:p.A460T, SIGLEC10:p.T250M, SLC13A5:p.Q273P, SLC17A9:p.V324I, SLC22A9:p.R407Q, SLC26A3:p.V88I, SLC5A3:p.A302fs, SLC9A4:p.R631H, SPAM1:p.R346Q, SPEN:p.E803fs, SPTA1:p.A2011V, SUSD5:p.T513M, SYNE1:p.R8468H, TARSL2:p.G366D, TAS2R41:p.A255T, TAT:p.R367H, TFPI2:p.R206C, THSD7B:p.R90C, TMEM147:p.A92V, TMEM156:p.R81C, TMPRSS6:p.V302I, TNFSF9:p.A232T, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.V216M, TP53:p.H179R, TP53:p.T155N, TRAPPC10:p.K133fs, TTN:p.R21402W, TTN:p.V16403M, TUBBP5:p.V102M, TYRP1:p.T352fs, UBC:p.R73L, UGT2B28:p.P289H, USH2A:p.R3719H, WASH6P:p.L211V, ZFP42:p.V227I, ZFP42:p.T264M, ZNF181:p.V305G, ZNF280B:p.E400K, ZNF534:p.N583K, ZNF563:p.W208fs, ZNF844:p.F487L, and ZPBP:p.R154C.

50. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from HNSC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofPIK3CA:p.E545K, PIK3CA:p.E542K, TP53:p.R175H, PIK3CA:p.H1047R, TP53:p.R282W, TP53:p.R248Q, TP53:p.R273H, TP53:p.R248W, TP53:p.G245S, RHOA:p.E40Q, EP300:p.D1399N, HRAS:p.G13V, MB21D2:p.Q311E, NFE2L2:p.E79Q, TP53:p.H179Y, FBXW7:p.R505G, HIST1H2BF:p.E77K, HRAS:p.G12D, MAPK1:p.E322K, NFE2L2:p.D29H, TP53:p.P278S, TP53:p.C242F, TP53:p.Y220C, TP53:p.H193L, TP53:p.H179R, TP53:p.V157F, TP53:p.R110L, AKNAD1:p.K620R, ANXA6:p.R231Q, AP1G2:p.D243N, ATAD5:p.D441N, ATP6AP2:p.E119Q, B2M:p.M1I, BCL11A:p.E579K, C1orf172:p.Y30fs, C7orf57:p.E30K, CCDC135:p.E313K, CDH12:p.P706T, CDH7:p.Q225K, CDK11B:p.E79del, CDKN2A:p.H83Y, CHCHD4:p.T79M, CIRH1A:p.S250I, CLSTN2:p.P759L, CRB1:p.L628fs, DENND5B:p.G1023E, DNAH5:p.Q1797E, DSP:p.R160G, EDA:p.L58F, EFCAB6:p.E1002K, ELF4:p.S415L, EP300:p.C1164Y, EPHA3:p.T802R, EPHA6:p.D952H, ERBB2:p.M916I, ESRRA:p.D219N, FAM101A:p.I89del, FBXO24:p.M553V, FCAR:p.V233M, GPANK1:p.Y351fs, GPR20:p.V300I, GPRASP1:p.S706L, GPRIN3:p.R633fs, GRID2:p.T649fs, GRM3:p.F682L, GUCY2F:p.S404L, HCRTR2:p.D100Y, HIST1H3C:p.K37M, HIST1H4C:p.R68P, HLX:p.S12T, HOXD10:p.Y151C, HPS3:p.K812N, HRAS:p.G12A, HRAS:p.G12S, IFT140:p.E664K, INPPL1:p.T493M, ITGA10:p.R669Q, ITGB1:p.D158N,

KIAA1429:p.D1526N, KIAA1429:p.S138F, KPRP:p.E553fs, KSR2:p.T555M, LINGO2:p.P410T, LPCAT1:p.V187del, MAGEB3:p.V75A, MAP3K7:p.E524Q, MAP4K3:p.P657fs, MAP9:p.K485N, MARS2:p.R481Q, MBOAT7:p.R424W, MUC16:p.R12774H, MUC5B:p.T4388M, MYH11:p.E993K, MYOCD:p.T493M, MYOM1:p.R63Q, NANOS3:p.S183L, NCOR1:p.R1561Q, NCOR1:p.Q169E, NCR1:p.D213N, NFE2L2:p.E79K, ODZ1:p.R366M, OPN1MW:p.A285T, OR2M2:p.A95fs, OR2M3:p.M273I, OR2T33:p.R120S, OR6V1:p.I248fs, PABPC5:p.P58L, PACSIN1:p.E359K, PIK3CA:p.M1043V, PIK3CA:p.H1047L, PIWIL1:p.V699M, PLIN5:p.430_431insNG, PLXNA3:p.P58S, PRB1:p.R274fs, PRSS1:p.D107N, RAC1:p.A159V, RGS7:p.L21fs, RPA1:p.R31H, RPL18:p.R178fs, SFI1:p.R821Q, SLC35D3:p.*417S, SLC5A7:p.G336C, SMARCA4:p.P913L, STAT3:p.D661V, SYCP2:p.K474N, SYT6:p.R249H, TBX21:p.E494K, THSD7A:p.R1046C, THSD7A:p.C728F, TMC3:p.R934S, TMTC2:p.T409R, TP53:p.E285K, TP53:p.C275F, TP53:p.R273C, TP53:p.G266E, TP53:p.G262V, TP53:p.R249S, TP53:p.G245V, TP53:p.C238F, TP53:p.M237I, TP53:p.Y236C, TP53:p.Y236D, TP53:p.R196P, TP53:p.PHHERC177del, TP53:p.V173L, TP53:p.V173M, TP53:p.Y163C, TP53:p.P151T, TP53:p.V143M, TP53:p.P58fs, URI1:p.S13fs, ZNF177:p.K384N, ZNF750:p.S96fs, and ZZZ3:p.R5Q.

51. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from KIRC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of WASH3P:p.G175S, VHL:p.L89H, VHL:p.S111N, WDR52:p.V1227G, KRT1:p.552_559YGSGGSSY>Y, KRTAP1-1:p.S34C, PALM2-AKAP2:p.1075_1076insEA, ZNF814:p.D404E, DOPEY2:p.Y2048S, KAT2B:p.W111fs, PABPC1:p.E156fs, PCDHGC5:p.G599V, PIK3CA:p.E545K, RRAD:p.A278E, SIRPA:p.D131del, UQCRFS1:p.I83V, VHL:p.P45L, VHL:p.V74D, VHL:p.R82P, VHL:p.L116fs, VHL:p.L158V, VHL:p.L169P, WDR73:p.DGTRSQ315del, ABCA3:p.E95D, ABCC5:p.L1090fs, ACADS:p.R330H, ACAN:p.G952E, ACSM2A:p.L402fs, ADAM23:p.K380M, ADH1A:p.D154V, AFF3:p.SA620del, AGAP6:p.D69fs, AGAP7:p.E71fs, AHNAK:p.5_6insE, AIDA:p.K247M, ALAS1:p.G302R, ANAPC16:p.R95fs, ANK2:p.N453S, ANKRD36:p.K378R, ARHGEF5:p.E487G, ARSD:p.AGV234del, ARSD:p.A234G, ATP2A1:p.G704C, ATP7A:p.Q990fs, AVIL:p.G299fs, AXDND1:p.EQ991del, BAP1:p.N78S,

BAP1:p.M1I, BLM:p.H660Q, BMPER:p.RIAL444del, BRK1:p.K70Q, BTRC:p.I416M, C16orf55:p.D118A, C19orf33:p.K102E, C20orf132:p.E382D, C2orf71:p.1225_1226insS, C6orf132:p.173_182PPPLLLEPPP>P, CASP5:p.R23fs, CATSPER4:p.T425M, CCDC120:p.I8V, CCR5:p.S185I, CCZ1:p.E214D, CD7:p.P174fs, CDAN1:p.L646fs, CDH23:p.F1132Y, CDK5RAP2:p.H1592Q, CENPB:p.E410V, CERCAM:p.A85fs, CHEK2:p.K373E, CHIT1:p.P284fs, CLCN2:p.645_645R>RR, CLUL1:p.G463R, CNTNAP4:p.Y436S, CUL9:p.D1726E, CWC25:p.K364E, CXorf51B:p.V43I, DDX39B:p.F149fs, DIRAS1:p.G79C, DISP2:p.F1021S, DNMBP:p.T78P, DOCK8:p.A177fs, DPCR1:p.H383N, DPCR1:p.L768del, EGFR:p.L838M, ENPEP:p.F289C, ESPNP:p.W122fs, FAM105A:p.H126N, FAM186A:p.IPPQAQELEIPL1556del, FAM194B:p.EEEEYL135del, FAM22F:p.S691del, FAM22F:p.P690fs, FAM47A:p.LRPEPPETGVSH235del, FAM47C:p.P388S, FAM78A:p.W192L, FBXO34:p.Q294fs, FGFR3:p.R571fs, FGFR3:p.P716H, FMN2:p.AIPPPPPLPGA956del, FOXD4L4:p.C405fs, FUT6:p.S140fs, GJA1:p.A311fs, GOLGA5:p.L492I, GPM6A:p.A50V, GPRIN1:p.231_239RKEDPGSLR>R, GRAMD1B:p.P356H, GREB1:p.S344Y, GRM6:p.A718fs, GUSB:p.L501V, GUSB:p.C500R, HBB:p.F86C, HDAC6:p.G977D, HEXDC:p.T482P, HNF1B:p.N302K, HNRPLL:p.M327V, HRC:p.P439fs, HSFX2:p.D92E, IL1RAP:p.F50C, IVL:p.EQQEGQLKHP167del, KANK4:p.S253P, KCNJ18:p.E378K, KIAA1751:p.K97N, KRT1:p.SSYGSGG557del, KRT2:p.L299W, KRT4:p.F154fs, KRTAP10-6:p.49_49P>PSCCAP, KRTAP5-7:p.C120Y, KRTAP9-2:p.CCQP140del, LARS:p.P185fs, LCP1:p.P445fs, LOC338651:p.PHRSHSPPWS102del, LRCH2:p.D717G, LTA4H:p.F107L, LYST:p.Q710H, MAFA:p.207_208HH>H, MAGEC1:p.P239del, MAP2K5:p.Q445R, MAPKAPK2:p.T214fs, MARCKS:p.K152fs, MED12L:p.P2071S, MEGF6:p.A582fs, MGST3:p.G143fs, MLXIPL:p.S790R, MOCOS:p.S849P, MST1R:p.M464V, MTOR:p.C1483F, MTOR:p.L1460P, MUC16:p.P11260A, MUC17:p.R1227fs, MUC17:p.H1228fs, MUC2:p.1480_1481insI, MUC6:p.P1569fs, MYO3A:p.N525S, NBPF3:p.D491V, NCOR1P1:p.L52P, NDUFA4L2:p.G3fs, NEFH:p.651_651K>KAKSPEK, NES:p.V611L, NFAT5:p.Q906E, NOXO1:p.G3fs, NR2C1:p.S270I, NSMCE2:p.Q31fs, NUDT21:p.W13fs, ODZ2:p.W628fs, ONECUT1:p.L424M, OR10A3:p.F73V, OR4F4:p.E15G, OR4N2:p.L150fs, OR51B5:p.A66fs, OR7C1:p.F104fs, PABPC1:p.Y408F, PABPC1:p.K333fs, PABPC1:p.A181T, PABPC3:p.P191T, PALLD:p.A996T, PALM2-AKAP2:p.G1118fs, PARD6A:p.G84fs,

PASK:p.T62I, PCDH15:p.C1713F, PCNT:p.G136S, PGM5:p.G426fs, PGPEP1L:p.R164fs, PIK3C2B:p.F1473L, PIK3CA:p.N1044K, PIK3R5:p.L371R, PITRM1:p.P816T, PLIN4:p.T347I, PODXL:p.28_30PSP>P, POLR1C:p.K332Q, POTED:p.I214V, PPM1E:p.R311W, PRKCE:p.Q157fs, PROX1:p.V225D, PRRC2C:p.P1883T, PRX:p.P549L, PSD3:p.T563P, PTCH1:p.P689H, RANBP3:p.L386W, RASGEF1C:p.A188T, RGPD6:p.F946L, RHEB:p.Y35N, RIMBP3:p.A396del, RIN3:p.L449V, RLIM:p.S501L, RNF17:p.S351C, RUNX2:p.P466H, SCAF1:p.P208fs, SDK1:p.K508fs, SECISBP2:p.D608E, SERPINB3:p.S209C, SESTD1:p.I306M, SFRP4:p.P325fs, SH3KBP1:p.P563fs, SIPA1L3:p.G777A, SLC13A2:p.L493fs, SLC16A9:p.CVLLGG470del, SLC25A5:p.A118T, SLC44A5:p.V70F, SLC4A8:p.N229K, SLC52A1:p.G370del, SLC52A2:p.G399fs, SLC6A10P:p.K88N, SLC6A14:p.A85fs, SLC9B1:p.V446fs, SON:p.VLESSAVT1359del, SP8:p.G165del, SPAG1:p.353_354insD, SPATA9:p.C189F, SPEG:p.A992fs, SPTB:p.T1864I, SRA1:p.V110L, STAT6:p.P354fs, STK11IP:p.A155E, STXBP3:p.E279G, SVIL:p.M93T, SYNE1:p.R8468S, SYNJ2:p.K832T, SYNPO:p.G619fs, TAOK2:p.Q899fs, TAS2R38:p.I311T, TBC1D12:p.F608Y, TBC1D1:p.H277R, TBC1D3:p.A556fs, TBC1D3C:p.A495fs, TBC1D3F:p.A556fs, TCF7:p.H140P, TDRD10:p.W276C, THRAP3:p.K551R, TMEM102:p.A110P, TMEM161B:p.L142P, TMEM230:p.D140G, TMEM47:p.G87S, TRDN:p.*730Y, TTBK1:p.T1065S, UBE2O:p.R1118fs, UBR5:p.T1306fs, UPK3A:p.G272fs, VHL:p.G39S, VHL:p.S65L, VHL:p.N78D, VHL:p.R79P, VHL:p.W88L, VHL:p.L89P, VHL:p.R107P, VHL:p.S111R, VHL:p.H115N, VHL:p.D121Y, VHL:p.G123fs, VHL:p.D126fs, VHL:p.L128H, VHL:p.L135F, VHL:p.I151T, VHL:p.L153P, VHL:p.L158P, VHL:p.Q164fs, VHL:p.L184P, VHL:p.L188P, WASH6P:p.315_316insAPP, WASH6P:p.T201M, WWP2:p.G458A, ZCCHC6:p.K937N, ZFAND2B:p.I149T, ZFR2:p.Y107N, ZNF273:p.N319K, ZNF462:p.S650T, ZNF516:p.A256D, ZNF519:p.H431Y, ZNF687:p.F858C, ZNF732:p.E227Q, ZNF880:p.Q406R, ZP3:p.V362fs, and ZRANB1:p.*735fs.

52. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LAML; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NPM1:p.W288fs, DNMT3A:p.R882H, NPM1:p.L287fs, IDH2:p.R140Q, IDH1:p.R132C, FLT3:p.D835Y, DNMT3A:p.R882C, FLT3:p.600_601insFREYEYD, IDH1:p.R132H, NRAS:p.G13D, U2AF1:p.S34F, KIT:p.D816V,

FLT3:p.D835E, IDH2:p.R172K, NRAS:p.G12D, WT1:p.S381fs, ABTB1:p.L249fs, DNMT3A:p.R736H, FLT3:p.D835H, KRAS:p.G12D, NPM1:p.L287fs, NRAS:p.Q61H, NRAS:p.Q61K, PHACTR1:p.V251fs, RBBP4:p.E330K, RUNX1:p.R135G, and U2AF1:p.S34Y.

53. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LUAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12C, KRAS:p.G12V, EGFR:p.L858R, U2AF1:p.S34F, KRAS:p.G12A, TP53:p.R158L, KRAS:p.G12D, PIK3CA:p.E545K, TP53:p.R273L, EGFR:p.ELREA746del, KRAS:p.G13D, A2ML1:p.S654fs, BRAF:p.G469V, CTNNB1:p.S37F, EGFR:p.G719A, KRAS:p.G13C, MYOF:p.G165fs, EGFR:p.S768I, FAM47C:p.G948W, KRAS:p.Q61L, MYH10:p.L1091fs, NRAS:p.Q61L, OR4C3:p.H130fs, PI15:p.V22F, RAD50:p.D69Y, RIT1:p.M90I, TP53:p.C275F, TP53:p.R249M, TP53:p.R249G, TP53:p.R248P, TP53:p.R175H, TP53:p.Y163C, TP53:p.A159P, TP53:p.V157F, TP53:p.G154V, ABCB1:p.R467L, ACBD3:p.R224L, ACTA1:p.G275C, ACTN2:p.D893Y, ADAM30:p.Q741H, ADAMTS14:p.G238C, ADAMTS20:p.R1251S, ADAMTS20:p.R541L, ADAMTS5:p.L549M, ADAMTS9:p.G659W, ADCY2:p.P1016T, ADCY5:p.G623C, AFP:p.A182G, AHDC1:p.P155Q, AKAP1:p.LDRNEEG317del, ALKBH1:p.K137E, ANK2:p.Q3076L, ANKRD44:p.G339C, ANO3:p.A41S, AP1G1:p.R723L, APBB2:p.T243fs, APOB:p.L973M, APOBR:p.R840L, AQP10:p.Q261L, ARAP3:p.R1226L, ARFIP2:p.R86L, ARHGAP36:p.P16H, ARL13B:p.R358L, ASCC2:p.R365L, ASPM:p.S240F, ASXL3:p.P1470Q, ATRN:p.P197Q, AVIL:p.G64W, AXDND1:p.W101R, B3GAT1:p.R125L, BARX2:p.R68P, BCL9L:p.G980C, BCOR:p.N1459S, BEND2:p.P536Q, BMS1:p.G455V, BRAF:p.V600E, BRAF:p.G466V, BRD9:p.G330W, BRF1:p.V469L, BRWD3:p.H160N, BTRC:p.G260W, C11orf68:p.V135L, C15orf2:p.V753F, C15orf2:p.G906W, C18orf8:p.M61I, C1GALT1:p.G299V, C1orf173:p.G1454S, C1orf173:p.S688Y, C1orf87:p.R541L, C2orf53:p.P272H, C3orf20:p.R740L, C7:p.R687S, C7orf58:p.G140W, C7orf58:p.R238L, CACNA1A:p.S772Y, CACNA1D:p.R1073L, CACNA1E:p.R2089Q, CACNA2D1:p.A352E, CACNG3:p.R232W, CADPS:p.R959S, CALB2:p.R258C, CAMK2B:p.G131V, CARD11:p.I1065M, CCDC111:p.R417L, CCDC141:p.E1204V, CCDC19:p.R279L, CCDC19:p.R207L, CCKAR:p.L271M, CD1B:p.W41L, CDH10:p.S577R, CDH10:p.R472C, CDH10:p.R128S,

CDH18:p.A721S, CDH20:p.P433H, CDH6:p.Q237K, CDK13:p.R880S, CDK4:p.R24L, CELF4:p.A309P, CFDP1:p.P129fs, CHN1:p.K264N, CHRNA4:p.S396R, CHRNA9:p.P361Q, CLCNKA:p.P124Q, CLEC12B:p.W217L, CLK4:p.R68L, CNTFR:p.D252Y, CNTN6:p.R807M, CNTNAP2:p.F395L, COL19A1:p.P538Q, COL5A2:p.G612W, COL5A2:p.G516W, COL9A1:p.P211Q, CPE:p.P290Q, CPNE8:p.Q127H, CPSF4:p.P219Q, CRIPAK:p.S180fs, CROT:p.Q580H, CRTC3:p.S363L, CSMD2:p.P1855Q, CSMD3:p.T2810N, CSMD3:p.P2727T, CSMD3:p.Q174H, CUBN:p.G596C, CUL4B:p.R91S, CUL7:p.L371F, CXCL9:p.K122N, CXCR4:p.E345Q, CXorf59:p.R198M, CYP11B1:p.R498G, CYP27A1:p.P112Q, CYP2B6:p.A444E, DACH2:p.R539L, DCC:p.R446H, DDX56:p.R329L, DEFA1:p.W90C, DENND2A:p.R688Q, DENND2A:p.R499L, DMBT1:p.R1521L, DNAH5:p.R3822L, DNAH9:p.S2993R, DNAI2:p.V231L, DPP6:p.L757F, DSG4:p.R128L, DST:p.A4410S, DZIP3:p.M322L, EBF3:p.R231S, EFCAB4B:p.E265Q, EHHADH:p.Q704H, ELAVL2:p.L263F, EMR1:p.R493H, ENAH:p.R514L, ENPP1:p.G738E, EPB41L3:p.A896S, EPG5:p.R2289L, EPHA1:p.G111V, EPHB6:p.R337H, EPRS:p.V1151L, ERBB2:p.S310Y, ERBB2:p.774_775insAYVM, ERBB2:p.776_776G>VC, ERN2:p.T295K, FAM120B:p.P467H, FAM127C:p.F52L, FAM135B:p.W240C, FAM210B:p.L112F, FAM47A:p.R690L, FAM47B:p.W163C, FAM47B:p.L567F, FAM5C:p.R457G, FAM70B:p.P277T, FAM71B:p.L583M, FAM75A6:p.R304S, FAM75A6:p.P54L, FAM75D1:p.R1265S, FARP1:p.R299L, FAT1:p.R4359L, FAT3:p.R1266H, FAT3:p.G1899V, FAT3:p.H3574N, FBXO18:p.M144I, FBXO31:p.G443fs, FCGBP:p.A1022S, FCRL2:p.V505L, FERD3L:p.P92H, FGB:p.E339Q, FGFR2:p.E116K, FGFRL1:p.R243L, FGFRL1:p.V274L, FKBPL:p.R320L, FLG2:p.G1545V, FLG2:p.L572F, FLG:p.P3254H, FLG:p.P2466Q, FMN2:p.P992T, FOLH1:p.A643S, FOXRED1:p.R136L, FRAS1:p.C382F, FRG2B:p.D142Y, FRMPD1:p.E1093Q, FSHB:p.T43N, GABRA5:p.Q224K, GADL1:p.L352I, GAL3ST3:p.A271S, GALNT14:p.D234E, GAS8:p.R313S, GATA3:p.M443I, GCDH:p.R82C, GEM:p.R268L, GFRAL:p.Q308K, GIT2:p.R123L, GJB4:p.R22S, GLB1L2:p.I407M, GLOD4:p.Q223fs, GNAO1:p.P283Q, GPNMB:p.I174M, GPR137B:p.G240C, GPR158:p.P762T, GPR98:p.G4307W, GRB7:p.R239L, GRHL1:p.G608W, GRID1:p.R683L, GRIK1:p.R368Q, GRM5:p.P895fs, GTF2E1:p.R192L, H3F3C:p.R131L, HAO2:p.H12N, HCN1:p.P231Q, HECW1:p.A183S, HGF:p.M686T, HIP1:p.R940L, HIST1H1E:p.R25P, HLA-DMA:p.A236fs, HOXA5:p.G11C, HS3ST3A1:p.G399W, HSD17B6:p.F209L,

HSPA13:p.V85L, HSPBAP1:p.R282L, HTR5A:p.W298C, IGHMBP2:p.R615S, IL2:p.R103M, IL2RA:p.G61W, IL32:p.P215T, ING1:p.A220S, INMT:p.G56V, ITGA8:p.G616C, ITGAD:p.L528fs, ITGAX:p.R283H, ITIH1:p.G254W, ITIH2:p.L842V, ITK:p.R29L, ITPR2:p.P358Q, JMJD1C:p.R1198S, KCNA1:p.G376C, KCNH8:p.M455I, KCNJ3:p.L430F, KCNK18:p.G23V, KCNK2:p.R166L, KEAP1:p.G603W, KEAP1:p.R260L, KEAP1:p.S144F, KHDRBS2:p.S203L, KIAA1211:p.P1203Q, KIAA1549:p.L1272F, KIAA1755:p.Q108H, KIF15:p.E252Q, KIF9:p.G480R, KIRREL:p.G604C, KLF5:p.E419Q, KRAS:p.Q61H, KRTAP10-12:p.R64P, KRTAP27-1:p.M124I, KRTAP4-5:p.C91F, KRTAP5-1:p.S193Y, L1CAM:p.R632S, L3MBTL4:p.W162L, LAMA1:p.D1030Y, LAMB1:p.T1610fs, LAMB4:p.G1239W, LAMB4:p.G588W, LEF1:p.I53V, LEKR1:p.Q450K, LIM2:p.S150T, LIPJ:p.P236Q, LPHN3:p.E740D, LPPR4:p.R527S, LRFN5:p.N132K, LRP1B:p.G3563C, LRP2:p.M4039I, LRRC4C:p.Q10L, LRRIQ1:p.W792L, LRRTM4:p.S243Y, MAGEA10:p.R7H, MAGEC2:p.W109C, MAGI1:p.G1156V, MAGI2:p.P1044T, MAK:p.P373Q, MAP2K1:p.K57N, MARCH11:p.R193L, MEPE:p.G142C, MKI67:p.R1081S, MKRN3:p.P448H, MLL3:p.N393K, MLL3:p.Q356K, MMRN1:p.A1013S, MOGAT2:p.Q66fs, MXRA5:p.D324Y, MYH4:p.T790M, MYH8:p.R1117C, MYH8:p.H1006N, MYO5B:p.R708L, MYO7B:p.P2040H, MYO9B:p.R94L, MYT1L:p.P351Q, NAA11:p.T184K, NAB1:p.L72F, NAV1:p.R938L, NBPF15:p.G665E, NCAM2:p.G698C, NCAPD2:p.R220L, NDST3:p.V427I, NEK2:p.R239S, NFIA:p.L294F, NLRP3:p.R157C, NOTCH2:p.R2105L, NR4A2:p.R314L, NRG1:p.V481L, NRXN1:p.R813S, NRXN1:p.A660S, NRXN3:p.P23H, NRXN3:p.R103C, NTM:p.G333C, NUAK1:p.G173C, NYAP2:p.P437L, ODZ3:p.P218Q, OIT3:p.R508S, OOEP:p.R101C, OPN1LW:p.P283H, OR10H4:p.M199I, OR10J1:p.L157Q, OR10X1:p.L298I, OR10Z1:p.L205F, OR14A16:p.G160C, OR2A25:p.M80I, OR2AG2:p.G249W, OR2AK2:p.W37C, OR2H2:p.L205F, OR2J2:p.G234W, OR2L13:p.M106I, OR2L13:p.T242A, OR2L3:p.M1I, OR2L3:p.L67I, OR2L8:p.R121C, OR2L8:p.R171S, OR2M2:p.F177L, OR2M2:p.F323L, OR2M5:p.V205L, OR2T12:p.M258L, OR2T27:p.D11Y, OR2T33:p.P165Q, OR2T34:p.C246F, OR2T6:p.V213L, OR4C12:p.D309Y, OR4C12:p.M279I, OR4C16:p.L162M, OR4M2:p.A119S, OR4M2:p.A161S, OR51V1:p.P298T, OR5AS1:p.M39I, OR5B12:p.S289C, OR5B17:p.M266I, OR5D14:p.H246N, OR5D16:p.P264T, OR5D18:p.R123H, OR5F1:p.G44V, OR5J2:p.A36S, OR5L1:p.T275N, OR6C65:p.I154fs, OR6C75:p.G94W, OR6K2:p.P79Q, OR8D2:p.R306M, OR9A2:p.R289W, OR9G9:p.R169L, P2RX7:p.P142Q, P2RY10:p.T10K,

P2RY10:p.V196L, PABPC5:p.R99S, PAPPA2:p.P917T, PAPPA2:p.P1706H, PBLD:p.P55Q, PCDH10:p.R587S, PCDH10:p.V986L, PCDH11X:p.R1010I, PCDHAC2:p.A742V, PCDHB5:p.P649S, PCDHGC5:p.K12N, PCDHGC5:p.P684H, PCLO:p.P3946T, PCMTD1:p.R271M, PDPR:p.G793W, PDYN:p.G191W, PDZD2:p.R565S, PDZD8:p.S980G, PFKM:p.R118S, PIGM:p.R225L, PIK3CA:p.E542K, PIK3CG:p.V165I, PILRA:p.S291fs, PLCE1:p.G564C, PLCL1:p.M564I, PLEKHA6:p.R110L, PNKP:p.G174W, POGZ:p.G75W, POLE:p.R573L, POM121L12:p.P231T, POM121L12:p.P242H, POTEE:p.V288M, POTEM:p.S78R, POU3F3:p.D321Y, PPT2:p.R265L, PRDM16:p.P1036L, PRELP:p.D201Y, PRPF40B:p.R160S, PRPF6:p.R763L, PTEN:p.R234L, PTPN11:p.G503V, PTPN13:p.E2067K, PTPRJ:p.G334W, PTPRT:p.R928L, PTPRU:p.P559S, PXDNL:p.P1456T, QSOX1:p.R401L, QSOX2:p.R683L, RAB13:p.R167L, RAB8A:p.G20W, RAPGEFL1:p.R356L, RBM19:p.G390W, RCL1:p.P112Q, REG1B:p.W57L, REG3A:p.S150L, REG4:p.G110V, RIMS2:p.R55L, RIT2:p.R85L, RLN2:p.S138C, RNF20:p.P529Q, RORB:p.G94W, RPL10L:p.K187T, RPRD2:p.R97S, RTN1:p.S103W, RUNX2:p.R337M, RYR2:p.K2413N, RYR2:p.M4334I, RYR3:p.P1670T, S100PBP:p.R5L, S1PR1:p.L104F, SAGE1:p.H298Q, SALL1:p.E965K, SALL1:p.R898W, SALL4:p.R187L, SBSPON:p.G133W, SCAF8:p.G740C, SCG2:p.P252Q, SCML4:p.L261F, SCN2A:p.T155K, SEC24D:p.A50fs, SEC61A2:p.G126V, SERPINA12:p.D253Y, SERPINA9:p.M414I, SERPINC1:p.R45L, SGIP1:p.R502L, SH3GL3:p.R174L, SH3PXD2A:p.S759L, SI:p.V1217F, SKOR1:p.Y883C, SLC1A2:p.F348fs, SLC24A5:p.R35S, SLC25A48:p.R101S, SLC35E2:p.R201L, SLC39A12:p.C628S, SLC39A6:p.R53L, SLC4A5:p.I533V, SLC5A1:p.G53W, SLC5A7:p.G442V, SLC6A11:p.W299L, SLC6A2:p.S354C, SLC8A1:p.G433C, SLIT1:p.R1460L, SLITRK5:p.R68L, SLITRK5:p.R468M, SLITRK6:p.N741K, SORL1:p.R205L, SOS1:p.N233Y, SOX9:p.E75K, SPAG16:p.V439L, SPIN4:p.Y171C, SPRR2D:p.P30fs, SPTA1:p.G2367C, SPTA1:p.D2243Y, SSX3:p.P127T, ST18:p.H778Q, STAC3:p.G117W, STOML3:p.D86Y, STX2:p.R107L, SUMF2:p.G110E, SUN3:p.P339Q, SV2C:p.P60Q, SYNDIG1:p.D135Y, SYNE1:p.K8632E, TARS2:p.E199K, TAS2R16:p.Q177H, TCOF1:p.K264R, TCTE1:p.S127I, TDO2:p.Q197H, THSD7A:p.G810W, THSD7A:p.R801L, TIFAB:p.D43E, TIGD4:p.S312F, TLL1:p.P53Q, TMPRSS11E:p.G259C, TMTC1:p.A864D, TMTC1:p.G212V, TMX3:p.R151C, TNNI1:p.R67L, TNR:p.L692I, TOP2A:p.R736L, TP53:p.R337L, TP53:p.E285K, TP53:p.R283P, TP53:p.D281N, TP53:p.C277F, TP53:p.V274F, TP53:p.R273H, TP53:p.I255F,

TP53:p.R249S, TP53:p.M237I, TP53:p.S215I, TP53:p.C176F, TP53:p.R110L, TP53:p.G105C, TP53:p.P72fs, TPO:p.E558K, TRAF6:p.R502S, TRIM42:p.Q127K, TRIM48:p.A93D, TRIM4:p.R398L, TRIM51:p.W131C, TRIM9:p.R337S, TRIML1:p.H399Q, TRPM3:p.G298W, TSC1:p.G378C, TSG101:p.R276S, TSHZ1:p.K501N, TSHZ3:p.G677V, TTF2:p.R761S, TUBA3C:p.Q176fs, UBAC1:p.K330N, UBE2J2:p.G193W, UBR1:p.G1647W, UGT2B7:p.M214I, VMP1:p.E369Q, VPS13B:p.G2575W, VSTM2A:p.G75V, VWA3B:p.R557L, WBP11:p.P227fs, WDR52:p.G612C, WDR59:p.R837S, WDR75:p.P287Q, WDR88:p.G100W, ZCCHC5:p.G335W, ZFHX4:p.L811F, ZFHX4:p.T1663N, ZFHX4:p.H2511Q, ZFP14:p.Q17L, ZIC1:p.A112E, ZNF154:p.T408N, ZNF223:p.G23W, ZNF295:p.S732C, ZNF322:p.K106N, ZNF385D:p.T226S, ZNF454:p.S190I, ZNF492:p.P392H, ZNF521:p.G640C, ZNF521:p.P270H, ZNF536:p.G186C, ZNF536:p.G663W, ZNF644:p.G21W, ZNF716:p.H263L, ZNF71:p.V411L, ZNF782:p.G484W, ZNF831:p.Q617K, ZNF98:p.C492F, and ZSWIM2:p.S214Y.

54. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LUSC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, TP53:p.R158L, KRTAP5-5:p.GCG47del, NFE2L2:p.E79Q, CDKN2A:p.D108Y, DHX9:p.V40G, MAFA:p.207_208HH>H, NFE2L2:p.R34Q, PBX2:p.Y262F, PIK3CA:p.E542K, TP53:p.R273L, TP53:p.C242F, TP53:p.R175G, TP53:p.Y163C, TP53:p.V157F, AICDA:p.R131G, ALPK2:p.D53N, ANKFN1:p.M280I, ARPC1A:p.F212L, ASXL2:p.S1081L, C1orf74:p.D254N, C3orf30:p.D227E, CCDC121:p.W397L, CHN2:p.I43M, CLEC4C:p.R179L, CLN3:p.G206S, CNTN5:p.T178N, COL12A1:p.G2753C, CPS1:p.T855K, CSMD3:p.T1094K, CSMD3:p.Q691K, DDX11:p.R167T, EGFR:p.L861Q, EME1:p.D570H, EP300:p.D1399N, ESYT3:p.S574F, FAM135B:p.L648M, FAM135B:p.Q285H, FAM47A:p.G372W, FBXW7:p.R505G, FGFR3:p.S249C, GALNT13:p.G358C, GNL3L:p.K20N, GPC5:p.R347L, HCN1:p.A714S, HCN1:p.R659L, HCN1:p.G499V, HCN1:p.P326T, HERC2P3:p.A803V, HEXDC:p.T482P, HIST1H3B:p.E74K, HIST2H2BE:p.G54D, IFNA10:p.V79A, IL7R:p.S54L, INADL:p.P1340A, ISX:p.C2F, ITGAX:p.R685H, ITPR1:p.E1883Q, KCNN3:p.80_81insQQ, KEAP1:p.G480W, KEAP1:p.R470C, KEAP1:p.V155F, KIAA1751:p.L63F, KIAA2022:p.C345F, KIR3DL2:p.K229E, KLF5:p.E419Q, LAMA4:p.M1293I,

LMLN:p.G199C, LRP2:p.A516V, LRRC66:p.F458L, LSG1:p.R517L, LUM:p.R310L, MB21D2:p.Q311E, MCHR1:p.S306F, MKRN3:p.G270V, MUC16:p.N11594K, NFE2L2:p.G81S, NFE2L2:p.G31A, NFE2L2:p.L30F, NFE2L2:p.D29H, OR2B11:p.G10V, OR2T2:p.F13V, OR4K2:p.C254F, OR51F2:p.R67P, OR51S1:p.R159Q, OR5D18:p.T271K, OR8H2:p.L166F, OR8J3:p.S160L, OR8K3:p.K235N, PCDHB1:p.N568K, PHIP:p.I1681M, PIK3CA:p.E726K, PIK3CA:p.H1047R, PLCE1:p.G439C, PRSS57:p.E39Q, PYHIN1:p.G148A, RANBP6:p.I984L, RBMXL1:p.G305C, REG1B:p.M67I, RGS6:p.W366L, RNF5:p.T136I, RP1:p.S1771L, RRP15:p.L214F, RYR2:p.E711K, SAMD3:p.Q206H, SLITRK3:p.R214L, SON:p.S908L, SP4:p.E11del, STK11:p.G279fs, TARBP1:p.L782V, TBCD:p.R476C, TMPRSS11F:p.R274Q, TP53:p.R337L, TP53:p.E271K, TP53:p.R267P, TP53:p.G245V, TP53:p.Y234C, TP53:p.Y220C, TP53:p.H214R, TP53:p.H193L, TP53:p.H179L, TPTE:p.M541I, TRIM7:p.L332I, TTN:p.T32425M, ZFP36L2:p.D240N, ZNF208:p.H883Q, ZNF48:p.R235H, ZNF626:p.K473R, ZNF676:p.P43T, ZZZ3:p.R162Q.

55. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from OV; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R273H, TP53:p.Y220C, TP53:p.R248Q, TP53:p.R175H, TP53:p.R273C, TP53:p.I195T, TP53:p.R248W, TP53:p.R282W, TP53:p.C176Y, TP53:p.V157F, TP53:p.S241F, TP53:p.H179R, TP53:p.G245S, TP53:p.H193R, ADCY2:p.V888I, B2M:p.M1V, BAP1:p.R227C, CYP4A11:p.V185F, DNAH5:p.R3197Q, GART:p.K807fs, GRIN2B:p.R519Q, HRNR:p.M1fs, KLHL29:p.L716fs, KRAS:p.G12V, MGA:p.R2435Q, MYO3A:p.N525S, NPAS2:p.Q201R, NRAS:p.Q61R, PDAP1:p.K55fs, PGAP1:p.F565C, TP53:p.S315fs, TP53:p.C275Y, TP53:p.R273L, TP53:p.V272M, TP53:p.G266V, TP53:p.G266R, TP53:p.D259Y, TP53:p.P250L, TP53:p.G245D, TP53:p.G245V, TP53:p.G244C, TP53:p.C238fs, TP53:p.Y236C, TP53:p.Y234C, TP53:p.V216M, TP53:p.S215R, TP53:p.Y205C, TP53:p.L194R, TP53:p.P191del, TP53:p.Y163C, TP53:p.A159V, TP53:p.K132N, TRPC7:p.D210V, UXS1:p.V100L, WNT11:p.C344Y, and ZNF295:p.E885A.

56. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from READ; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12V, TP53:p.R273H, KRAS:p.A146T, KRAS:p.G12D, TP53:p.R175H, AKAP9:p.L3482I, APBA1:p.E624K, BAG5:p.D439N, C17orf97:p.E230D, CDH23:p.F177L, CERS3:p.E95D, DNAH5:p.R982H, ERBB2:p.V842I, GABRB3:p.D500N, KRAS:p.G13D, KRAS:p.G12C, KRAS:p.G12S, LRP6:p.R675Q, MACF1:p.F722L, MBOAT2:p.R43Q, MYO1D:p.E246K, NLRC4:p.E409K, NRAP:p.E327K, NRAS:p.Q61K, PCDH15:p.R1552I, PIK3CA:p.N345K, PIK3CA:p.E545K, POLE:p.S459F, PPP2R2B:p.P326L, SMAD4:p.R361H, TP53:p.R248W, ZFP2:p.R150I, and ZNF563:p.K26N.

57. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from SKCM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, NRAS:p.Q61K, HSD17B7P2:p.N175S, BRAF:p.V600K, DISP1:p.G732L, IDH1:p.R132C, NRAS:p.Q61L, MUC16:p.P5119S, RAC1:p.P29S, WASH3P:p.G175S, AGAP9:p.M248V, C15orf23:p.S24F, DNAH5:p.D3236N, SPTLC3:p.R97K, TMC5:p.R276C, CFB:p.R314M, FRG1B:p.A50P, INMT:p.S212F, LOC649330:p.G93E, MAP2K1:p.P124S, RGS7:p.R44C, STK19:p.D89N, ADAM30:p.G97L, ARL16:p.G6R, ARMC4:p.E22K, BRAF:p.K601E, CAPN13:p.P405S, CD1C:p.R89C, CLCC1:p.P406Q, CNTN5:p.S379F, DNAH5:p.R742Q, EEF1B2:p.S43G, FRG1B:p.I59V, GABRG1:p.E205K, IARS2:p.R832C, IL32:p.D218fs, ISX:p.R86C, KLHDC7A:p.E635K, NAP1L4:p.P285Q, NBPF10:p.Q908E, OR2A5:p.S71L, OR4E2:p.R226Q, OR4M1:p.G41E, OR4M2:p.S268F, OR4N2:p.G41E, OR51B2:p.S163L, PCDHGC5:p.R293C, PCLO:p.R4133C, PHGDH:p.G173L, POTEG:p.D51N, PPP6C:p.R301C, PRAMEF11:p.C84S, PSG9:p.E404K, PTPRB:p.D1560N, RNF152:p.P95S, SPAG16:p.P488S, SPATA8:p.E18K, TAF1A:p.R172M, TCEB3C:p.E308K, THSD7B:p.E126K, TTN:p.E12129K, XIRP2:p.D2439N, and ZNF831:p.R1393Q.

58. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from UCEC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RPL22:p.K15fs, PTEN:p.R130G, PTEN:p.R130Q, KRAS:p.G12D, KRAS:p.G12V, PIK3CA:p.H1047R, PIK3CA:p.R88Q,

PIK3CA:p.E545K, PTEN:p.V317fs, FGFR2:p.S252W, PIK3CA:p.E542K, CTNNB1:p.S37F, POLE:p.P286R, PPP2R1A:p.P179R, CTNNB1:p.S37C, KRAS:p.G13D, CTNNB1:p.D32N, CTNNB1:p.S33F, CTNNB1:p.G34R, KIAA2026:p.R574C, LIMCH1:p.R806fs, PIK3CA:p.H1047L, ALPK2:p.K523fs, CTNNB1:p.S33C, FBXW7:p.R505C, HPD:p.R284fs, KRAS:p.G12A, PIK3CA:p.R93Q, POLE:p.V411L, TP53:p.R248W, ABCA11P:p.R385I, ABI1:p.K445N, ACSM2B:p.K195N, APOB:p.F3102L, ASCC3:p.R136Q, C12orf4:p.R335Q, CCDC132:p.R838C, CHD4:p.R975H, CSDE1:p.R220C, CTNNB1:p.D32Y, CTNNB1:p.S33Y, CTNNB1:p.T41I, EXOC1:p.R588C, FBXW7:p.R465H, FGFR2:p.N549K, FUBP1:p.R430C, GEN1:p.S509L, IK:p.E90fs, KIF20B:p.E54K, MAX:p.H28R, MBOAT2:p.R43Q, METTL14:p.R298P, MFGE8:p.D170N, MS4A8B:p.S3L, NSMCE1:p.D244N, OXR1:p.E122K, PCDH19:p.E530K, PIK3CA:p.R108H, PIK3CA:p.N345K, PIK3CA:p.C420R, PIK3CA:p.Q546P, PIK3CA:p.Q546R, PTEN:p.R130L, RBL2:p.E127K, RXFP1:p.S223Y, SF3B1:p.R957Q, SLC20A1:p.P328fs, SOX17:p.S403I, TNS1:p.Q659del, TP53:p.R273H, TP53:p.R273C, TP53:p.R248Q, TTN:p.D16823N, TXNL1:p.R234C, ZFHX3:p.R1893fs, ZNF180:p.R625I, ZNF257:p.R392I, ZNF354B:p.D609N, ZNF43:p.R280C, ZNF709:p.R468I, ZNF765:p.S254L, ABCA5:p.R1476Q, ACVR1:p.R206H, ADAD1:p.S11L, ADAM9:p.R256Q, ADD3:p.E570K, ADGB:p.S1124L, AGXT2:p.R502C, AMBN:p.S225Y, ANKDD1A:p.R24H, ARHGEF33:p.R46I, ATP10B:p.L1304I, ATP2C1:p.E724K, ATP9A:p.R290Q, ATR:p.R1814fs, AVL9:p.F34L, BMPER:p.R241Q, BTN3A2:p.E153K, C14orf118:p.R279I, C14orf166B:p.F230L, C3orf23:p.R217C, C3orf62:p.R185Q, CACNA1C:p.S710L, CAGE1:p.E539K, CARD10:p.KE272del, CCDC144A:p.S1264L, CCDC168:p.D5020Y, CCDC36:p.R209I, CD55:p.E156K, CEP44:p.S253L, CIITA:p.E728K, CREBBP:p.P2094L, CTNNB1:p.S37A, CTTNBP2:p.S420L, DCT:p.R532Q, DIAPH2:p.E121K, DLG2:p.S624L, DNAH10:p.R1888Q, DNAH14:p.R1367C, DNAH7:p.R2961Q, DNAH8:p.R1347H, DNAJC13:p.E1248K, DNMT1:p.E51K, DST:p.S1767Y, DYNC2H1:p.E883D, EMR1:p.R631Q, EPHX4:p.R282Q, ERCC6L2:p.L445I, F10:p.E117K, FAM155B:p.E158K, FAM83B:p.R206Q, FARP1:p.S383L, FAT3:p.A4159T, FBXW7:p.R689W, FBXW7:p.R465C, FBXW7:p.G423V, FN1:p.R290C, FZD6:p.R416Q, GABRA3:p.R73H, GABRA4:p.R460Q, GALNTL2:p.E395K, GFAP:p.A233T, GGA2:p.A63V, GIGYF2:p.R227H, GNPTAB:p.R1189Q, GPR112:p.S1283Y, GPR98:p.R4142W, GRIA3:p.S646Y, GRM6:p.E363D, HMCN1:p.S133Y, HSPA4L:p.R483C, HTR2A:p.S219L, INTS7:p.R940C, INTS7:p.R106I, ITM2C:p.E167K, JAKMIP2:p.R283I,

KCND3:p.S438L, KCNS2:p.D211N, KDM1B:p.F361L, KIAA0556:p.L330I, KIAA1147:p.A149V, KIF23:p.R150Q, KIF27:p.K925N, KIF9:p.R594Q, KLHL13:p.E213K, KLHL28:p.E33K, LIN9:p.R183W, LRBA:p.E2103K, LRP2:p.R2432I, MAGI2:p.L450M, MC5R:p.A109T, MEGF10:p.S1053L, MKI67:p.T1664fs, MKLN1:p.F485L, MMRN1:p.F917L, MSH4:p.E730K, MTOR:p.S2215Y, MUC7:p.S336L, MYBPC2:p.R646H, N4BP2L2:p.R506C, NAPSA:p.R121Q, NCOA7:p.E369D, NCR1:p.R258W, NEK11:p.R374Q, NHEJ1:p.R109Q, NNMT:p.E233K, NOTCH4:p.15_16LL>L, NPY1R:p.A371T, NRAS:p.Q61R, OGDHL:p.R57C, OMA1:p.R445Q, OPRM1:p.R462C, OR4C12:p.F248L, OR5AK2:p.K89N, OSBPL6:p.R577Q, PCDHAC2:p.K138N, PCDHB12:p.R289C, PCDHGC5:p.A70T, PIK3CA:p.R38H, PIK3CA:p.E39K, PIK3CA:p.E110del, PIK3CA:p.K111E, PIK3CA:p.Q546K, PIK3CA:p.M1043V, PIK3CA:p.M1043I, PLA2G3:p.R201Q, PLXNA1:p.E1295K, PON1:p.R306Q, POTEE:p.R303I, POTEF:p.K674N, PPP2R1A:p.S256F, PPP2R3B:p.F310L, PRAM1:p.A268T, PREX1:p.E1246K, PRKCQ:p.A324V, PTEN:p.R130P, PVRL4:p.A358T, RAI2:p.S385Y, RBM39:p.T353I, RELN:p.F2722L, RFPL1:p.R148Q, ROBO2:p.D1018N, ROS1:p.R245I, RPS6KA6:p.S394Y, RSBN1:p.E572K, RYR1:p.A2576T, SACS:p.R2906Q, SCAPER:p.R366Q, SELP:p.R429W, SENP7:p.S673Y, SEPHS1:p.E13K, SFRP4:p.R232Q, SGK1:p.K367del, SIX1:p.E191K, SLC10A7:p.S261L, SLC12A2:p.R828Q, SLC16A14:p.R495Q, SLC7A2:p.R322W, SMCR8:p.E175K, SOS1:p.N233Y, SPOP:p.E50K, STRN3:p.K218N, STXBP6:p.D92N, SULT1E1:p.R77Q, SUN3:p.L124I, SUSD1:p.R343C, SYNM:p.R516Q, TAF1:p.R843W, TDRD3:p.R322Q, THADA:p.S1941L, TLN2:p.S208L, TMEM161B:p.R315Q, TMPRSS3:p.R16Q, TP53:p.Y220C, TPTE:p.S423L, TRANK1:p.E846K, TRPC5:p.S490L, TRPM3:p.R429W, TSSK1B:p.E301K, TTLL7:p.R751H, TTN:p.S20317L, TTN:p.E6404K, TTN:p.R4434Q, TTN:p.R2506Q, UGT8:p.E102K, USF1:p.R52Q, USP16:p.R455Q, USP25:p.R873H, USP33:p.R36Q, VPRBP:p.R802Q, VPS13B:p.R692Q, WDR65:p.F110C, YTHDC2:p.E185K, ZFYVE1:p.R266Q, ZKSCAN1:p.R541fs, ZNF117:p.R157I, ZNF180:p.R569I, ZNF195:p.R59Q, ZNF254:p.K179N, ZNF263:p.R510I, ZNF333:p.R554Q, ZNF354B:p.R402I, ZNF442:p.R309Q, ZNF454:p.R376I, ZNF485:p.R374I, ZNF488:p.R206Q, ZNF559:p.E284K, ZNF594:p.R287I, ZNF611:p.R390I, ZNF645:p.R154C, ZNF649:p.R338Q, ZNF649:p.R198I, ZNF674:p.R405I, ZNF675:p.R220I, ZNF678:p.R564I, ZNF732:p.R354I, ZNF780A:p.R466Q, ZNF823:p.R547I, ZNF836:p.R854I, ZNF836:p.R630I, ZNF841:p.R757I, and ZNF98:p.R370I.

59. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from ACC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ZFPM1:p.EPL444del, GARS:p.P42A, ZNF517:p.V349A, LRIG1:p.L24V, CCDC102A:p.R96W, OPRD1:p.C27F, SOWAHA:p.R124P, LACTB:p.M5L, TOR3A:p.F13L, ZFPM1:p.E444fs, ZNF787:p.D367del, LRIG1:p.L26V, IRX3:p.L422P, TRIOBP:p.H1300R, TUBA1C:p.L146F, ZFPM1:p.P445fs, ZFPM1:p.446_447LA>P, TPO:p.S398T, USP42:p.R779P, ERCC2:p.D312N, GLTPD2:p.D209E, OTOP1:p.LLW104del, RINL:p.P402L, AMDHD1:p.S3G, ASPDH:p.Q266R, KCNK17:p.S21G, TMEM247:p.Q128E, MUC5B:p.D682G, OBSCN:p.R4516W, FAM184B:p.R784W, SEMA5B:p.V840D, ZNF598:p.E25G, ADAD2:p.G44E, C1orf106:p.R538C, ZAR1:p.Q42H, PANK2:p.G126A, PODXL:p.28_30PSP>P, SALL3:p.L593V, THEM4:p.L17R, C2orf81:p.T315P, CLDN23:p.V210M, FAM109A:p.GGG156del, FPGS:p.I22V, HHIPL1:p.V692A, MUC5B:p.M2869T, PLEC:p.R1386Q, SYT8:p.R373W, TAF5:p.S130A, TMEM189-UBE2V1:p.N6D, UQCRFS1:p.S6A, B3GNT6:p.L316fs, CCDC105:p.P499T, CLIC6:p.Q298E, IDUA:p.T374P, NOTCH2:p.C19W, RGS9BP:p.A96S, RREB1:p.G783V, SP8:p.G165del, WDR34:p.W60G, C19orf10:p.G12R, CELSR2:p.16_17insP, FAM75C1:p.71_71H>HLVSQRH, GPRIN2:p.R446H, KBTBD13:p.A81V, OGFR:p.S557T, PODXL:p.30_30P>PSP, BHLHE22:p.L62Q, C4orf32:p.G32E, C5orf65:p.Q245R, KNDC1:p.V806D, KRTAP10-6:p.49_49P>PSCCAP, LRP11:p.P92R, MAP1S:p.S411C, NOL9:p.S58A, RASIP1:p.R601C, RGMB:p.S63R, SARM1:p.R23P, TSC22D2:p.A419T, ZNF628:p.T230A, ZNF814:p.A337V, AATK:p.A541T, BTBD11:p.G265A, CRIPAK:p.C143R, KCTD3:p.F9V, KRT8:p.S59A, MUC5B:p.S681G, NCOR2:p.1846_1847insSSG, OGFR:p.E556K, APOE:p.C130R, C10orf95:p.A85S, C13orf33:p.R59G, CRIPAK:p.C174R, FAM18B2:p.C51Y, GLI3:p.P998L, GLTSCR2:p.Q389R, HECTD2:p.P19A, IRF2BPL:p.123_125QQQ>Q, MEX3C:p.179_182AAAA>A, NEFH:p.EE658del, RNF149:p.S9G, RNF222:p.A133T, SEZ6L2:p.R74P, TNIP2:p.R73G, ARRDC4:p.T79A, B3GNT6:p.P330fs, BAG1:p.G45R, C22orf26:p.P28L, CHDH:p.E40A, COQ2:p.V66L, CTGF:p.H83D, DLEU7:p.A83V, EPPK1:p.D2378H, FAM86C1:p.R30P, FZD1:p.93_94insP, GPRIN2:p.V241M, GPX1:p.11_13AAA>A, HES3:p.P96T, JMJD4:p.A11V, KANK3:p.R359H, LPPR2:p.A186S,

NEFH:p.665_666insEE, NOM1:p.R24G, RNF39:p.G263C, SCRT1:p.S133A, SNED1:p.L1228P, TTLL11:p.122_123insKA, ZCCHC3:p.A159del, ZNF219:p.QP233del, ASB16:p.T249A, ASB2:p.H515P, ATP9B:p.S39G, AVL9:p.G7fs, C17orf96:p.L63V, C19orf29:p.A499V, CRB2:p.T1110M, CRIPAK:p.P173R, CRIPAK:p.I190L, CSGALNACT2:p.L362F, CTBS:p.LAL31del, CTNNB1:p.S45P, DMRT1:p.S45T, DOK7:p.G461D, FBRSL1:p.A836V, FEZ2:p.P50L, FRG1:p.S169N, HSD17B1:p.G313S, IBA57:p.S130R, KIF1A:p.E917D, KRTAP9-1:p.160_160Q>QPSCGSSCCQ, LURAP1L:p.55_56insGGG, NMU:p.A19E, NMU:p.A18E, NOXA1:p.D6E, NPTX1:p.G100D, PLIN5:p.R306W, TBP:p.95_96insQ, TMEM200C:p.S498G, TNXB:p.V706fs, VARS:p.P51S, ZC3H12D:p.P405S, and ZZEF1:p.V30A.

60. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from CESC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, PIK3CA:p.E542K, MAPK1:p.E322K, EP300:p.D1399N, ERBB2:p.S310F, ERBB3:p.V104M, KRAS:p.G12D, ANKRD12:p.E721Q, ANKRD36:p.M1144T, MICA:p.G318fs, PIK3CA:p.E726K, PTEN:p.R130Q, ABCD1:p.S606P, ACTL7B:p.E211K, ADAM21:p.F129C, ADAMTS12:p.P1053A, AKT1:p.E17K, ANKLE1:p.V643L, ANO3:p.M956I, AOAH:p.R326T, APOD:p.S115L, ASCC1:p.H207Y, ATM:p.S800F, AURKA:p.S387L, BAG5:p.M286I, C12orf43:p.E28Q, C16orf3:p.G65S, C3orf70:p.S6L, C4orf21:p.E800Q, CALB2:p.K60N, CALCB:p.R81T, CCDC152:p.E153Q, CCDC53:p.R58C, CDC27:p.P242S, CFHR5:p.R441H, CLOCK:p.L123fs, CMYA5:p.E2733K, CNTRL:p.P185S, CSHL1:p.R117Q, CSMD3:p.H952Y, CTNNB1:p.D32G, CTSH:p.E254Q, DHPS:p.F49L, DMPK:p.R44H, DNAH14:p.F622fs, DNAH3:p.E3367Q, DNAH8:p.E587D, DNASE1L1:p.D212N, ECE2:p.D254N, FAM71B:p.H445D, FAM73A:p.G23V, FAS:p.E261K, FBXW7:p.R505G, FBXW7:p.R465C, FEZF2:p.E82K, FKBPL:p.E161Q, FMNL1:p.E927Q, GPATCH3:p.E275Q, GPR142:p.R304T, GPRIN2:p.T100P, GRAMD2:p.I123M, HERC2:p.S329F, HGF:p.G229A, HIF3A:p.A72T, HIST1H1B:p.K188N, HIST1H2AL:p.R30P, HIST2H2AC:p.R30P, HLA-C:p.N104K, HLA-DPB1:p.G114fs, HRNR:p.G2539S, INVS:p.R799K, JPH3:p.Q433H, JUP:p.S627L, KIAA1211:p.R308fs, KIAA1211:p.E309fs, KLK2:p.E161K, KRAS:p.G13D, KRAS:p.G12V, LIN9:p.E231K, LOC151174:p.P90S, LRRC37A3:p.A406D, LRTM2:p.L176V, MEPE:p.S30T,

MUC12:p.R2634C, MUC4:p.S2936L, MYOM2:p.D988N, NFE2L2:p.D29H, NOTCH2:p.R2298W, NPIPL1:p.P250L, NR5A2:p.E80K, NYAP2:p.R197Q, OBSL1:p.E1642K, OR13C2:p.L9V, OSBP:p.Q721H, PAOX:p.H107Y, PDILT:p.E500K, PIAS3:p.D460N, PLEKHO2:p.E351Q, PNRC1:p.R73C, PPP4R1:p.L597F, PREP:p.F469L, PRKDC:p.Q3568E, PSME3:p.R231W, RANBP6:p.R915W, RCAN2:p.D440N, RNPC3:p.E116fs, SDHAP1:p.H66Y, SDHAP2:p.S37fs, SERPINA3:p.K158N, SERPINA4:p.R98C, SF1:p.R255W, SGSM1:p.E818K, SIM1:p.V213M, SLC10A4:p.F281L, SLC25A5:p.I79F, SLC35G2:p.K62fs, SLC4A9:p.R617C, SLCO2A1:p.M479I, SND1:p.Q38E, SPATA17:p.R72K, SRSF12:p.S150C, TADA2B:p.E67K, TCTEX1D2:p.S74L, TEDDM1:p.M166I, TEX15:p.E1652Q, TMC2:p.E92D, TMEM131:p.E1319Q, TNKS2:p.T619fs, TNS1:p.Q659del, TP53:p.E285K, TRAF3:p.S9F, TRIM61:p.K98N, TRPM1:p.M996I, TUFT1:p.L101F, U2AF1:p.S34F, UNC93B1:p.V498M, USP4:p.L259V, VCAN:p.S1308C, WDR17:p.P278S, ZBED4:p.S385L, ZEB2:p.E1094K, ZFYVE9:p.M1147I, ZNF16:p.R452W, ZNF677:p.R131T, and ZSWIM4:p.E407K.

61. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from CRC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12D, KRAS:p.G12V, BRAF:p.V600E, KRAS:p.G13D, TP53:p.R175H, PIK3CA:p.E545K, FBXW7:p.R465H, KRAS:p.A146T, PIK3CA:p.H1047R, TP53:p.R248W, CDC27:p.D555E, SMAD4:p.R361H, TP53:p.R273H, KRAS:p.G12C, NRAS:p.Q61K, ERBB2:p.V842I, ERBB3:p.V104M, FBXW7:p.R465C, PIK3CA:p.R88Q, PIK3CA:p.E542K, TP53:p.R273C, TP53:p.G245S, AXIN2:p.G665fs, C16orf45:p.T106N, C20orf26:p.R1088Q, DNMT1:p.E432K, FBXW7:p.R505C, HLCS:p.E362K, HPSE2:p.K58N, KIF14:p.R598Q, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KLK2:p.P57T, KRAS:p.G12A, KRAS:p.G12S, LPHN3:p.R1183Q, LRP6:p.R675Q, MYH8:p.R1048Q, NRAP:p.E327K, NRAS:p.G12C, PIK3CA:p.N345K, POSTN:p.R508C, PPP2R1A:p.R183W, PTEN:p.R130Q, RAF1:p.S257L, SDK1:p.T1181M, SGSM1:p.F1117L, TCF7L2:p.R482fs, TP53:p.R282W, TRIM23:p.R289Q, UGT8:p.E102K, ZNF491:p.R343Q, A2M:p.R732Q, AADACL4:p.A266T, ABCA8:p.E1158K, ABCA8:p.R842Q, ABCA8:p.A696T, ABCB8:p.R345H, ACACA:p.R1731C, ACADM:p.F48C, ACOT9:p.R50Q, ACPP:p.R105Q, ACTL7B:p.R354H, ACTL9:p.R331H, ACVR1:p.S290L, ADAM30:p.S314Y, ADAM32:p.R559Q, ADAMTS16:p.D817N, ADAMTS4:p.R156W,

ADCY5:p.R661H, AGMAT:p.V313M, AGPAT4:p.A212T, AKAP12:p.E1282K, AKAP9:p.L3482I, ALB:p.S294L, ALDH1L1:p.A870T, ALG2:p.S302Y, AMOTL1:p.R676Q, AMPD1:p.K502N, AMPH:p.R292W, ANKRD6:p.R479C, APBA1:p.K730N, APBA1:p.E624K, APC:p.E847fs, APC:p.F1354fs, APC:p.M1413fs, APOB:p.R3136C, APOB:p.A43V, APPL1:p.R668W, AQPEP:p.A309T, ARF4:p.R149H, ARFGEF1:p.D1632N, ARHGAP32:p.E1253K, ARHGAP36:p.R128C, ARHGAP36:p.A147V, ARHGAP5:p.D890fs, ARNTL:p.T395M, ARPP21:p.R338H, ARSG:p.V131I, ASCC3:p.R1197Q, ATP10D:p.R311H, ATP6V0A4:p.R191Q, ATP9B:p.R265Q, AXDND1:p.E930D, AXIN2:p.W663fs, B2M:p.L13fs, B3GALNT1:p.R145Q, BACH1:p.R538Q, BAG5:p.D439N, BBOX1:p.F176V, BCL2L11:p.R91Q, BCL7A:p.T52M, BCLAF1:p.R37fs, BEND5:p.R198C, BICD2:p.R162H, BLVRA:p.S44L, BMP3:p.R344W, BNC2:p.R512W, BRPF1:p.R66C, BRWD3:p.R787C, BTBD7:p.S436L, BUB1B:p.F996L, BZRAP1:p.V1627I, C11orf30:p.R1111C, C14orf101:p.E295K, C14orf102:p.D115N, C14orf105:p.R100I, C15orf2:p.V488I, C15orf33:p.D340N, C16orf87:p.R151I, C1RL:p.L351fs, C22orf40:p.P32fs, C3orf39:p.R333W, C5orf30:p.D4N, C5orf4:p.R114Q, C6orf170:p.K724T, C7orf63:p.A10T, CACHD1:p.S720Y, CACNA1A:p.T665M, CACNA2D3:p.A332T, CACNB2:p.R608H, CACNG3:p.V134I, CACNG3:p.A138V, CACNG5:p.G121R, CADM1:p.S190L, CADPS:p.A1073T, CAPRIN2:p.E13K, CARD11:p.R423Q, CASC1:p.R54Q, CASP14:p.R5W, CBFB:p.E152K, CC2D2A:p.R1284C, CCDC18:p.K615N, CCDC60:p.R230H, CCDC81:p.R259I, CCDC88C:p.P1851fs, CCKBR:p.V236M, CD101:p.D283Y, CD101:p.R594Q, CD180:p.N228T, CDC14B:p.R375C, CDCA7L:p.P405fs, CDH10:p.E349K, CDH12:p.D674N, CDH20:p.A134V, CDH23:p.F177L, CDH2:p.D547Y, CDH9:p.F523L, CDK16:p.R108C, CEACAM5:p.L640I, CEP152:p.E21K, CERS3:p.E95D, CHD4:p.R975H, CHD5:p.A801T, CIZ1:p.V668A, CLEC18A:p.R423H, CLTCL1:p.R481W, CMAS:p.R110Q, CNRIP1:p.R102W, COBLL1:p.K732N, COL14A1:p.R1082I, COL17A1:p.P1004L, COL4A6:p.L550I, COL6A3:p.D2792N, COPB1:p.R425C, CORO2A:p.*526R, COX15:p.L86I, CSMD1:p.S781Y, CTCFL:p.E423K, CTDNEP1:p.E126K, CTTNBP2:p.R164C, CYP4B1:p.E434D, DACH2:p.R539C, DBC1:p.V216I, DBF4B:p.S254Y, DCHS2:p.F2149L, DCLK2:p.S549Y, DDI1:p.R275Q, DENND4A:p.P357H, DENND4C:p.R1081Q, DHTKD1:p.R410Q, DISP1:p.R763C, DKK2:p.R230H, DKK4:p.R203Q, DLC1:p.A350V, DLC1:p.E222D, DMD:p.R3195H, DNAH5:p.R982H, DNAH5:p.R224Q, DNAH9:p.D1547N,

DNAJC24:p.E61K, DNM1:p.A251T, DNMT1:p.E1531Q, DNMT3B:p.R92W, DOCK10:p.A1830V, DOCK1:p.E864K, DOCK2:p.G170R, DOCK3:p.R1183C, DOCK5:p.E177K, DOK5:p.R274W, DPP8:p.G165R, DPY19L1:p.F378L, DUOX2:p.F880L, DVL2:p.A601fs, EBAG9:p.E187K, EBF3:p.G255fs, EDNRB:p.L450R, EGR2:p.R390H, EHD3:p.E44K, EIF2C1:p.R139Q, ELF3:p.F305fs, ELMOD2:p.T141M, EMR2:p.S75L, ENAM:p.R373H, ENOX2:p.R356W, ENTPD7:p.E327K, EPG5:p.D369N, EPHB2:p.R392H, ERCC6:p.V780I, ERCC6L:p.R505Q, ERRFI1:p.A421T, ESCO1:p.R300Q, ETV6:p.R369W, F8:p.S2269Y, FAM123B:p.F173fs, FAM135B:p.R884H, FAM169B:p.K165N, FAM170A:p.E56K, FAM171B:p.D459N, FAM181A:p.R109H, FAM5B:p.R402C, FBXO11:p.A432V, FBXW7:p.R689W, FBXW7:p.S582L, FBXW7:p.R14Q, FGF14:p.A236V, FHDC1:p.R254W, FHOD3:p.A225T, FHOD3:p.E813K, FMO3:p.F510L, FNDC1:p.R652H, FOXK1:p.R354W, FOXN3:p.P96fs, FPGT-TNNI3K:p.R455H, FZD3:p.D367N, GABRA4:p.R460Q, GABRA5:p.S126N, GABRB3:p.D500N, GALNTL5:p.R262I, GJA1:p.R362Q, GLRA3:p.L454I, GLRA3:p.F132L, GOLGA4:p.Q1536H, GP2:p.S41L, GPC6:p.A214T, GPLD1:p.R717Q, GPR125:p.R113Q, GPR156:p.F754L, GPR158:p.D566N, GPR21:p.R216H, GPR61:p.A62T, GPR98:p.R4142W, GPRC5A:p.V30I, GRAP2:p.E69D, GRIA1:p.R218C, GRIA2:p.R845Q, GRM7:p.R679Q, GTF3A:p.K306N, HAO1:p.R172C, HARS2:p.R168H, HBB:p.F42L, HCN4:p.R525H, HDAC5:p.A1044T, HGF:p.S467Y, HIPK4:p.R280H, HLA-DMA:p.E84K, HMG20A:p.E248D, HPS3:p.S468L, HRSP12:p.R120Q, HS3ST1:p.E287K, HTR3B:p.R236C, HTR5A:p.R152C, HTT:p.D1548N, HYDIN:p.R1187C, HYDIN:p.R939Q, HYDIN:p.R451Q, HYOU1:p.R158C, IFT172:p.A944V, IGJ:p.R77Q, IL17RA:p.Q803fs, IL1RAPL2:p.T647M, IL3:p.A90T, IL5RA:p.L47I, INPP5D:p.R523Q, INPP5K:p.R263C, IRAK3:p.R267Q, IREB2:p.R419Q, ITGA4:p.T673M, ITGA4:p.F900L, ITIH5:p.A912T, ITK:p.E196K, JAG1:p.A462T, JAK1:p.V310I, KAL1:p.V303I, KBTBD8:p.V549I, KCNA3:p.A415V, KCND3:p.S438L, KCNMB4:p.F209L, KCTD20:p.L314fs, KDELC1:p.L447I, KIAA0528:p.R181Q, KIAA0556:p.R1082W, KIAA1109:p.S4937Y, KIAA1804:p.V474M, KIAA1804:p.R477W, KIF16B:p.R145Q, KIF26B:p.A1114V, KPNA4:p.R29Q, KRAS:p.K117N, KRAS:p.Q61L, KRAS:p.Q61K, KRT6B:p.L197P, L1CAM:p.T186M, LALBA:p.A41T, LAMA4:p.A558V, LBX1:p.R176W, LPAR4:p.R145Q, LRP1B:p.K2623N, LRP2:p.R3043C, LRP2:p.S737L, LRRC18:p.R218W, LRRC31:p.K23T, LRRC7:p.R1389H, LZTS2:p.P100fs, MACF1:p.S292L, MACF1:p.F722L,

MAEL:p.R345C, MAGEE1:p.V380M, MAGI1:p.R1198C, MAP1B:p.E2046D, MAP2:p.K530N, MAP2K4:p.R287H, MAP3K4:p.R275Q, MAP7D2:p.R487C, MAPK8IP1:p.L217fs, MBOAT2:p.R43Q, MCF2L2:p.R926Q, MECOM:p.R969C, METTL16:p.R200Q, METTL21A:p.R174Q, METTL6:p.F56L, MFF:p.R162C, MFSD5:p.R280Q, MIA3:p.Q356H, MMAA:p.R326C, MORC1:p.D113Y, MORC2:p.R740H, MPDZ:p.L804I, MR1:p.S46L, MRPL47:p.L234I, MS4A8B:p.S3L, MSH4:p.K464N, MSH6:p.T1085fs, MSH6:p.R1095H, MUC16:p.R8606H, MYH13:p.D311N, MYH7:p.R1689C, MYO1D:p.E246K, MYO3A:p.N525H, MYO6:p.D1180N, MYO9A:p.R2179Q, MYO9A:p.R167Q, MYOZ2:p.E251K, MYT1:p.E226K, NAA25:p.S807Y, NCAM1:p.R474W, NCOA4:p.R562Q, NEB:p.D5434N, NEB:p.L1591I, NEB:p.E1214K, NEDD9:p.A798T, NEDD9:p.A316T, NEK1:p.R608C, NFASC:p.V256I, NINL:p.R1366C, NLRC4:p.D593N, NLRC4:p.E409K, NLRP4:p.V229I, NLRP5:p.R392H, NME9:p.E75K, NOLC1:p.T428M, NPC1:p.E451K, NPSR1:p.R235Q, NRAS:p.Q61L, NRAS:p.G13R, NRAS:p.G12D, NRG2:p.T246M, NTN4:p.E59K, NUB1:p.R373Q, NUDT15:p.S83Y, NUF2:p.S340L, NUP88:p.A302V, ODZ1:p.R2556W, OGDHL:p.A427T, OGFRL1:p.E427K, OLFM4:p.K132N, OPRM1:p.R353H, OR10A3:p.S93Y, OR2M3:p.R235H, OR52W1:p.R133C, OR5AU1:p.R312H, OR5B17:p.R163H, OR8S1:p.A99V, OSTN:p.R115Q, OTOL1:p.V431I, OTUD3:p.R277I, PAN3:p.S580N, PANK3:p.R260I, PAX3:p.T424M, PCBP1:p.L102Q, PCDH10:p.V477M, PCDH15:p.R1552I, PCDHAC2:p.A519T, PCDHAC2:p.E190K, PCDHAC2:p.A266T, PCDHAC2:p.A156V, PCDHAC2:p.E271K, PCDHAC2:p.A736V, PCDHB5:p.D51Y, PCDHB8:p.D235N, PCDHGC5:p.S289L, PCDHGC5:p.V662M, PCNXL2:p.R135Q, PCOLCE2:p.A348V, PCOLCE2:p.R87H, PDE4B:p.S417L, PGAM1:p.R240H, PHF3:p.R1410I, PIAS2:p.S519L, PIGR:p.A580T, PIK3CA:p.D350G, PIK3CA:p.E545A, PIK3CA:p.E545G, PIK3CA:p.Q546K, PIP4K2C:p.R204H, PKHD1L1:p.F1856L, PLA2G4A:p.E443K, PLCG2:p.E544K, PLCG2:p.D973N, PLEKHA6:p.V328fs, PLEKHG4B:p.E384K, PLK1:p.D233G, PLOD3:p.R297fs, PLSCR3:p.E77K, PLXNC1:p.S462L, PLXNC1:p.R819C, POLA1:p.E603D, POLE:p.S459F, POLE:p.V411L, POLQ:p.R860Q, PPP2R2B:p.P326L, PPP2R5C:p.S259Y, PRAMEF4:p.R248H, PREX1:p.V731I, PRKAA2:p.R407Q, PRKAR2B:p.S309L, PRKCI:p.R480C, PRKRA:p.K122N, PSG8:p.R397C, PSG8:p.R320C, PSMD12:p.R201Q, PTPDC1:p.R430W, PTPN12:p.R765Q, PTPN13:p.S887L, PTPRD:p.L1053I,

PTPRU:p.D1434N, PXDN:p.P856fs, PXDNL:p.T1312M, QRSL1:p.S226L, RAB7L1:p.R79W, RALGAPA1:p.R398C, RANBP2:p.R1231C, RBBP7:p.E313K, RBBP7:p.E274K, RBFOX2:p.A340T, RBMXL1:p.R331Q, RHOBTB1:p.T464M, RIMS2:p.R599Q, RIN3:p.S708L, RLBP1:p.D281N, RLBP1:p.A72V, RNASET2:p.A127V, RNF113B:p.A172V, RNF150:p.R236Q, RNF150:p.S208L, RNF43:p.S216L, ROR2:p.D672N, RPL6:p.F193C, RPS6KA5:p.E166K, RSPO2:p.R28C, RUVBL1:p.E431K, RUVBL1:p.R117C, RWDD2B:p.R254H, RXFP3:p.R113C, RYR3:p.R2705Q, SAGE1:p.R229C, SCFD2:p.R545W, SCML4:p.R194Q, SCN10A:p.T1570M, SCN11A:p.A1688T, SCN11A:p.V1289I, SCN11A:p.V566I, SCUBE2:p.V342M, SEMA3A:p.D81N, SEMA4D:p.R252Q, SEPHS1:p.R371Q, SEZ6L:p.S207L, SFPQ:p.R611Q, SFSWAP:p.S617Y, SGCG:p.A220V, SGCZ:p.I41M, SH3TC2:p.R89C, SIGLEC11:p.S363F, SIPA1L1:p.R1063Q, SIPA1L1:p.S1227Y, SLC12A1:p.S292L, SLC22A15:p.S201L, SLC24A2:p.A134V, SLC25A40:p.R96Q, SLC2A7:p.A65T, SLC30A9:p.R194H, SLC33A1:p.S542L, SLC35F3:p.A280T, SLC39A7:p.R382C, SLC43A1:p.P133L, SLC43A3:p.R216H, SLC44A5:p.R185H, SLC6A2:p.A562T, SLC8A1:p.R431H, SLFN12L:p.F232fs, SLITRK1:p.R52H, SLITRK3:p.S298L, SMAD2:p.R321Q, SMARCA4:p.R381Q, SOCS5:p.S464L, SORBS1:p.V1156M, SORBS1:p.F570L, SORCS2:p.R320W, SOX6:p.R719W, SPATA22:p.S150L, SPEG:p.A944V, SPTB:p.R86C, SPTBN4:p.A1993V, STIM2:p.R572Q, STT3B:p.D583Y, SULT1C4:p.R85Q, SUN3:p.E128K, SUPT6H:p.A957T, SYNE1:p.I1249L, SYNE1:p.R170W, SYNE2:p.K3103N, SYNGR4:p.R169Q, SYT7:p.T349M, TANK:p.S380L, TAS1R2:p.R270C, TAS2R1:p.F183L, TCF7L2:p.R488C, TDRD10:p.S322L, TECTB:p.L29I, TEKT5:p.R401H, TGFBR1:p.S241L, THAP5:p.S287Y, THSD7B:p.R90H, TLL1:p.T153M, TLL2:p.S872L, TM9SF2:p.R91H, TMCC3:p.R110H, TMEM132A:p.R481C, TMEM132D:p.R578W, TMEM55A:p.R189Q, TMEM74:p.R125Q, TMPRSS11A:p.S288L, TNIP2:p.A139T, TOP2B:p.R656H, TOX:p.S354L, TP53:p.G244D, TP53:p.R175C, TPO:p.A826T, TPR:p.S2155L, TPTE2:p.R258Q, TPTE:p.S423L, TRAK1:p.D627N, TRAPPC11:p.R568Q, TRIM23:p.R396Q, TRIM44:p.D331N, TRIO:p.R661W, TRPA1:p.K54N, TRPC5:p.S490L, TRPM6:p.R995H, TRPM7:p.R1862C, TRPM7:p.R843Q, TRPS1:p.R1125W, TRPV5:p.R492H, TRRAP:p.R3515W, TSHZ1:p.R881M, TTC21A:p.S270Y, TTN:p.R22795C, TTN:p.R3193Q, TTN:p.R328H, TUBA3D:p.R243Q, TUFT1:p.A340T, TXNDC15:p.R343Q, UBE2NL:p.R86I, UBIAD1:p.A97T, UGT2A1:p.N97fs, USH2A:p.F2369L, USP11:p.A286T,

USP25:p.R1119Q, USP26:p.R861Q, USP29:p.F81L, USP31:p.D391N, USP40:p.S851L, UTP14A:p.V148I, VAV3:p.E685K, VCAN:p.R1125H, VPS13C:p.D1359Y, WBSCR17:p.R228C, WDR3:p.E841K, WDR52:p.A157T, XKR6:p.R268Q, XPOT:p.R541W, YTHDC1:p.R267Q, YTHDC2:p.E634K, ZBBX:p.R596I, ZBTB24:p.L607I, ZC3H13:p.R103Q, ZCWPW2:p.D144N, ZEB2:p.R156H, ZFHX4:p.E237D, ZFP14:p.R386C, ZFP28:p.R525I, ZFP2:p.R150I, ZFP3:p.R273I, ZFP90:p.R330Q, ZHX2:p.V790I, ZIC4:p.S305L, ZIM3:p.D352N, ZKSCAN4:p.R319Q, ZMYM4:p.R1446Q, ZNF117:p.R185I, ZNF167:p.R683I, ZNF180:p.R401I, ZNF19:p.R349I, ZNF205:p.R384C, ZNF236:p.S1480L, ZNF248:p.R568I, ZNF259:p.R174I, ZNF266:p.R512Q, ZNF266:p.R344Q, ZNF280B:p.E363K, ZNF283:p.R392Q, ZNF32:p.S62L, ZNF345:p.R82Q, ZNF345:p.R334I, ZNF350:p.R310Q, ZNF434:p.R306C, ZNF439:p.E239D, ZNF439:p.R262I, ZNF443:p.R301I, ZNF445:p.L682M, ZNF470:p.R641I, ZNF471:p.R282I, ZNF484:p.R138C, ZNF528:p.R279Q, ZNF563:p.K26N, ZNF573:p.R350I, ZNF583:p.R344I, ZNF585A:p.E638K, ZNF585A:p.E491D, ZNF625:p.R235Q, ZNF652:p.K327N, ZNF677:p.R451I, ZNF678:p.R368I, ZNF699:p.R41I, ZNF70:p.R244I, ZNF770:p.S441P, ZNF774:p.R423Q, ZNF782:p.K247T, ZNF7:p.R337I, and ZNF831:p.E949D.

62. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from DLBCL; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of EZH2:p.Y641F, MYD88:p.L273P, BCL2:p.G33R, CARD11:p.E626K, ADCY2:p.A87V, BCL2:p.N172S, BCL2:p.H20Q, BRAF:p.K601E, BTG1:p.L31F, CACNA1E:p.R1458C, CARD11:p.E93D, CD79B:p.Y197D, CD79B:p.Y197H, CREBBP:p.R1446H, GRID1:p.E622K, HIST1H1C:p.A65V, HIST1H1E:p.G133A, HIST1H3B:p.A48S, KRAS:p.G13D, MYD88:p.S251N, PABPC1:p.R94C, PIM1:p.L164F, PIM1:p.L184F, POU2F2:p.T239A, POU2F2:p.T239S, RELN:p.R2971Q, SLC25A48:p.A67T, STAT6:p.D468H, TNF:p.L47F, and TRAF7:p.R11H.

63. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from KICH; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ACR:p.W279C, AGRN:p.1284_1285VT>A, C7orf25:p.R384fs, CAMSAP1:p.T466fs, CBWD6:p.E102fs, DOCK8:p.L1111fs,

EBPL:p.Q196P, EBPL:p.L189V, GFM1:p.A17fs, GOLGA6L6:p.D570E, ITGA5:p.A48D, LUZP2:p.S154fs, MTMR9:p.K193fs, MUC16:p.P10452fs, MUC4:p.S2832P, ODF2L:p.K407fs, RHBDD3:p.G34fs, RILPL1:p.S358R, TAS2R30:p.L236fs, TRRAP:p.A973S, UBR5:p.K2120fs, URGCP:p.G639fs, ZNF98:p.A222T, and ZSWIM6:p.Q610fs.

64. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from KIRP; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, ZNF598:p.E25G, NEFH:p.E645K, EEF1B2:p.S43G, NEFH:p.AKSPEKEE652del, OBP2B:p.K61N, SKI:p.A62G, C14orf126:p.R6W, KRT8:p.S59A, ACSBG2:p.I250M, ASIC2:p.R46L, CSGALNACT2:p.L362F, FRG1B:p.A50P, IDUA:p.H33Q, KRTAP4-5:p.S74C, SCAF11:p.E926fs, SYN2:p.A34del, ZNF814:p.R322K, BMS1:p.E878D, JMY:p.P822T, KIF1A:p.E917D, KRTAP4-7:p.S57P, LAMA5:p.L2223R, LRP1:p.P1058T, MED16:p.H449Q, MUC2:p.T1488P, MUC5B:p.D682G, NACA2:p.R75K, NEFH:p.665_666insEE, OR2L8:p.S201fs, RGPD5:p.P1760A, RRN3:p.P11S, RRN3:p.R9C, STAG3L2:p.L81fs, ZNF814:p.G320E, ACP6:p.V29G, AHNAK2:p.S2166F, AHNAK2:p.P1215S, AP1G1:p.I782fs, AQP2:p.N68T, BAIAP2L2:p.V396M, BMP6:p.Q118L, BST1:p.G36A, CDR1:p.V31A, CLDN7:p.S172A, CLIP1:p.S1018fs, COL18A1:p.G884fs, CROCC:p.A355P, CTAGE15P:p.A364V, CUBN:p.I2816M, DMRT2:p.T106S, DPY19L1:p.V249L, DSPP:p.D1047N, EBPL:p.L189V, EIF4G1:p.E465del, EXOSC2:p.R11P, FAM216A:p.P36S, FCGR2A:p.V222G, FMOD:p.S331R, FOLR2:p.Q112R, FRG1B:p.L20P, GAGE2B:p.9_10insY, GDPD5:p.G593fs, GIMAP8:p.A544S, GLUD2:p.R300G, GLUD2:p.S496R, GPR135:p.Q5P, HOXD8:p.Q67H, IER5:p.R194G, IL25:p.C168fs, JSRP1:p.V92A, KRAS:p.G12D, KRTAP1-1:p.Y86C, KRTAP4-11:p.L161V, LTBP1:p.L163P, MAML2:p.Q591K, MAPK7:p.A501D, MEF2A:p.P99S, MET:p.H1094Y, MET:p.M1250T, MST1:p.N435fs, MUC2:p.T1582R, MUC2:p.T1722I, MUC4:p.A4222T, MUC4:p.T2335M, MUC4:p.P1138L, MUC5B:p.S1098A, MUC5B:p.S3431N, MYH7:p.A1487T, NBPF10:p.R39fs, NBPF10:p.Y638S, NEFH:p.654_654S>SPEKAKS, PARG:p.A584T, PBX2:p.Y262F, PIP4K2A:p.R219K, RLIM:p.S471P, RUNX2:p.Q71E, SGK223:p.R63S, SMARCB1:p.L365fs, SRCAP:p.Q1875fs, TBC1D2B:p.R920Q, TCF7L2:p.R482fs, TMEM131:p.K640fs, TMEM60:p.K77fs, TPPP:p.R30K, TRPV3:p.A218E, TTBK2:p.C83W, UBXN11:p.S510G, UGT1A1:p.T4A,

UTS2R:p.A289E, YBX1:p.P250L, ZNF514:p.V81G, ZNF516:p.A256D, ZNF681:p.K405Q, ZNF814:p.D404E, ZNF814:p.P323H, ZXDB:p.G206R.

65. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LIHC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R249S, CTNNB1:p.D32V, CTNNB1:p.D32G, CTNNB1:p.S33P, CTNNB1:p.K335I, CTNNB1:p.H36P, EEF1A1:p.T432L, GNAS:p.R844C, OR2T4:p.V137L, TP53:p.H193R, ATXN1:p.Q217H, CSMD3:p.F2383fs, CTNNB1:p.D32N, CTNNB1:p.S33C, CTNNB1:p.G34V, CTNNB1:p.S45P, CTNNB1:p.N387K, DHRS4:p.I218T, DNM2:p.E378D, F5:p.Q426L, GALNTL5:p.A45T, GPX1:p.P77R, GRM8:p.R852C, IDH1:p.R132C, KIF26B:p.A2033T, KRT8:p.S59A, LOC100132247:p.T532P, NEB:p.D3854H, PIK3CA:p.H1047R, SOLH:p.R714H, TP53:p.R158H, TP53:p.V157F, and ZNF638:p.D400N.

66. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from MM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NRAS:p.Q61R, KRAS:p.Q61H, KRAS:p.G13D, NRAS:p.Q61K, BRAF:p.V600E, NRAS:p.Q61H, NRAS:p.G13R, ZNF717:p.W315C, ATP13A4:p.V431G, DNAJC12:p.R135K, IRF4:p.K123R, KRAS:p.A146T, KRAS:p.Q61R, KRAS:p.G12A, KRAS:p.G12D, ZNF717:p.N594I, ACTG1:p.A22P, ARL6IP1:p.M75L, BEND2:p.E630K, BRAF:p.G469A, CDHR1:p.R218G, DIS3:p.R780K, DMXL2:p.D2412E, DNAJC10:p.I80K, EGR1:p.Q9H, FGFR3:p.*807S, IDH1:p.R132C, IL6ST:p.P216H, INTS12:p.M1V, KRAS:p.K117N, KRAS:p.A59G, KRAS:p.G12R, MAX:p.R36W, MLL5:p.G492E, NBPF1:p.E810K, NRAS:p.Q61L, NRAS:p.G12D, ODF2L:p.E294K, PADI2:p.T114P, PNLIP:p.T37M, PRDM1:p.S588C, PTPN11:p.E76K, PTPN14:p.E286K, RBM6:p.V675G, SCN10A:p.R1142H, SRGAP1:p.T61M, SUSD1:p.T168P, TAS2R16:p.V231I, TINAG:p.E403K, TRIP12:p.L1775P, and ZNF717:p.C844S.

67. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from PRAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, RGPD5:p.P1760A,

FRG1B:p.L52S, EEF1B2:p.S43G, FRG1B:p.I10T, FRG1B:p.A53T, LRRC37A2:p.T102S, NBPF10:p.E3455K, PTH2:p.L22V, CYP2D7P1:p.S32A, FAM47C:p.N648D, MAP3K9:p.E38del, MUC4:p.H4205Q, CHEK2:p.K373E, FRG1B:p.A11T, FRG1B:p.A50P, HLA-J:p.R124W, KRTAP1-5:p.I88T, KRTAP4-9:p.D18V, NPIP:p.A271V, PDGFRA:p.R483fs, ZNF780A:p.Q600H, ZNF845:p.R925H, ZNF91:p.R333H, ARFGAP3:p.N299fs, BTN2A3P:p.P3S, FNBP4:p.TT58del, HLA-A:p.Q78R, LOC554223:p.RAPWMEQ147del, PODXL:p.28_30PSP>P, POLI:p.D17del, SPOP:p.F133L, SYN2:p.A34del, TMEM52:p.23_26LLPL>L, UBC:p.L149R, ZNF208:p.I647S, ZNF799:p.E589G, ZNF814:p.D404E, ASTN2:p.L221del, B4GALNT1:p.G88fs, C16orf74:p.S21del, CCDC15:p.H458P, CD209:p.R129W, CNTNAP1:p.S1029I, DBR1:p.541_542DD>D, FAM22F:p.S691del, FRG1B:p.D32V, FRG1B:p.I34T, FRG1B:p.N55D, FRG1B:p.I59V, FRG1B:p.S71N, KIF25:p.W3R, KRTAP4-11:p.L161V, KRTAP4-11:p.M93V, KRTAP4-11:p.R51K, KRTAP4-6:p.S153Y, LILRB5:p.S598P, LMOD2:p.E124del, LOC645752:p.L40P, LRP1:p.P1058T, LRRIQ3:p.K244fs, LURAP1L:p.55_56insGGG, MLLT10:p.V463E, MYOCD:p.Q310del, NBPF10:p.N1369D, OTUD4:p.T909I, PARG:p.A584T, PEX1:p.I370fs, POTEC:p.K507E, POTEC:p.R477Q, POU4F2:p.68_69insG, PRG4:p.T417P, SDHAP2:p.R31C, SPOP:p.F133C, SPOP:p.W131G, TIMD4:p.T152del, TMEM121:p.P299del, TP53:p.G245S, UBC:p.R73L, UBC:p.I191T, WASH3P:p.G175S, ZMIZ1:p.D1048fs, ZNF709:p.T413I, ACADS:p.R330H, ADAMTS7:p.K1357fs, AFF2:p.R597H, AGAP6:p.S127I, AK302238:p.A44T, AK302879:p.Q191R, ALDH1A2:p.R85C, ANAPC1:p.T537A, ANKRD36C:p.H438R, AP4B1:p.R276W, ARFGAP2:p.S38N, BBS9:p.F268fs, BC139719:p.L133R, BRAF:p.G469A, C22orf43:p.D171del, CANT1:p.K131R, CHD3:p.E35del, CLEC4A:p.R209H, CNOT3:p.E20K, CNPY3:p.17_18LL>L, CNTNAP3B:p.S317T, CNTNAP3B:p.M1247I, CTNNB1:p.T41A, DDX10:p.D788del, DLC1:p.S741T, DPY19L2:p.M210V, EDC4:p.S617del, EFCAB6:p.R379K, ERC2:p.927_928HH>H, FAM111B:p.S269fs, FEM1A:p.L620M, FHOD3:p.A632fs, FLJ43860:p.L850fs, FMN2:p.G59del, FNBP4:p.914_915PP>P, FRG1:p.E86del, FRG1B:p.K13N, FRG1B:p.P42Q, GABRB1:p.R416C, GABRR2:p.A368V, GAGE2B:p.9_10insY, GOLGA8DP:p.N84H, GOT2:p.R355W, GPATCH4:p.K210fs, HDGFL1:p.188_189insA, HLA-DQB2:p.G250S, HLA-DQB2:p.R247H, IDH1:p.R132H, IL27:p.E176del, IRF2BPL:p.123_125QQQ>Q, KANK3:p.DGDS489del, KIAA1462:p.858_859SS>S, KRTAP4-11:p.S48R, KRTAP4-7:p.S57P,

KRTAP4-8:p.C95S, LPHN3:p.R826H, LRP10:p.L11del, LRP5:p.S1609P, LRRC16B:p.R787W, MAS1L:p.R324G, MECOM:p.R915Q, MED12:p.L1224F, MED12L:p.Q2115del, MESP2:p.GQGQGQGQ195del, MGAT4C:p.T345M, MLEC:p.E238del, MSLNL:p.T68P, MUC7:p.S173P, MYC:p.Q37del, NBPF10:p.N440D, NLRP6:p.E611del, NOX3:p.C404fs, OR1M1:p.V69I, OR7E24:p.L7fs, OTUD4:p.A153del, PANK2:p.T417fs, PCLO:p.S496P, PCNT:p.S162G, PCSK9:p.23_24insL, PHOSPHO1:p.S32del, POU4F1:p.H108del, PRAMEF8:p.R319H, PRDM7:p.M387L, PRG4:p.T597P, PTPRD:p.R1323C, PTPRF:p.R1174Q, ROBO3:p.RS1367del, ROCK1:p.T518S, RPTN:p.G296S, RTL1:p.152_152E>EE, SIRPA:p.V233I, SLC2A6:p.A230D, SLC8A2:p.E710del, SMG7:p.E846fs, SNAPC4:p.S542del, SP8:p.G165del, SPOP:p.F133I, SPOP:p.F133V, SPOP:p.F102C, SPOP:p.F102V, SRSF11:p.G17fs, SRSF4:p.K396del, SSPO:p.S4198fs, STAG3L2:p.L81fs, STK19:p.R18fs, TBC1D2B:p.R920Q, TBC1D9:p.P1233T, TCHH:p.P1158R, TCOF1:p.K1366del, TNRC18:p.2664_2665SS>S, TP53:p.R248Q, TP53:p.R175H, TP53:p.C141G, TSPAN4:p.L92V, UBXN11:p.GPGPGPSP504del, UTP3:p.E81del, WASH3P:p.L187V, ZAN:p.P717L, ZAN:p.L878P, ZFP90:p.R591fs, ZNF761:p.H373R, and ZNF91:p.H305R.

68. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from STAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RNF43:p.G659fs, BZRAP1:p.P1416fs, XYLT2:p.Y526fs, LARP4B:p.T163fs, PGM5:p.I98V, ZBTB20:p.P692fs, ARID1A:p.G1848fs, FHOD3:p.P334fs, KIAA0182:p.T120fs, ATP6V1B1:p.Y383fs, PIK3CA:p.H1047R, FRMD4A:p.P1005fs, PIK3CA:p.E545K, CDC14A:p.N123fs, KRAS:p.G13D, MLL2:p.T172fs, BCORL1:p.S1679fs, PLEKHA6:p.V328fs, C9orf131:p.P342fs, CD4:p.Q164fs, FBXW7:p.R465C, GNG12:p.T68fs, IRS4:p.G591fs, JARID2:p.V422fs, KIAA0195:p.I902fs, MBD6:p.P732fs, MVK:p.P138fs, PAMR1:p.G101fs, WNT16:p.W165fs, ZNF43:p.N251fs, ABCA6:p.L306fs, ADAM28:p.K73fs, AOC3:p.L79fs, ATP2A1:p.R819fs, B2M:p.L13fs, C6orf89:p.P58fs, CNTLN:p.K1305fs, CR2:p.V206fs, DYRK4:p.K468fs, ERBB3:p.V104M, GLI1:p.W272fs, KRAS:p.G12D, MLL2:p.T172fs, MSH6:p.T1085fs, NLK:p.C190fs, OR5M3:p.T89fs, PAX6:p.P375fs, PTEN:p.L265fs, RABGAP1:p.K928fs, RAD51AP2:p.T316fs, SVIL:p.G1862fs, TP53:p.R273H, WNK4:p.G606fs, ARID1A:p.P2139fs, AXIN2:p.G665fs,

C13orf33:p.R67fs, C1QTNF5:p.P308fs, CELSR1:p.G614fs, CRYGD:p.G159fs, DCHS1:p.R235fs, DDC:p.I433fs, EDNRB:p.Y383fs, EPHA2:p.P460fs, FOXN3:p.P96fs, HDAC4:p.P901fs, INF2:p.S527fs, KIRREL2:p.V649fs, KLF3:p.I104fs, KLHL14:p.P231fs, MAP7D3:p.Q308fs, OTX2:p.R44fs, PAFAH1B1:p.K302fs, PLAGL2:p.P10fs, POLM:p.P97fs, PRPF40B:p.I31fs, RALGAPB:p.T379fs, SBNO1:p.N1139fs, SERPINI1:p.L81fs, SH3KBP1:p.L574fs, SLC12A7:p.H686fs, SLC27A3:p.P643fs, TBX4:p.S370fs, TP53:p.R273C, TP53:p.R175H, TRAM1L1:p.R345fs, WBP1:p.P138fs, ABCC4:p.L883fs, AKAP13:p.K2785fs, ALDH3A1:p.P562fs, ALPK2:p.L356fs, ARFGEF1:p.P1552fs, ARID1A:p.G1848fs, AVPR1A:p.F351fs, BAX:p.M38fs, C14orf43:p.P313fs, C1QTNF5:p.G194fs, C7orf50:p.L179fs, CDC25C:p.K322fs, CETN3:p.K63fs, CHD3:p.P597fs, CTCF:p.K202fs, CTSC:p.F105fs, DDX17:p.G163fs, DLGAP3:p.G377fs, EBF3:p.G255fs, FHDC1:p.F100fs, FILIP1L:p.K749fs, FLNB:p.W529fs, GBP7:p.G431fs, GCC2:p.E700fs, GPR161:p.G517fs, IWS1:p.S802fs, KIAA0240:p.K895fs, KIAA1967:p.P415fs, LRRC43:p.D558fs, MACF1:p.R707fs, MBD6:p.G780fs, MLL3:p.F4496fs, MPRIP:p.A351fs, MUC6:p.2129_2130SS>S, NOX5:p.P467fs, OPTN:p.P24fs, OR4K5:p.F177fs, PIK3CA:p.N345K, PIK3CA:p.E542K, PLXNA1:p.P1016fs, PNPLA7:p.P1199fs, PODN:p.I301fs, PPP2R3B:p.T389fs, PRSS36:p.L680fs, RGL2:p.G203fs, RHOQ:p.V190fs, RNF111:p.R771fs, RTN2:p.P313fs, SALL4:p.V995fs, SBF1:p.P1076fs, SETDB2:p.R715fs, SNAPC2:p.T292fs, SPG20:p.F232fs, SRCAP:p.P1876fs, STAT2:p.P489fs, TCHP:p.E172fs, TP53:p.R282W, TP53:p.R248Q, USP21:p.K474fs, WDR7:p.G262fs, ZBTB7C:p.E157fs, ZFC3H1:p.K385fs, ZNF124:p.T339fs, ZNF626:p.K115fs, ADNP2:p.S322fs, AGAP1:p.G127fs, ALDH2:p.L286fs, ARHGAP5:p.D890fs, ARHGEF17:p.A615fs, ARID1A:p.Y1324fs, ART1:p.I243fs, ASCL4:p.D35fs, ATXN2L:p.G998fs, B3GNT5:p.F30fs, BCKDHA:p.H37fs, BCL9L:p.P1127fs, BEND3:p.D265fs, BNC2:p.S575R, BRD3:p.P24fs, C12orf51:p.P4235fs, C1R:p.P216fs, C7orf49:p.G130fs, CA2:p.I145fs, CABP5:p.R145fs, CASD1:p.F781fs, CASP8:p.R471fs, CCDC153:p.P200fs, CD93:p.D280fs, CROT:p.L32fs, CSF3R:p.P468fs, CTCF:p.K202fs, ERBB2:p.S310F, FAM46D:p.S69R, FBN3:p.G601fs, FBXO21:p.F144fs, GAS6:p.G150fs, GLYR1:p.G380fs, GXYLT1:p.L223fs, HAUS6:p.S530fs, IGF2R:p.T1314fs, ITGB1:p.L378I, KDM3B:p.P1316fs, KIF13A:p.K1115fs, KLF3:p.S224fs, LARP1:p.A223fs, LRP1:p.G1488fs, LRP1:p.G1488fs, MAGEE2:p.Q45fs, MAMSTR:p.P162fs, MAPK15:p.Q511fs, MLL2:p.P647fs, MOCS2:p.P22fs, MTG1:p.L105fs, MTG1:p.H327fs, MTIF2:p.N109fs,

NID2:p.R1035fs, PAX2:p.P395fs, PCCA:p.R230H, PDZD2:p.R101fs, PFKP:p.M593fs, PIK3CA:p.R88Q, PLA2G1B:p.L53fs, PLAU:p.R201fs, PMEPA1:p.P208fs, POP1:p.K750fs, PTCH1:p.P1307fs, PTPRT:p.P1075fs, RDBP:p.P6fs, RNMT:p.K392fs, ROBO2:p.P1080fs, RUNDC3B:p.L6fs, SDAD1:p.K275fs, SLC10A6:p.G109fs, SNAPC1:p.D211fs, SPATA5L1:p.C685fs, SPTA1:p.K1732T, STAT5B:p.P367fs, SYT4:p.M1fs, TAF1L:p.K851fs, TAP2:p.L75fs, TBL1XR1:p.N126fs, THEMIS:p.K406fs, TMEM79:p.P161fs, TP53:p.C176F, TP53BP2:p.K69fs, TP53RK:p.L174fs, UBQLN2:p.A523fs, UHRF1BP1:p.I1330fs, VPRBP:p.K939fs, VPS13B:p.T56fs, WASF3:p.P305fs, YLPM1:p.E1178fs, ZC3H13:p.K1006fs, ZC3H18:p.P825fs, ZC3H4:p.E779Q, ZNF48:p.P247fs, ZNF608:p.A465fs, ZNF878:p.S238fs, ZSCAN18:p.P225fs, ABCB1:p.R527fs, ABCB6:p.G318fs, ACACB:p.G255fs, ACP1:p.Q123fs, ACTL6A:p.L88fs, ADAMTSL4:p.G778fs, AGBL5:p.I420fs, AHI1:p.K303fs, AKAP9:p.M3743fs, AKD1:p.R1209fs, ANKRD40:p.D99E, ARHGEF5:p.S1512fs, ARID1A:p.K1071fs, ARID3A:p.S557G, ARPP21:p.I130fs, ASPN:p.F67fs, ASXL3:p.E873fs, ATP6V1C2:p.R312fs, BEST3:p.P444fs, BRAF:p.P403fs, BRMS1:p.G107fs, BTBD11:p.T451fs, BTBD11:p.A561V, C11orf9:p.S261fs, C14orf102:p.R90fs, C14orf43:p.Q36fs, C15orf52:p.G98fs, C19orf21:p.R262C, C19orf70:p.P50fs, C20orf160:p.P46fs, C3:p.P890fs, CADPS2:p.N468fs, CASC3:p.S232F, CASC3:p.P603L, CASC3:p.P645L, CASC3:p.S658L, CASKIN2:p.P727fs, CBLL1:p.E138fs, CBLN3:p.P69fs, CCDC108:p.P1164fs, CCDC148:p.K420fs, CCDC153:p.P200fs, CCDC169-SOHLH2:p.K162R, CCDC88A:p.K677fs, CD1E:p.F85V, CD3EAP:p.K218fs, CDH11:p.K357T, CDH1:p.D254Y, CDH23:p.V403I, CFI:p.K37fs, CHPF2:p.D645fs, CIC:p.R507fs, CIC:p.A1114fs, CIC:p.A1114fs, CLSTN1:p.T615M, CNBD1:p.L396P, CNGA4:p.K510T, CNOT6:p.S248fs, CNTROB:p.R920fs, COL9A1:p.P283fs, CPAMD8:p.P784fs, CR1L:p.L79fs, CRB1:p.F630V, CSMD1:p.L3410V, CTNNA3:p.K856fs, CTNND1:p.I447fs, CTSD:p.P89fs, CUX1:p.A439fs, CYP7B1:p.K332T, DAB2IP:p.D994fs, DNAH11:p.T871fs, DNAH8:p.K1688fs, DNAJC1:p.K193fs, DNM2:p.P791fs, DSTN:p.F101fs, DYRK1B:p.Q545fs, EAF2:p.V109fs, EDNRB:p.A104V, EEA1:p.N570fs, EFHA1:p.F290fs, EGR1:p.P332fs, EIF4G3:p.K563fs, ELK3:p.S173fs, ENTPD2:p.G204fs, EOMES:p.G332fs, EPHA10:p.P868fs, EPHB6:p.G54fs, EPHX1:p.P132fs, EPPK1:p.G2015fs, ERBB4:p.M1fs, ESF1:p.T99fs, EXOSC8:p.L160fs, FAM113B:p.R51fs, FAM116A:p.L441fs, FAM135B:p.S645R, FAM151A:p.P117fs, FAM193A:p.D428fs, FAM193A:p.D428fs, FAM214B:p.A42fs, FAM40B:p.R740C,

FAM70B:p.S19L, FASTKD1:p.K3fs, FBXW7:p.R479Q, FBXW9:p.G298fs, FER:p.L474fs, FERMT2:p.K152fs, FGGY:p.G138fs, FIGNL1:p.K309fs, FLG:p.K159fs, FLNB:p.W529fs, FOLH1:p.S501fs, FYB:p.G324fs, GABRD:p.Q412fs, GALNTL1:p.W317fs, GANAB:p.L23fs, GCDH:p.L389fs, GIMAP7:p.V276fs, GIPC3:p.G227fs, GLI3:p.P1033fs, GLIPR1L2:p.G92fs, GNPNAT1:p.F54fs, GON4L:p.M134fs, GPATCH4:p.K210fs, GRK4:p.K22fs, GTF3C1:p.S767fs, GTF3C4:p.E562fs, H2AFY2:p.K144fs, HCFC1R1:p.P83fs, HCRTR2:p.S9fs, HCRTR2:p.S9fs, HDLBP:p.G747fs, HECA:p.R333fs, HIVEP3:p.H554fs, HIVEP3:p.P534fs, HLA-C:p.P209fs, HOOK1:p.L361fs, HOXD8:p.P122fs, HTT:p.G697fs, IBTK:p.K1213fs, IDE:p.K37fs, IFT172:p.A837T, INPPL1:p.A974fs, INPPL1:p.P1154fs, INSM2:p.T533fs, INTS12:p.L14fs, INVS:p.R815fs, IPO11:p.S844fs, IRX6:p.A425V, ISG20L2:p.P288fs, ITGB8:p.A7fs, JARID2:p.G394fs, JHDM1D:p.R97fs, KBTBD6:p.G442fs, KCNC1:p.K455fs, KCNH2:p.G149A, KCNJ10:p.P102fs, KCNMB2:p.N151K, KCTD21:p.T6M, KIAA0586:p.A1592fs, KIAA1009:p.F406fs, KIAA1109:p.E1588fs, KIAA2026:p.K690fs, KIF26B:p.S1065fs, KIF6:p.L204fs, KIRREL:p.P335fs, KLC2:p.T568fs, KRAS:p.Q61H, KRAS:p.G12S, MAN1C1:p.G431fs, MAP1A:p.P2063fs, MAP2:p.K1472fs, MAP3K12:p.R449del, MAP7D1:p.A80fs, MGST2:p.K102fs, MKI67:p.T1664fs, MKL1:p.P307fs, MLL2:p.P2354fs, MLL2:p.L656fs, MLL2:p.P647fs, MLL2:p.L1877fs, MMP3:p.I64fs, MPDZ:p.K1582fs, MTUS2:p.R1005W, MUC16:p.A6156T, MYB:p.R481fs, MYEOV:p.L269fs, MYH11:p.K1263del, MYO18A:p.P209fs, MYO7A:p.I539fs, MYOCD:p.G226fs, NAA16:p.H514fs, NBEA:p.V2247fs, NCAPD3:p.Q909fs, NCAPH:p.T466fs, NCOR2:p.P1308fs, NEFM:p.A213V, NEK8:p.V690fs, NF1:p.T676fs, NHLRC1:p.F204fs, NKD1:p.P286fs, NPR3:p.Y138H, NT5M:p.P206fs, NUFIP2:p.R224fs, NUP210:p.L135fs, NYNRIN:p.G113fs, OBSCN:p.G997fs, OGDH:p.Y948fs, OR4C16:p.S135R, OR51A7:p.L124R, OR7C1:p.C179fs, OSBP2:p.H627fs, OTOF:p.E1304K, P2RX1:p.R20fs, PALB2:p.M296fs, PALB2:p.N280fs, PANK1:p.K400fs, PAPD4:p.C225fs, PAPPA2:p.I1683fs, PARP15:p.K461fs, PARP4:p.K847fs, PCDH10:p.N118fs, PCDH10:p.P225fs, PCGF3:p.H63fs, PELI2:p.G197fs, PHACTR1:p.V251fs, PHACTR2:p.S237fs, PHACTR4:p.S354fs, PHKB:p.K642fs, PIAS3:p.H116fs, PIGO:p.P787fs, PIGT:p.A346fs, PIK3R3:p.M341fs, PITPNM1:p.P295fs, PKN2:p.K76fs, PLA2G15:p.W230fs, PLAG1:p.K184fs, PLEKHO1:p.T254fs, PLOD3:p.R297fs, PLOD3:p.P296fs, PLXNA2:p.P464fs, POLQ:p.L1430fs, PPARGC1B:p.P135fs, PPL:p.P454fs, PPM1H:p.P226fs, PPP1R12C:p.P372fs,

PREX2:p.R562fs, PRICKLE4:p.Q109fs, PRKAR1B:p.P87fs, PRKCG:p.R345C, PRMT8:p.S28fs, PROX1:p.F592fs, PRRG3:p.R163fs, PSD2:p.G256fs, PTCHD3:p.F588fs, PTPN4:p.N319fs, PTPRC:p.Q895H, PWWP2B:p.S84fs, PYGO2:p.Q150fs, RABGAP1:p.K928fs, RB1CC1:p.N1171fs, RBM6:p.R96fs, RHOA:p.Y42C, RIMS1:p.R71G, RIMS2:p.V401fs, RING1:p.G171fs, RINT1:p.L107fs, RNF43:p.P116fs, ROBO2:p.K1293fs, RPS6KA6:p.K109fs, RRS1:p.N45fs, RSF1:p.K386fs, RUSC2:p.P486fs, RXFP3:p.A60V, SAFB:p.W798fs, SCARF1:p.R614Q, SCLT1:p.K109fs, SERPINB12:p.Q168fs, SGK3:p.L61fs, SGOL2:p.E407fs, SIGLEC1:p.P318fs, SIK1:p.Q678fs, SLC16A6:p.G98fs, SLC25A17:p.F28fs, SLC26A7:p.I629fs, SLC32A1:p.V494I, SLC4A3:p.L1061fs, SLC7A10:p.P157fs, SLC9A2:p.T746fs, SLITRK1:p.K45fs, SND1:p.H721fs, SOAT1:p.F64fs, SORBS2:p.E1158fs, SOX7:p.L309fs, SPAG17:p.Q1264fs, SPTY2D1:p.P485fs, SRCIN1:p.P865fs, SREBF2:p.H763fs, SRRT:p.G102fs, STAB1:p.P1120fs, STRADA:p.R333fs, STX2:p.K252fs, SV2A:p.E138fs, SYCP2:p.M176fs, SYNJ2:p.P1111fs, TAS2R10:p.L196fs, TBC1D22B:p.A175fs, TEAD2:p.P298fs, TFE3:p.G482fs, TGM6:p.T358fs, TIMM44:p.K83fs, TIMP3:p.A199fs, TLR4:p.L498V, TMEM132D:p.P206fs, TMEM41A:p.F156fs, TMEM41B:p.F230fs, TMTC4:p.R611C, TNK2:p.P632fs, TOPBP1:p.I1381fs, TP53:p.E286K, TP53:p.P152fs, TRIP11:p.K541fs, TRPA1:p.T673fs, TRPM8:p.H765fs, TTF1:p.K336fs, TTI1:p.R707H, TTN:p.E15192D, U2AF2:p.L175fs, UBC:p.G684fs, UBR4:p.P2802fs, UPF2:p.E1033D, UPK2:p.P49fs, USP13:p.I116fs, USP15:p.K782fs, VASH1:p.G3fs, VEZF1:p.355_356insN, VPS13A:p.F2883fs, WAPAL:p.R522fs, WDFY3:p.L1842fs, WDR59:p.N160fs, WDR5:p.N214fs, WDR60:p.Q412fs, WDTC1:p.M287fs, WHSC1L1:p.K418fs, WNT1:p.W167fs, XIRP2:p.E1007D, YBX2:p.P226fs, YIF1A:p.R131fs, ZBBX:p.E151del, ZBTB40:p.L262fs, ZBTB7C:p.G342fs, ZBTB7C:p.D154fs, ZC3H18:p.T701fs, ZDHHC5:p.E651del, ZDHHC7:p.P316fs, ZFHX3:p.R1893fs, ZFHX3:p.E763fs, ZFHX4:p.L408fs, ZHX3:p.N249K, ZIM3:p.I384fs, ZKSCAN5:p.D13fs, ZMYM4:p.K345fs, ZNF236:p.T1410M, ZNF23:p.F122fs, ZNF334:p.K426fs, ZNF358:p.T130fs, ZNF701:p.L296fs, ZNF711:p.L737fs, and ZNF831:p.A49fs.

69. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from TGCT; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, BTN2A3P:p.P3S,

MUC2:p.G1715S, NBPF10:p.L44V, SP8:p.G156S, DCP1B:p.Q252H, DEK:p.E41D, ERC1:p.K692R, FAM104B:p.D75H, FRG1B:p.M49V, KRTAP10-10:p.V234M, LRRCC1:p.A6V, NRAS:p.Q61R, PNPLA4:p.L223P, ANKLE1:p.C644fs, ANKLE1:p.C644fs, KIT:p.D816H, KIT:p.D816Y, MUC2:p.T1597I, PSMD11:p.A5V, RHPN2:p.V73M, RUNX2:p.Q71E, SP4:p.E7K, TUBA1C:p.L146F, ZNF814:p.Y324H, ADAMTS17:p.N572T, ATRX:p.K1936R, BCL11B:p.E535D, BMP2K:p.Q460H, BMP2K:p.H487Q, C12orf32:p.D60V, C22orf43:p.K19E, CDC27:p.N571I, CDC27:p.P242S, DDX11:p.K208fs, EBPL:p.L189V, EZH2:p.K510R, FAM86A:p.A141T, GAS2L2:p.D189A, GRID2IP:p.LS754del, HGC6.3:p.E171G, KIT:p.D816V, KIT:p.N822Y, KIT:p.N822K, KRAS:p.Q61R, KRAS:p.G12V, KRTAP1-1:p.I116V, LRRC37BP1:p.Y166D, MEF2A:p.R127Q, MFF:p.S7F, MST1:p.R347W, MUC4:p.S3048L, MUC6:p.H2000Q, MUC6:p.P1977H, NAT10:p.I393T, OPLAH:p.A900D, PIEZO1:p.Q749E, PRAMEF4:p.F300V, RBM10:p.E184D, SERINC2:p.T121P, SPIN2A:p.M150V, SRRM2:p.A2257S, SSBP3:p.K6R, ZNF680:p.R501W, ABCC8:p.Y512C, ABCC9:p.L466P, ABCD1:p.H169Q, ABL2:p.P19T, ACVR2B:p.R48C, AHDC1:p.P33fs, AHNAK2:p.L1640M, ALPPL2:p.W31S, AMMECR1:p.G77C, ANK3:p.D1322E, ANKHD1-EIF4EBP3:p.G60S, ANKRD11:p.Y2015S, ANKRD11:p.K369R, ANKRD50:p.V637M, APBB3:p.L450P, ARHGAP24:p.T35A, ARID4B:p.G1076A, ARMC3:p.A514T, ARRB2:p.T99P, ATAD5:p.I305V, ATXN3:p.305_306insQQQQQQ, AVPR1B:p.G39R, AXDND1:p.E994Q, BAI2:p.A231G, BEST3:p.P383L, BIRC6:p.V414L, BIRC8:p.A225M, BRWD1:p.K1319R, BTN2A2:p.L15F, C12orf51:p.A2644T, C12orf65:p.K143T, C16orf62:p.L244I, C1QBP:p.T225I, C1orf167:p.S123G, C5orf25:p.Y4F, CACNA1E:p.G2080S, CAPNS1:p.LV303del, CCDC159:p.A332S, CDKAL1:p.P409L, CDYL:p.V48A, CDYL:p.A60G, CELSR2:p.L17P, CHD4:p.E138D, CKAP5:p.G576A, CLCC1:p.K52R, CMTM8:p.S26T, CNKSR2:p.P249L, CNTN5:p.I501T, COG5:p.H617R, COL15A1:p.K708R, COL6A3:p.A2378D, CRYGB:p.R143G, CSGALNACT2:p.L362F, CUL4A:p.I438F, CXXC1:p.Q156H, CYP19A1:p.F406L, DCLRE1B:p.F28I, DDX11:p.A376T, DDX11:p.E680D, DEPDC5:p.R1525Q, DLC1:p.S741T, DNMT1:p.R995Q, DOCK11:p.Q169E, DSPP:p.D1047N, E2F7:p.I91S, EBF1:p.D353G, ECI2:p.K55R, EEF1A2:p.Y418S, EIF3J:p.A8G, EML6:p.K805R, EPAS1:p.S474T, EPRS:p.L1335I, ERICH1:p.E327K, FAM101B:p.L5P, FAM104A:p.M1R, FAM110D:p.R71H, FAM155A:p.Q95R, FAM186A:p.G1492E, FAM194B:p.Y139H, FAM21B:p.P1231S, FAM32A:p.K9R,

FAM46B:p.H416R, FAM48B1:p.I499V, FAM48B1:p.A516P, FAM5C:p.S425W, FAM86C2P:p.C120Y, FBXL14:p.V48G, FRMPD3:p.Q832del, FRS2:p.L47S, GDF5:p.E105fs, GPNMB:p.C3fs, GPT2:p.R10P, H2AFV:p.Q125R, HDLBP:p.R503C, HERC2:p.R2129C, HIST1H2BJ:p.K13R, HLX:p.N231K, HMGB3:p.E198D, HSF4:p.R169W, HSF4:p.S491P, HYAL4:p.D222N, INO80E:p.P206fs, INTS4:p.S460A, IQCF6:p.R3H, ITPR1:p.M1569I, ITPR3:p.R1698G, KANSL3:p.G376E, KCNA4:p.E627del, KDM5A:p.P423S, KDM6A:p.Y362fs, KIAA0020:p.K63R, KIDINS220:p.N851S, KIT:p.W557G, KLHDC2:p.W321S, KRAS:p.A146T, KRAS:p.Q61H, KRAS:p.Q61L, KRAS:p.G12A, KRAS:p.G12R, KRBA1:p.R839G, KRTAP4-8:p.T63S, L2HGDH:p.P441del, LAMC3:p.P174Q, LHCGR:p.L16Q, LOC401296:p.L144M, LPHN2:p.F906I, LRP12:p.G310C, LTB4R:p.F73L, LTBP3:p.L35del, LUC7L3:p.S148T, LYPD4:p.T64K, MAMLD1:p.Q572L, MAP4K2:p.R341G, MAPK7:p.A501D, MAT2A:p.E166G, MED12L:p.C1292Y, MESP2:p.Q182E, MEX3C:p.R534S, MIER2:p.L131F, MLL5:p.Y66C, MLLT3:p.177_178SS>S, MMS19:p.D1005N, MRPS25:p.E119del, MSH6:p.D576A, MTIF3:p.G65E, MUC17:p.M1807T, MUC17:p.T2279N, MUC17:p.G2474S, MUC2:p.TTPSPP1475del, MUC2:p.T1568M, MUC2:p.T1580N, MUC2:p.T1704I, MUC2:p.T1706M, MUC4:p.H1117D, MUC5B:p.R1097H, MYEF2:p.K323E, MYEOV:p.L302H, MYH8:p.A785V, MYO1A:p.N584K, NAP1L3:p.P353R, NAV1:p.I1433M, NCAM1:p.E131G, NEB:p.D3107N, NEFH:p.V670E, NELL2:p.G170D, NHS:p.D1561N, NKD2:p.H447del, NSD1:p.T461R, NT5C3:p.A3P, NYAP1:p.P480S, OBSCN:p.A908T, OR10J1:p.R244Q, OR1S2:p.M298I, OR2L3:p.K294R, OR6K6:p.F311L, PABPC3:p.V325fs, PBX2:p.Y262F, PCDHB4:p.P255F, PCMTD1:p.V281A, PCP4L1:p.K64R, PDE3A:p.A98E, PDIA6:p.N56K, PDS5A:p.L1309F, PHLDA2:p.R28S, PIGR:p.V183G, PIK3CA:p.E545K, PIK3CD:p.C381R, PKD1:p.T938M, PLEKHM1:p.A895V, PLEKHN1:p.A600D, PLXND1:p.R367L, PMS2:p.K651R, PNMA3:p.E200G, POTEF:p.S112G, PRAMEF8:p.I448V, PRDM2:p.E278D, PRODH:p.L527V, PRPF31:p.R289W, PSME4:p.N495D, PTGR1:p.E40A, PTPRB:p.Q726H, RABGEF1:p.N207D, RAC1:p.P34R, RANBP17:p.M900I, REV3L:p.A30S, RFC3:p.I82N, RFC3:p.K296N, RIMBP3:p.Q1154R, RPL19:p.R151C, RPL5:p.R58fs, RPTN:p.M538I, RRAD:p.A278E, RYR1:p.D668Y, RYR2:p.L2023F, SAFB:p.G799V, SCRIB:p.G332V, SDK1:p.Y2146C, SEC16A:p.T443K, SEC31B:p.P905S, SELO:p.R565Q, SELP:p.A297T, SI:p.I1681K, SLC2A7:p.H268Q, SLC37A1:p.V528I, SLC38A1:p.G100R, SMARCA2:p.D1158A, SMARCA5:p.T156fs,

SMC3:p.E970Q, SMG1:p.P2696H, SNRNP200:p.A2129G, SPIN2B:p.M150V, ST6GALNAC1:p.S354N, STAMBPL1:p.Y143H, STARD8:p.G662A, STON1-GTF2A1L:p.N451S, SYMPK:p.A336G, TAS2R8:p.W98C, TCHH:p.W1016R, TET1:p.T1472S, TIAM1:p.G247M, TNS1:p.P183S, TOR1AIP2:p.G146R, TPRX1:p.S216P, TPRX1:p.S200P, TRMT61A:p.S244I, TSPAN4:p.L92V, TTF1:p.Q530R, UBE2M:p.G131D, UBR5:p.R2517S, UGT2B11:p.R447I, UMODL1:p.M559I, UNC93A:p.V445A, USP46:p.Q137R, VWA2:p.G317D, VWA7:p.V792G, WASH3P:p.L187V, WNT5B:p.K327E, WRN:p.E510D, XDH:p.P410S, ZAN:p.S755P, ZC3H11A:p.I777T, ZC3H7A:p.C575S, ZDHHC11:p.H250Q, ZFHX4:p.D3239N, ZKSCAN3:p.K200A, ZMYM4:p.T367I, ZNF174:p.P353T, ZNF322:p.Y353C, ZNF592:p.K324Q, ZNF592:p.P500T, ZNF782:p.C145F, ZNF799:p.C453R, ZNF804B:p.P644S, and ZNRF3:p.R889W.

70. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from THCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, HRAS:p.Q61R, NRAS:p.Q61K, OTUD4:p.T909I, HRAS:p.Q61K, NLRP6:p.E611G, AKT1:p.E17K, ANKMY1:p.N302I, ATP6V1A:p.L237P, CYP19A1:p.S113I, DCUN1D4:p.L275P, DGCR8:p.E518K, DLC1:p.S741T, DNAH10:p.C1853F, EIF1AX:p.G9D, FAM75D5:p.L222P, FCGRT:p.P40A, KRAS:p.Q61K, LMX1B:p.Q285del, MAS1L:p.R324G, MED15:p.S35I, MEGF6:p.Y393C, ODZ2:p.A1529V, OR5L1:p.R122H, OR6K6:p.F311L, OTX1:p.D315N, POTEE:p.S75G, SCN5A:p.D1978H, TOP2A:p.K1199E, and TSG101:p.K265R.

71. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from UCS; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R248Q, ZNF814:p.D404E, BTN2A3P:p.P3S, FBXW7:p.R465C, FRG1B:p.G65E, MUC4:p.H4205Q, NBPF10:p.V99F, PIK3CA:p.E545K, PIK3CA:p.H1047R, PPP2R1A:p.P179R, DDX11L2:p.*128Q, FBXW7:p.R479Q, FRG1B:p.K13N, FRG1B:p.L52S, HSD17B7P2:p.N175S, KRAS:p.G12V, LOC283788:p.S37G, TP53:p.R273H, TP53:p.S241Y, ADAMTS12:p.E359K, BCL2L11:p.L187fs, CDC27:p.L460fs, CHEK2:p.K373E, ESPNP:p.W122fs, FBXW7:p.R689W,

FBXW7:p.R505G, FBXW7:p.R465H, FCGBP:p.V4019M, FRG1B:p.I10T, FRG1B:p.D32V, FRG1B:p.R37K, KRAS:p.G12D, LOC100233156:p.R21C, LOC283788:p.I46M, LRP1B:p.L1392F, MAMLD1:p.Q572L, MST1P9:p.L319P, MUC4:p.A2390T, MUC4:p.G2172S, NBPF10:p.E3455K, PIK3CA:p.G106V, PODXL:p.28_30PSP>P, POTEC:p.R477Q, PPP2R1A:p.R183W, PPP2R1A:p.S219L, PTPN18:p.TG378del, RGPD3:p.N756D, RPL13AP20:p.G107R, SAMD4B:p.R477W, SMAP1:p.E169fs, TP53:p.H193R, TP53:p.H179R, TP53:p.R175H, TUBBP5:p.R119H, and U2AF1:p.S34F.

72. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from PAAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RBM14:p.AAAAAAA286del, KRAS:p.G12D, JMY:p.PPPPPPPPPPPP811del, RIOK1:p.D69del, LCE2A:p.SSGGCCGSSSGGCC47del, KRAS:p.G12V, C1QB:p.GPKGPMGPKGGPGAPGAP90del, ZFHX3:p.V777del, DBR1:p.541_542DD>D, AEBP1:p.K1133del, KRAS:p.G12R, RBM47:p.495_502AAAAAAAA>A, AP3S1:p.K41fs, MLL2:p.AEGPHLSPQPEELHLSPQ792del, RFX1:p.386_401GGGGGGGGGGGGGGSG>G, AXDND1:p.EQ991del, HERC2P3:p.A803V, RGPD3:p.N756D, FNDC1:p.D1180del, ANAPC1:p.T537A, IRS4:p.21_22AA>A, GIGYF2:p.Q1005del, NCOA3:p.Q1253fs, SIK3:p.950_951QQ>Q, GPR6:p.AAAAATAAGGPDTGEWGPPA36del, NBPF12:p.D1323fs, SHROOM4:p.1156_1157EE>E, ZMIZ2:p.VAAAAATATATATAT153del, DGKK:p.PAPP41del, LZTS1:p.RTQDLEGALRTKGLEL432del, CASQ2:p.395_396DD>D, DCP1B:p.251_252insH, ESPNP:p.296_317PPPPSFPPPPPPPPGTQLPPPPP>P, KBTBD6:p.T403K, NBPF16:p.D449fs, ANKRD36C:p.H438R, ESPN:p.PPPPPPSFPPPPPPPPGTQLPP430del, FCGBP:p.A2493V, KRAS:p.Q61H, NCOA3:p.Q1276del, OR2T2:p.C203fs, TMCC1:p.Q565L, BCKDHA:p.G129fs, ESPNP:p.H64fs, GNAS:p.R844H, NBPF14:p.R25C, OGFOD1:p.G477fs, RBM12:p.P693S, SLC38A10:p.1071_1072II>I, SORBS2:p.P866S, TP53:p.R248W, TP53:p.R175H, and UBAC1:p.E269del.

73. The pharmaceutical composition of any of paragraphs 30-72, wherein the composition comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least

17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 neoantigenic peptides.

74. The pharmaceutical composition of paragraph 73, wherein the composition comprises 15 to 20 neoantigenic peptides.

75. The pharmaceutical composition of paragraphs 73 or 74, further comprising at least one additional neoantigenic peptide which is specific for an individual patient's tumor.

76. The pharmaceutical composition of paragraph 75, wherein the patient specific neoantigenic peptide is selected by identifying sequence differences between the genome, exome, and/or transcriptome of the patient's tumor sample and the genome, exome, and/or transcriptome of a non-tumor sample.

77. The pharmaceutical composition of paragraph 75, wherein the samples are fresh or formalin-fixed paraffin embedded tumor tissues, freshly isolated cells, or circulating tumor cells.

78. The pharmaceutical composition of paragraph 75, wherein the sequence differences are determined by Next Generation Sequencing.

79. The pharmaceutical composition of any of paragraphs 30-78, wherein each neoantigenic peptide is from about 5 to about 50 amino acids in length.

80. The pharmaceutical composition of paragraph 79, wherein each neoantigenic peptide is between about 15 to about 35 amino acids in length; is about 15 amino acids or less in length; is about 8 and about 11 amino acids in length; or is 9 or 10 amino acids in length.

81. The pharmaceutical composition of paragraph 79 or 80, wherein each neoantigenic peptide binds major histocompatibility complex (MHC) class I.

82. The pharmaceutical composition of any one of paragraphs 30-81, wherein each neoantigenic peptide binds to MHC class I with a binding affinity of less than about 500 nM, or optionally each neoantigenic peptide binds to HLA-A, -B or –C with a K_D of less than 500 nM.

83. The pharmaceutical composition of paragraph 79, wherein each neoantigenic peptide is about 30 amino acids or less in length; is between about 6 and about 25 amino acids in length; is between about 15 and about 24 amino acids in length; or is between about 9 and about 15 amino acids in length.

84. The pharmaceutical composition of paragraph 79, 82 or 83, wherein each neoantigenic peptide binds major histocompatibility complex (MHC) class II.

85. The pharmaceutical composition of paragraph 84, wherein each neoantigenic peptide binds to MHC class I with a binding affinity of less than about 500 nM, or optionally each neoantigenic peptide binds to HLA-A, -B or –C with a K_D of less than 500 nM.

86. The pharmaceutical composition of any of paragraphs 30-85, wherein at least one neoantigenic peptide further comprises flanking amino acids.

87. The pharmaceutical composition of paragraph 86, wherein the flanking amino acids are not native flanking amino acids.

88. The pharmaceutical composition of any of paragraphs 30-87, which at least one neoantigenic peptide is linked to at least a second neoantigenic peptide.

89. The pharmaceutical composition of paragraph 88, wherein peptides are linked using a poly-glycine or poly-serine linker.

90. The pharmaceutical composition of paragraph 88 or 89, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 1000 nM.

91. The pharmaceutical composition of any of paragraphs 88-90, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 500 nM.

92. The pharmaceutical composition of any of paragraphs 88-91, wherein both of the neoepitopes bind to human leukocyte antigen (HLA) -A, -B, -C, -DP, -DQ, or -DR.

93. The pharmaceutical composition of any of paragraphs 88-92, wherein the isolated neoantigenic peptide and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide and the second neoantigenic peptide binds a class II HLA.

94. The pharmaceutical composition of any of paragraphs 88-92, wherein the isolated neoantigenic peptide binds a class II HLA and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide binds a class I HLA and the second neoantigenic peptide binds a class II HLA.

95. The pharmaceutical composition of any of paragraphs 30-94, wherein at least one neoantigenic peptide further comprises modifications which increase in vivo half-life, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation.

96. The pharmaceutical composition of paragraph 95, wherein the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids.

97. The pharmaceutical composition of paragraph 95, wherein the cells that are targeted are antigen presenting cells.

98. The pharmaceutical composition of paragraph 97, wherein the antigen presenting cells are dendritic cells.

99. The pharmaceutical composition of paragraph 98, wherein the dendritic cells are targeted using DEC205, XCR1, CD197, CD80, CD86, CD123, CD209, CD273, CD283, CD289, CD184, CD85h, CD85j, CD85k, CD85d, CD85g, CD85a, CD141, CD11c, CD83, TSLP receptor, or CD1a marker.

100. The pharmaceutical composition of paragraph 99, wherein the dendritic cells are targeted using the CD141, DEC205, or XCR1 marker.

101. The pharmaceutical composition of any of paragraphs 30-100, which is an immunogenic or vaccine composition.

102. The pharmaceutical composition of paragraph 101, further comprising an immunomodulator or adjuvant.

103. The pharmaceutical composition of paragraph 102, wherein the immunodulator or adjuvant is selected from the group consisting of Poly(I:C), Poly-ICLC, STING agonist, 1018 ISS, aluminium salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312 VG, Montanide ISA 206 VG, Montanide ISA 50 V2, Montanide ISA 51 VG, OK-432, OM-174, OM-197-MP-EC, ISA-TLR2 agonist, ONTAK, PepTel®. vector system, PLG microparticles, resiquimod, SRL172, virosomes and other virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Pam3CSK4, acrylic or methacrylic polymers, copolymers of maleic anhydride, and QS21 stimulon.

104. An isolated polynucleotide encoding the isolated neoantigenic peptide of any of paragraphs 1-24.

105. The isolated polynucleotide of paragraph 104, which is RNA.

106. The isolated polynucleotide of paragraph 105, wherein the RNA is modified to increase stability, increase cellular targeting, increase translation efficiency, adjuvanticity, cytosol accessibility, and/or decrease cytotoxicity.

107. The isolated polynucleotide of paragraph 106, wherein the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, codon optimization, increased GC-content, incorporation of modified nucleosides, incorporation of 5'-cap or cap analog, and/or incorporation of an unmasked poly-A sequence.

108. A cell comprising the polynucleotide of any of paragraphs 104-107.

109. A vector comprising the polynucleotide of any one of paragraphs 104-107.

110. The vector of paragraph 110, in which the polynucleotide is operably linked to a promoter.

111. The vector of paragraphs 109 or 110, which is a plasmid, phage, transposon, cosmid, virus, or virion.

112. The vector of paragraph 111, which is an adeno-associated virus, herpesvirus, lentivirus, or pseudotypes thereof.

113. An in vivo delivery system comprising the isolated polynucleotide of any of paragraphs 104-107.

114. The delivery system of paragraph 113, wherein the delivery system includes spherical nucleic acids, viruses, virus-like particles, plasmids, bacterial plasmids, or nanoparticles.

115. A cell comprising the vector or delivery system of any of paragraphs 109-114.

116. The cell of paragraph 115, which is an antigen presenting cell.

117. The cell of paragraph 116, which is a dendritic cell.

118. The cell of paragraph 117, which is an immature dendritic cell.

119. A composition comprising at least one polynucleotide of any of paragraphs 104-107.

120. The composition of paragraph 119, wherein the composition comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least

20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 of the isolated polynucleotides.

121. The composition of paragraph 120, wherein the composition comprises between about 2 and about 20 polynucleotides.

122. The composition of any one of paragraphs 119-121, wherein the composition further comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 26, at least 27, at least 28, at least 29, or at least 30 additional neoantigenic polynucleotides encoding for additional neoantigenic peptides.

123. The composition of paragraph 122, wherein the composition comprises between about 4 and about 20 additional neoantigenic polynucleotides.

124. The composition of paragraph 122, wherein the isolated polynucleotides and the additional neoantigenic polynucleotides are linked.

125. The composition of paragraph 124, wherein the polynucleotides are linked using nucleic acids that encode a poly-glycine or poly-serine linker.

126. The composition of any of paragraphs 122-125, wherein at least one of the additional neoantigenic peptide is specific for an individual patient's tumor.

127. The composition of paragraph 126, wherein the patient specific neoantigenic peptide is selected by identifying sequence differences between the genome, exome, and/or transcriptome of the patient's tumor sample and the genome, exome, and/or transcriptome of a non-tumor sample.

128. The composition of paragraph 127, wherein the samples are fresh or formalin-fixed paraffin embedded tumor tissues, freshly isolated cells, or circulating tumor cells.

129. The composition of paragraphs 127 or 128, wherein the sequence differences are determined by Next Generation Sequencing.

130. A T cell receptor (TCR) capable of binding at least one neoantigenic peptide listed in any of paragraphs 1-27, optionally a neoantigenic peptide comprising FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

131. The TCR of paragraph 130, which is capable of binding the isolated neoantigenic peptide in the context of MHC class I or class II.

132. A chimeric antigen receptor comprising: (i) a T cell activation molecule; (ii) a transmembrane region; and (iii) an antigen recognition moiety capable of binding an isolated neoantigenic peptide of any one of paragraphs 1-27.

133. The chimeric antigen receptor of paragraph 132, wherein CD3-zeta is the T cell activation molecule.

134. The chimeric antigen receptor of paragraph 132 or 133, further comprising at least one costimulatory signaling domain.

135. The chimeric antigen receptor of any of paragraphs 132-134, wherein the signaling domain is CD28, 4-1BB, ICOS, OX40, ITAM, or Fc epsilon RI-gamma.

136. The chimeric antigen receptor of any of paragraphs 132-135, wherein the antigen recognition moiety is capable of binding the isolated neoantigenic peptide in the context of MHC class I or class II.

137. The chimeric antigen receptor of any of paragraphs 132-136, comprising the CD3-zeta, CD28, CTLA-4, ICOS, BTLA, KIR, LAG3, CD137, OX40, CD27, CD40L, Tim-3, A2aR, or PD-1 transmembrane region.

138. The chimeric antigen receptor of any of paragraphs 132-137, wherein the tumor-specific epitope is located in the extracellular domain of a tumor associated polypeptide, optionally the tumor-specific epitope comprises FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

139. A T cell comprising the T cell receptor or chimeric antigen receptor of any of paragraphs 130-138.

140. The T cell of paragraph 139, which is a helper or cytotoxic T cell.

141. A nucleic acid comprising a promoter operably linked to a polynucleotide encoding the T cell receptor of paragraph 130 or 131.

142. The nucleic acid of paragraph 141, wherein the TCR is capable of binding the at least one neoantigenic peptide in the context of major histocompatibility complex (MHC) class I or class II.

143. A nucleic acid comprising a promoter operably linked to a polynucleotide encoding the chimeric antigen receptor of any of paragraphs 132-138.

144. The nucleic acid of paragraph 143, wherein the antigen recognition moiety is capable of binding the at least one neoantigenic peptide in the context of major histocompatibility complex (MHC) class I or class II.

145. The nucleic acid of paragraphs 143 or 144, wherein the tumor-specific epitope is located in the extracellular domain of a tumor associated polypeptide.

146. The nucleic acid of any of paragraphs 143-145, comprising the CD3-zeta, CD28, CTLA-4, ICOS, BTLA, KIR, LAG3, CD137, OX40, CD27, CD40L, Tim-3, A2aR, or PD-1 transmembrane region.

147. An antibody capable of binding at least one neoantigenic peptide listed in Tables 1-9.

148. A modified cell transfected or transduced with the nucleic acid of any one of paragraphs 141-146.

149. The modified cell of paragraph 148, wherein the modified cell is a T cell, tumor infiltrating lymphocyte, NK-T cell, TCR-expressing cell, CD4+ T cell, CD8+ T cell, or NK cell.

150. A composition comprising the T cell receptor or chimeric antigen receptor of any of paragraphs 130-138.

151. A composition comprising autologous patient T cells containing the T cell receptor or chimeric antigen receptor of any of paragraphs 130-138.

152. The composition of paragraph 150 or 151, further comprising an immune checkpoint inhibitor.

153. The composition of paragraph 150 of 151, further comprising at least two immune checkpoint inhibitors.

154. The composition of paragraph 152 or 153, wherein the immune checkpoint inhibitor inhibits a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

155. The composition of paragraph 154, wherein the immune checkpoint inhibitor interacts with a ligand of a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

156. The composition of any of paragraphs 119-129 or 150-156, further comprising an immune modulator or adjuvant.

157. The composition of paragraph 156, wherein the immune modulator is a co-stimulatory ligand, a TNF ligand, an Ig superfamily ligand, CD28, CD80, CD86, ICOS, CD40L, OX40, CD27, GITR, CD30, DR3, CD69, or 4-1BB.

158. The composition of paragraph 156, wherein the immune modulator is at least one cancer cell or cancer cell extract.

159. The composition of paragraph 158, wherein the cancer cell is autologous to the subject in need of the composition.

160. The composition of paragraph 159, wherein the cancer cell has undergone lysis or been exposed to UV radiation.

161. The composition of paragraph 156, wherein the composition further comprises an adjuvant.

162. The composition of paragraph 161, wherein the adjuvant is selected from the group consisting of: Poly(I:C), Poly-ICLC, STING agonist, 1018 ISS, aluminium salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312 VG, Montanide ISA 206 VG, Montanide ISA 50 V2, Montanide ISA 51 VG, OK-432, OM-174, OM-197-MP-EC, ISA-TLR2 agonist, ONTAK, PepTel®. vector system, PLG microparticles, resiquimod, SRL172, virosomes and other virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Pam3CSK4, acrylic or methacrylic polymers, copolymers of maleic anhydride, and QS21 stimulon.

163. The composition of paragraph 161 or 162, wherein the adjuvant induces a humoral immune response when administered to a subject.

164. The composition of paragraph 162, wherein the adjuvant induces a T helper cell type 1 response when administered to a subject.

165. An in vivo delivery system comprising the pharmaceutical composition of any of paragraphs 30-103.

166. The delivery system of paragraph 165, wherein the delivery system includes cell-penetrating peptides, nanoparticulate encapsulation, virus like particles, or liposomes.

167. The delivery system of paragraph 166, wherein the cell-penetrating peptide is TAT peptide, herpes simplex virus VP22, transportan, or Antp.

168. A cell comprising the isolated neoantigenic peptide of any of paragraphs 1-29.

169. The cell of paragraph 168, which is an antigen presenting cell.

170. The cell of paragraph 169, which is a dendritic cell.

171. A method of treating cancer or initiating, enhancing, or prolonging an anti-tumor responses in a subject in need thereof comprising administering to the subject the peptide, polynucleotide, vector, composition, antibody, or cells of any of paragraphs 1-164.

172. A method of prophylactic cancer treatment comprising:

(a) selecting a cancer drug for a patient in need thereof, the drug selected from the group consisting of ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitors, and antiestrogen therapy; and

(b) administering prophylactically to the subject, a pharmaceutical composition according to any of paragraphs 30-103 wherein the at least one neoantigenic peptide is derived from drug resistant mutations associated with the selected cancer drug.

173. A method of treating or preventing a tumor in a population of subjects in need thereof, comprising administering to a subject an agent comprising an extracellular ligand-binding domain recognizing a tumor-specific neoepitope comprising a tumor-specific mutation having an incidence of at least 1% of subjects in the population.

174. The method according to any of paragraphs 171-173, wherein the tumor-specific mutation comprises a mutation listed for any population in Table 9.

175. The method according to any of paragraphs 171-173, wherein the tumor-specific mutation is within a gene containing an extracellular domain.

176. The method according to paragraph 175, wherein the tumor-specific mutation comprises FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

177. The method according to paragraph 176, wherein the tumor-specific mutation is within the extracellular domain.

178. The method according to paragraph 177, wherein the tumor-specific mutation comprises FGFR3 S249C or ERBB3 V104M.

179. The method of any of paragraph 171-178, wherein the subject is a human.

180. The method of paragraph 179, wherein the subject has cancer.

181. The method of paragraph 180, wherein the cancer is selected from the group consisting of urogenital, gynecological, lung, gastrointestinal , head and neck cancer, malignant glioblastoma, malignant mesothelioma, non-metastatic or metastatic breast cancer, malignant melanoma, Merkel Cell Carcinoma or bone and soft tissue sarcomas, haematologic neoplasias, multiple myeloma, acute myelogenous leukemia, chronic myelogenous leukemia, myelodysplastic syndrome and acute lymphoblastic leukemia, non-small cell lung cancer (NSCLC), breast cancer, metastatic colorectal cancers, hormone sensitive or hormone refractory prostate cancer, colorectal cancer, ovarian cancer, hepatocellular cancer, renal cell cancer, pancreatic cancer, gastric cancer, oesophageal cancers, hepatocellular cancers, cholangiocellular cancers, head and neck squamous cell cancer soft tissue sarcoma, and small cell lung cancer.

182. The method of any of paragraphs 171-181, wherein the subject has undergone surgical removal of the tumor.

183. The method of any of paragraphs 171-182, wherein the peptide, polynucleotide, vector, composition, or cells is administered via intravenous, intraperitoneal, intratumoral, intradermal, or subcutaneous administration.

184. The method of paragraph 183, wherein the peptide, polynucleotide, vector, composition, or cells is administered into an anatomic site that drains into a lymph node basin.

185. The method of paragraph 184, wherein administration is into multiple lymph node basins.

186. The method of any one of paragraphs 183-185, wherein administration is by a subcutaneous or intradermal route.

187. The method of paragraph 183, wherein peptide is administered.

188. The method of paragraph 187, wherein administration is intratumorally.

189. The method of paragraph 183, wherein polynucleotide, optionally RNA, is administered.

190. The method of paragraph 189, wherein the polynucleotide is administered intravenously.

191. The method of paragraph 183, wherein the cell is a T cell or dendritic cell.

192. The method of paragraph 191, wherein the peptide or polynucleotide comprises an antigen presenting cell targeting moiety.

193. The method of any of paragraphs 171-192, further comprising administering at least one immune checkpoint inhibitor to the subject.

194. The method of paragraph 193, wherein the checkpoint inhibitor is a biologic therapeutic or a small molecule.

195. The method of paragraph 193 or 194, wherein the checkpoint inhibitor is selected from the group consisting of a monoclonal antibody, a humanized antibody, a fully human antibody and a fusion protein or a combination thereof.

196. The method of any of paragraphs 193-195, wherein the checkpoint inhibitor inhibits a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

197. The method of any of paragraphs 193-196, wherein the checkpoint inhibitor interacts with a ligand of a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

198. The method of any of paragraphs 193-197, wherein two or more checkpoint inhibitors are administered.

199. The method of paragraph 198, wherein the checkpoint inhibitors are: (i) ipilimumab or tremelimumab, and (ii) nivolumab.

200. The method of any of paragraphs 193-199, wherein the checkpoint inhibitor and the composition are administered simultaneously or sequentially in any order.

201. The method of paragraph 200, wherein the peptide, polynucleotide, vector, composition, or cells is administered prior to the checkpoint inhibitor.

202. The method of paragraph 200, wherein the peptide, polynucleotide, vector, composition, or cells is administered after the checkpoint inhibitor.

203. The method of paragraph 200, wherein administration of the checkpoint inhibitor is continued throughout neoantigen peptide, polynucleotide, vector, composition, or cell therapy.

204. The method of any of paragraphs 193-203, wherein the neoantigen peptide, polynucleotide, vector, composition, or cell therapy is administered to subjects that only partially respond or do not respond to checkpoint inhibitor therapy.

205. The method of any one of paragraphs 193-204, wherein the checkpoint inhibitor is administered intravenously or subcutaneously.

206. The method of paragraph 205, wherein the checkpoint inhibitor is administered subcutaneously within about 2 cm of the site of administration of the composition.

207. The method of paragraph 206, wherein the composition is administered into the same draining lymph node as the checkpoint inhibitor.

208. The method of any of paragraphs 171-207, further comprising administering an additional therapeutic agent to the subject either prior to, simultaneously with, or after treatment with the peptide, polynucleotide, vector, composition, or cells.

209. The method of paragraph 208, wherein the additional agent is a chemotherapeutic agent, an immunomodulatory drug, an immune metabolism modifying drug, a targeted therapy, radiation an anti-angiogenesis agent, or an agent that reduces immune-suppression.

210. The method of paragraph 209, wherein the chemotherapeutic agent is an alkylating agent, a topoisomerase inhibitor, an anti-metabolite, or an anti-mitotic agent.

211. The method of paragraph 208, wherein the additional agent is an anti-glucocorticoid induced tumor necrosis factor family receptor (GITR) agonistic antibody or antibody fragment, ibrutinib, docetaxeol, cisplatin, or cyclophosphamide.

212. The method of any of paragraphs 171-211, which elicits a CD4+ T cell immune response.

213. The method of any of paragraphs 171-212, which elicits a CD4+ T cell immune response and a CD8+ T cell immune response.

214. A method for stimulating an immune response in a subject, comprising administering an effective amount of modified cells or composition of any of paragraphs 30-103, 108, 115-129, 139, 140, 148-164, and 168-170.

215. The method of paragraph 214, wherein the immune response is cytotoxic and/or humoral immune response.

216. The method of paragraph 214, wherein the method stimulates a T cell-mediated immune response in a subject.

217. The method of paragraph 216, wherein the T cell-mediated immune response is directed against a target cell.

218. The method of paragraph 217, wherein the target cell is a tumor cell.

219. The method of any of paragraphs 214-218, wherein the modified cells are transfected or transduced in vivo.

220. The method of any of paragraphs 214-219, wherein the modified cells are transfected or transduced ex vivo.

221. The method of any of paragraphs 214-220, wherein the modified cells are autologous patient T cells.

222. The method of paragraph 221, wherein the autologous patient T cells are obtained from a patient that has received a neoantigen peptide or nucleic acid vaccine.

223. The method of paragraph 222, wherein the neoantigen peptide or nucleic acid vaccine comprises at least one personalized neoantigen.

224. The method of paragraph 223, wherein the neoantigen peptide or nucleic acid vaccine comprises at least one additional neoantigenic peptide listed in Tables 1-9.

225. The method of paragraph 224, wherein the patient received a chemotherapeutic agent, an immunomodulatory drug, an immune metabolism modifying drug, targeted therapy or radiation prior to and/or during receipt of the neoantigen peptide or nucleic acid vaccine.

226. The method of any of paragraphs 222-225, wherein the patient receives treatment with at least one checkpoint inhibitor.

227. The method of any of paragraphs 222-226, wherein the autologous T cells are obtained from a patient that has already received at least one round of T cell therapy containing a neoantigen.

228. The method of any of paragraphs 222-227, wherein the method further comprises adoptive T cell therapy.

229. The method of paragraph 228, wherein the adoptive T cell therapy comprises autologous T-cells.

230. The method of paragraph 229, wherein the autologous T-cells are targeted against tumor antigens.

231. The method of paragraph 228 or 229 wherein the adoptive T cell therapy further comprises allogenic T-cells.

232. The method of paragraph 231, wherein the allogenic T-cells are targeted against tumor antigens.

233. The method of any of paragraphs 227-231, wherein the adoptive T cell therapy is administered before the checkpoint inhibitor.

234. A method for evaluating the efficacy of any of paragraphs 171-213, comprising: (i) measuring the number or concentration of target cells in a first sample obtained from the subject before administering the modified cell, (ii) measuring the number concentration of target cells in a second sample obtained from the subject after administration of the modified cell, and (iii) determining an increase or decrease of the number or concentration of target cells in the second sample compared to the number or concentration of target cells in the first sample.

235. The method of paragraph 234, wherein treatment efficacy is determined by monitoring a clinical outcome; an increase, enhancement or prolongation of anti-tumor activity by T cells; an increase in the number of anti-tumor T cells or activated T cells as compared with the number prior to treatment; B cell activity; CD4 T cell activity; or a combination thereof.

236. The method of paragraph 235, wherein treatment efficacy is determined by monitoring a biomarker.

237. The method of paragraph 236, wherein the biomarker is selected from the group consisting of CEA, Her-2/neu, bladder tumor antigen, thyroglobulin, alpha-fetoprotein, PSA, CA 125, CA19.9, CA 15.3, leptin, prolactin, osteopontin, IGF-II, CD98, fascin, sPIgR, 14-3-3 eta, troponin I, and b-type natriuretic peptide.

238. The method of paragraph 235, wherein clinical outcome is selected from the group consisting of tumor regression; tumor shrinkage; tumor necrosis; anti-tumor response by the immune system; tumor expansion, recurrence or spread; or a combination thereof.

239. The method of paragraph 235, wherein the treatment effect is predicted by presence of T cells or by presence of a gene signature indicating T cell inflammation or a combination thereof.

240. A kit comprising a neoantigen therapeutic of any of paragraphs 1-164.

[0051] Accordingly, it is an object of the invention not to encompass within the invention any previously known product, process of making the product, or method of using the product such that Applicants reserve the right and hereby disclose a disclaimer of any previously known product, process, or method. It is further noted that the invention does not intend to encompass within the scope of the invention any product, process, or making of the product or method of using the product, which does not meet the written description and enablement requirements of

the USPTO (35 U.S.C. §112, first paragraph) or the EPO (Article 83 of the EPC), such that Applicants reserve the right and hereby disclose a disclaimer of any previously described product, process of making the product, or method of using the product. It may be advantageous in the practice of the invention to be in compliance with Art. 53(c) EPC and Rule 28(b) and (c) EPC. All rights to explicitly disclaim any embodiments that are the subject of any granted patent(s) of applicant in the lineage of this application or in any other lineage or in any prior filed application of any third party is explicitly reserved Nothing herein is to be construed as a promise.

[0052] It is noted that in this disclosure and particularly in the claims and/or paragraphs, terms such as "comprises", "comprised", "comprising" and the like can have the meaning attributed to it in U.S. Patent law; e.g., they can mean "includes", "included", "including", and the like; and that terms such as "consisting essentially of" and "consists essentially of" have the meaning ascribed to them in U.S. Patent law, e.g., they allow for elements not explicitly recited, but exclude elements that are found in the prior art or that affect a basic or novel characteristic of the invention. Nothing herein is intended as a promise.

[0053] These and other embodiments are disclosed or are obvious from and encompassed by, the following Detailed Description.

DETAILED DESCRIPTION OF THE INVENTION

[0054] To facilitate an understanding of the present invention, a number of terms and phrases are defined herein:

[0055] Unless specifically stated or obvious from context, as used herein, the term "about" is understood as within a range of normal tolerance in the art, for example within 2 standard deviations of the mean. About can be understood as within 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, or 0.01% of the stated value. Unless otherwise clear from context, all numerical values provided herein are modified by the term about.

[0056] Unless specifically stated or obvious from context, as used herein, the term "or" is understood to be inclusive. Unless specifically stated or obvious from context, as used herein, the terms "a," "an," and "the" are understood to be singular or plural.

[0057] All gene name symbols refer to the gene as commonly known in the art. Gene symbols may be those refered to by the HUGO Gene Nomenclature Committee (HGNC). Any reference to the gene symbol is a reference made to the entire gene or variants of the gene. The HUGO Gene Nomenclature Committee is responsible for providing human gene naming guidelines and approving new, unique human gene names and symbols. All human gene names and symbols can be searched at www.genenames.org, the HGNC website, and the guidelines for their formation are available there (www.genenames.org/guidelines).

[0058] By "agent" is meant any small molecule chemical compound, antibody, nucleic acid molecule, or polypeptide, or fragments thereof.

[0059] By "ameliorate" is meant decrease, suppress, attenuate, diminish, arrest, or stabilize the development or progression of a disease (e.g., a neoplasia, tumor, etc.).

[0060] By "alteration" is meant a change (increase or decrease) in the expression levels oractivity of a gene or polypeptide as detected by standard art known methods such as those described herein. As used herein, an alteration includes a 10% change in expression levels, preferably a 25% change, more preferably a 40% change, and most preferably a 50% or greater change in expression levels.

[0061] By "analog" is meant a molecule that is not identical, but has analogous functional or structural features. For example, a tumor specific neo-antigen polypeptide analog retains the biological activity of a corresponding naturally-occurring tumor specific neo-antigen polypeptide, while having certain biochemical modifications that enhance the analog's function relative to a naturally-occurring polypeptide. Such biochemical modifications could increase the analog's protease resistance, membrane permeability, or half-life, without altering, for example, ligand binding. An analog may include an unnatural amino acid.

[0062] "Combination therapy" is intended to embrace administration of therapeutic agents (e.g. neoantigenic peptides described herein) in a sequential manner, that is, wherein each therapeutic agent is administered at a different time, as well as administration of these therapeutic agents, or at least two of the therapeutic agents, in a substantially simultaneous manner. Substantially simultaneous administration can be accomplished, for example, by administering to the subject a single capsule having a fixed ratio of each therapeutic agent or in multiple, single capsules for each of the therapeutic agents. For example, one combination of the present invention may comprise a pooled sample of neoantigenic peptides administered at the

same or different times, or they can be formulated as a single, co-formulated pharmaceutical composition comprising the peptides. As another example, a combination of the present invention (e.g., a pooled sample of tumor specific neoantigens) may be formulated as separate pharmaceutical compositions that can be administered at the same or different time. As used herein, the term "simultaneously" is meant to refer to administration of one or more agents at the same time. For example, in certain embodiments, the neoantigenic peptides are administered simultaneously. Simultaneously includes administration contemporaneously, that is during the same period of time. In certain embodiments, the one or more agents are administered simultaneously in the same hour, or simultaneously in the same day. Sequential or substantially simultaneous administration of each therapeutic agent can be effected by any appropriate route including, but not limited to, oral routes, intravenous routes, sub-cutaneous routes, intramuscular routes, direct absorption through mucous membrane tissues (e.g., nasal, mouth, vaginal, and rectal), and ocular routes (e.g., intravitreal, intraocular, etc.). The therapeutic agents can be administered by the same route or by different routes. For example, one component of a particular combination may be administered by intravenous injection while the other component(s) of the combination may be administered orally. The components may be administered in any therapeutically effective sequence. The phrase "combination" embraces groups of compounds or non-drug therapies useful as part of a combination therapy.

[0063] The term "neoantigen" or "neoantigenic" means a class of tumor antigens that arises from a tumor-specific mutation(s) which alters the amino acid sequence of genome encoded proteins.

[0064] By "neoplasia" is meant any disease that is caused by or results in inappropriately high levels of cell division, inappropriately low levels of apoptosis, or both. For example, cancer is an example of a neoplasia. Examples of cancers include, without limitation, leukemia (e.g., acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic myelocytic leukemia, chronic lymphocytic leukemia), polycythemia vera, lymphoma (e.g., Hodgkin's disease, non-Hodgkin's disease), Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors such as sarcomas and carcinomas (e.g., fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma,

lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, nile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, uterine cancer, testicular cancer, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodenroglioma, schwannoma, meningioma, melanoma, neuroblastoma, and retinoblastoma). Lymphoproliferative disorders are also considered to be proliferative diseases.

[0065] The term "vaccine" is meant to refer in the present context to a pooled sample of tumor-specific neoantigenic peptides, for example at least two, at least three, at least four, at least five, or more neoantigenic peptides. A "vaccine" is to be understood as meaning a composition for generating immunity for the prophylaxis and/or treatment of diseases (e.g., neoplasia/tumor). Accordingly, vaccines are medicaments which comprise antigens and are intended to be used in humans or animals for generating specific defense and protective substance by vaccination. A "vaccine composition " can include a pharmaceutically acceptable excipient, carrier or diluent.

[0066] The term "pharmaceutically acceptable" refers to approved or approvable by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, including humans.

[0067] A "pharmaceutically acceptable excipient, carrier or diluent" refers to an excipient, carrier or diluent that can be administered to a subject, together with an agent, and which does not destroy the pharmacological activity thereof and is nontoxic when administered in doses sufficient to deliver a therapeutic amount of the agent.

[0068] A "pharmaceutically acceptable salt" of pooled tumor specific neoantigens as recited herein may be an acid or base salt that is generally considered in the art to be suitable for use in contact with the tissues of human beings or animals without excessive toxicity, irritation, allergic response, or other problem or complication. Such salts include mineral and organic acid salts of basic residues such as amines, as well as alkali or organic salts of acidic residues such as carboxylic acids. Specific pharmaceutical salts include, but are not limited to, salts of acids such

as hydrochloric, phosphoric, hydrobromic, malic, glycolic, fumaric, sulfuric, sulfamic, sulfanilic, formic, toluenesulfonic, methanesulfonic, benzene sulfonic, ethane disulfonic, 2-hydroxyethylsulfonic, nitric, benzoic, 2-acetoxybenzoic, citric, tartaric, lactic, stearic, salicylic, glutamic, ascorbic, pamoic, succinic, fumaric, maleic, propionic, hydroxymaleic, hydroiodic, phenylacetic, alkanoic such as acetic, HOOC-(CH2)n-COOH where n is 0-4, and the like. Similarly, pharmaceutically acceptable cations include, but are not limited to sodium, potassium, calcium, aluminum, lithium and ammonium. Those of ordinary skill in the art will recognize from this disclosure and the knowledge in the art that further pharmaceutically acceptable salts for the pooled tumor specific neoantigens provided herein, including those listed by Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Company, Easton, PA, p. 1418 (1985). In general, a pharmaceutically acceptable acid or base salt can be synthesized from a parent compound that contains a basic or acidic moiety by any conventional chemical method. Briefly, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in an appropriate solvent.

[0069] By a "polypeptide" or "peptide" is meant a polypeptide that has been separated from components that naturally accompany it. Typically, the polypeptide is isolated when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, a polypeptide. An isolated polypeptide may be obtained, for example, by extraction from a natural source, by expression of a recombinant nucleic acid encoding such a polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method, for example, column chromatography, polyacrylamide gel electrophoresis, or by HPLC analysis.

[0070] As used herein, the terms "prevent," "preventing," "prevention," "prophylactic treatment," and the like, refer to reducing the probability of developing a disease or condition in a subject, who does not have, but is at risk of or susceptible to developing a disease or condition.

[0071] The term "prime/ boost" or "prime/ boost dosing regimen" is meant to refer to the successive administrations of a vaccine or immunogenic or immunological compositions. The priming administration (priming) is the administration of a first vaccine or immunogenic or immunological composition type and may comprise one, two or more administrations. The boost administration is the second administration of a vaccine or immunogenic or immunological

composition type and may comprise one, two or more administrations, and, for instance, may comprise or consist essentially of annual administrations. In certain embodiments, administration of the neoplasia vaccine or immunogenic composition is in a prime/ boost dosing regimen.

[0072] Ranges provided herein are understood to be shorthand for all of the values within the range. For example, a range of 1 to 50 is understood to include any number, combination of numbers, or sub-range from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50, as well as all intervening decimal values between the aforementioned integers such as, for example, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. With respect to sub-ranges, "nested sub-ranges" that extend from either end point of the range are specifically contemplated. For example, a nested sub-range of an exemplary range of 1 to 50 may comprise 1 to 10, 1 to 20, 1 to 30, and 1 to 40 in one direction, or 50 to 40, 50 to 30, 50 to 20, and 50 to 10 in the other direction.

[0073] A "receptor" is to be understood as meaning a biological molecule or a molecule grouping capable of binding a ligand. A receptor may serve, to transmit information in a cell, a cell formation or an organism. The receptor comprises at least one receptor unit and frequently contains two or more receptor units, where each receptor unit may consist of a protein molecule, in particular a glycoprotein molecule. The receptor has a structure that complements the structure of a ligand and may complex the ligand as a binding partner. Signaling information may be transmitted by conformational changes of the receptor following binding with the ligand on the surface of a cell. According to the invention, a receptor may refer to particular proteins of MHC classes I and II capable of forming a receptor/ligand complex with a ligand, in particular a peptide or peptide fragment of suitable length.

[0074] The term "subject" refers to an animal which is the object of treatment, observation, or experiment. By way of example only, a subject includes, but is not limited to, a mammal, including, but not limited to, a human or a non-human mammal, such as a non-human primate, bovine, equine, canine, ovine, or feline.

[0075] The terms "treat," "treated," "treating," "treatment," and the like are meant to refer to reducing or ameliorating a disorder and/or symptoms associated therewith (e.g., a neoplasia or tumor). "Treating" may refer to administration of the therapy to a subject after the onset, or suspected onset, of a cancer. "Treating" includes the concepts of "alleviating", which refers to

lessening the frequency of occurrence or recurrence, or the severity, of any symptoms or other ill effects related to a cancer and/or the side effects associated with cancer therapy. The term "treating" also encompasses the concept of "managing" which refers to reducing the severity of a particular disease or disorder in a patient or delaying its recurrence, e.g., lengthening the period of remission in a patient who had suffered from the disease. It is appreciated that, although not precluded, treating a disorder or condition does not require that the disorder, condition, or symptoms associated therewith be completely eliminated.

[0076] The term "therapeutic effect" refers to some extent of relief of one or more of the symptoms of a disorder (e.g., a neoplasia or tumor) or its associated pathology. "Therapeutically effective amount" as used herein refers to an amount of an agent which is effective, upon single or multiple dose administration to the cell or subject, in prolonging the survivability of the patient with such a disorder, reducing one or more signs or symptoms of the disorder, preventing or delaying, and the like beyond that expected in the absence of such treatment. "Therapeutically effective amount" is intended to qualify the amount required to achieve a therapeutic effect. A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the "therapeutically effective amount" (e.g., ED50) of the pharmaceutical composition required. For example, the physician or veterinarian could start doses of the compounds of the invention employed in a pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved.

[0077] The terms "spacer" or "linker" as used in reference to a fusion protein refers to a peptide that joins the proteins comprising a fusion protein. Generally, a spacer has no specific biological activity other than to join or to preserve some minimum distance or other spatial relationship between the proteins or RNA sequences. However, in certain embodiments, the constituent amino acids of a spacer may be selected to influence some property of the molecule such as the folding, net charge, or hydrophobicity of the molecule.

[0078] Suitable linkers for use in an embodiment of the present invention are well known to those of skill in the art and include, but are not limited to, straight or branched-chain carbon linkers, heterocyclic carbon linkers, or peptide linkers. The linker is used to separate two neoantigenic peptides by a distance sufficient to ensure that, in a preferred embodiment, each neoantigenic peptide properly folds. Preferred peptide linker sequences adopt a flexible extended

conformation and do not exhibit a propensity for developing an ordered secondary structure. Typical amino acids in flexible protein regions include Gly, Asn and Ser. Virtually any permutation of amino acid sequences containing Gly, Asn and Ser would be expected to satisfy the above criteria for a linker sequence. Other near neutral amino acids, such as Thr and Ala, also may be used in the linker sequence. Still other amino acid sequences that may be used as linkers are disclosed in Maratea et al. (1985), Gene 40: 39-46; Murphy et al. (1986) Proc. Nat'l. Acad. Sci. USA 83: 8258-62; U.S. Pat. No. 4,935,233; and U.S. Pat. No. 4,751,180.

[0079] The recitation of a listing of chemical groups in any definition of a variable herein includes definitions of that variable as any single group or combination of listed groups. The recitation of an embodiment for a variable or aspect herein includes that embodiment as any single embodiment or in combination with any other embodiments or portions thereof.

[0080] Any compositions or methods provided herein can be combined with one or more of any of the other compositions and methods provided herein.

[0081] The therapy disclosed herein constitutes a new method for treating various types of cancer. The therapy described herein also provides a method of therapy for achieving clinical benefit without an unacceptable level of side effects.

[0082] In one aspect the present invention relates to methods for the treatment of neoplasia, and more particularly tumors, by administering to a subject a vaccine or immunogenic composition comprising a plurality of tumor specific neoantigenic peptides. As described in more detail herein, in some embodiments the composition provides a specific, optimized subset of tumor-specific neoantigens suitable for the treatment of tumors in a high proportion of subjects suffering from cancer. In some embodiments, the tumor specific neoantigens may together bind to a high overall proportion of HLA allotypes present in the subject population.

[0083] The immune system can be classified into two functional subsystems: the innate and the acquired immune system. The innate immune system is the first line of defense against infections, and most potential pathogens are rapidly neutralized by this system before they can cause, for example, a noticeable infection. The acquired immune system reacts to molecular structures, referred to as antigens, of the intruding organism. There are two types of acquired immune reactions, which include the humoral immune reaction and the cell-mediated immune reaction. In the humoral immune reaction, antibodies secreted by B cells into bodily fluids bind to pathogen-derived antigens, leading to the elimination of the pathogen through a variety of

mechanisms, e.g. complement-mediated lysis. In the cell-mediated immune reaction, T-cells capable of destroying other cells are activated. For example, if proteins associated with a disease are present in a cell, they are fragmented proteolytically to peptides within the cell. Specific cell proteins then attach themselves to the antigen or peptide formed in this manner and transport them to the surface of the cell, where they are presented to the molecular defense mechanisms, in particular T-cells, of the body. Cytotoxic T cells recognize these antigens and kill the cells that harbor the antigens.

[0084] The molecules that transport and present peptides on the cell surface are referred to as proteins of the major histocompatibility complex (MHC). MHC proteins are classified into two types, referred to as MHC class I and MHC class II. The structures of the proteins of the two MHC classes are very similar; however, they have very different functions. Proteins of MHC class I are present on the surface of almost all cells of the body, including most tumor cells. MHC class I proteins are loaded with antigens that usually originate from endogenous proteins or from pathogens present inside cells, and are then presented to naïve or cytotoxic T-lymphocytes (CTLs). MHC class II proteins are present on dendritic cells, B- lymphocytes, macrophages and other antigen-presenting cells. They mainly present peptides, which are processed from external antigen sources, i.e. outside of the cells, to T-helper (Th) cells. Most of the peptides bound by the MHC class I proteins originate from cytoplasmic proteins produced in the healthy host cells of an organism itself, and do not normally stimulate an immune reaction. Accordingly, cytotoxic T-lymphocytes that recognize such self-peptide-presenting MHC molecules of class I are deleted in the thymus (central tolerance) or, after their release from the thymus, are deleted or inactivated, i.e. tolerized (peripheral tolerance). MHC molecules are capable of stimulating an immune reaction when they present peptides to non-tolerized T-lymphocytes. Cytotoxic T-lymphocytes have both T-cell receptors (TCR) and CD8 molecules on their surface. T-Cell receptors are capable of recognizing and binding peptides complexed with the molecules of MHC class I. Each cytotoxic T-lymphocyte expresses a unique T-cell receptor which is capable of binding specific MHC/peptide complexes.

[0085] The peptide antigens attach themselves to the molecules of MHC class I by competitive affinity binding within the endoplasmic reticulum, before they are presented on the cell surface. Here, the affinity of an individual peptide antigen is directly linked to its amino acid sequence and the presence of specific binding motifs in defined positions within the amino

acid sequence. If the sequence of such a peptide is known, it is possible to manipulate the immune system against diseased cells using, for example, peptide vaccines.

[0086] One of the critical barriers to developing curative and tumor-specific immunotherapy is the identification and selection of highly specific and restricted tumor antigens to avoid autoimmunity. Tumor neoantigens, which arise as a result of genetic change (e.g., inversions, translocations, deletions, missense mutations, splice site mutations, etc.) within malignant cells, represent the most tumor-specific class of antigens. Neoantigens have rarely been used in cancer vaccine or immunogenic compositions due to technical difficulties in identifying them, selecting optimized neoantigens, and producing neoantigens for use in a vaccine or immunogenic composition. These problems may be addressed by:

- identifying mutations in neoplasias/tumors which are present at the DNA level in tumor but not in matched germline samples from a high proportion of subjects having cancer;

- analyzing the identified mutations with one or more peptide-MHC binding prediction algorithms to generate a plurality of neoantigen T cell epitopes that are expressed within the neoplasia/tumor and that bind to a high proportion of patient HLA alleles; and

- synthesizing the plurality of neoantigenic peptides selected from the sets of all neoantigen peptides and predicted binding peptides for use in a cancer vaccine or immunogenic composition suitable for treating a high proportion of subjects having cancer.

[0087] For example, translating sequencing information into a therapeutic vaccine may include:

(1) *Prediction of mutated peptides that can bind to HLA molecules of a high proportion of individuals.* Efficiently choosing which particular mutations to utilize as immunogen requires the ability to predict which mutated peptides would efficiently bind to a high proportion of patient's HLA alleles. Recently, neural network based learning approaches with validated binding and non-binding peptides have advanced the accuracy of prediction algorithms for the major HLA-A and -B alleles.

(2) *Formulating the drug as a multi-epitope vaccine of long peptides.* Targeting as many mutated epitopes as practically possible takes advantage of the enormous capacity of the immune system, prevents the opportunity for immunological escape by down-modulation of a particular immune targeted gene product, and compensates for the known inaccuracy of epitope prediction approaches. Synthetic peptides provide a particularly useful means to prepare multiple immunogens efficiently and to rapidly translate identification of mutant epitopes to an effective vaccine. Peptides can be readily synthesized chemically and easily purified utilizing reagents free of contaminating bacteria or animal substances. The small size allows a clear focus on the mutated region of the protein and also reduces irrelevant antigenic competition from other components (unmutated protein or viral vector antigens).

(3) *Combination with a strong vaccine adjuvant.* Effective vaccines require a strong adjuvant to initiate an immune response. As described below, poly-ICLC, an agonist of TLR3 and the RNA helicase -domains of MDA5 and RIG3, has shown several desirable properties for a vaccine adjuvant. These properties include the induction of local and systemic activation of immune cells *in vivo,* production of stimulatory chemokines and cytokines, and stimulation of antigen-presentation by DCs. Furthermore, poly-ICLC can induce durable CD4+ and CD8+ responses in humans. Importantly, striking similarities in the upregulation of transcriptional and signal transduction pathways were seen in subjects vaccinated with poly-ICLC and in volunteers who had received the highly effective, replication-competent yellow fever vaccine. Furthermore, >90% of ovarian carcinoma patients immunized with poly-ICLC in combination with a NYES0-1 peptide vaccine (in addition to Montanide) showed induction of CD4+ and CD8+ T cell, as well as antibody responses to the peptide in a recent phase 1 study. At the same time, polyICLC has been extensively tested in more than 25 clinical trials to date and exhibited a relatively benign toxicity profile.

The above-described advantages of the invention are described further herein.

[0088] As described herein, there is a large body of evidence in both animals and humans that mutated epitopes are effective in inducing an immune response and that cases of spontaneous tumor regression or long term survival correlate with CD8+ T-cell responses to mutated epitopes (Buckwalter and Srivastava PK. "It is the antigen(s), stupid" and other lessons from over a decade of vaccitherapy of human cancer. Seminars in immunology 20:296-300 (2008); Karanikas et al, High frequency of cytolytic T lymphocytes directed against a tumor-

specific mutated antigen detectable with HLA tetramers in the blood of a lung carcinoma patient with long survival. Cancer Res. 61:3718-3724 (2001); Lennerz et al, The response of autologous T cells to a human melanoma is dominated by mutated neoantigens. Proc Natl Acad Sci U S A.102:16013 (2005)) and that "immunoediting" can be tracked to alterations in expression of dominant mutated antigens in mice and man (Matsushita et al, Cancer exome analysis reveals a T-cell-dependent mechanism of cancer immunoediting Nature 482:400 (2012); DuPage et al, Expression of tumor-specific antigens underlies cancer immunoediting Nature 482:405 (2012); and Sampson et al, Immunologic escape after prolonged progression-free survival with epidermal growth factor receptor variant III peptide vaccination in patients with newly diagnosed glioblastoma J Clin Oncol. 28:4722-4729 (2010)).

[0089] Sequencing technology has revealed that each tumor contains multiple, patient-specific mutations that alter the protein coding content of a gene. Such mutations create altered proteins, ranging from single amino acid changes (caused by missense mutations) to addition of long regions of novel amino acid sequence due to frame shifts, read-through of termination codons or translation of intron regions (novel open reading frame mutations; neoORFs). These mutated proteins are valuable targets for the host's immune response to the tumor as, unlike native proteins, they are not subject to the immune-dampening effects of self-tolerance. Therefore, mutated proteins are more likely to be immunogenic and are also more specific for the tumor cells compared to normal cells of the patient.

[0090] In one embodiment, the neoantigenic peptides in the composition together have affinity to a plurality of MHC molecules, e.g. which together cover a large proportion of the target population. Efficiently choosing which particular mutations to utilize as immunogen requires the ability to predict which mutated peptides would efficiently bind to the HLA alleles present in the patient population. Recently, neural network based learning approaches with validated binding and non-binding peptides have advanced the accuracy of prediction algorithms for the major HLA-A and -B alleles. Utilizing the recently improved algorithms for predicting which missense mutations create strong binding peptides to cognate MHC molecules, a set of peptides representative of optimal mutated epitopes (both neoORF and missense) for the patient population may be identified and prioritized (Zhang et al, Machine learning competition in immunology – Prediction of HLA class I binding peptides J Immunol Methods 374:1 (2011);

Lundegaard et al Prediction of epitopes using neural network based methods J Immunol Methods 374:26 (2011)).

[0091] Targeting as many mutated epitopes as practically possible takes advantage of the enormous capacity of the immune system, prevents the opportunity for immunological escape by down-modulation of a particular immune targeted gene product, and compensates for the known inaccuracy of epitope prediction approaches. Synthetic peptides provide a particularly useful means to prepare multiple immunogens efficiently and to rapidly translate identification of mutant epitopes to an effective vaccine or immunogenic composition. Peptides can be readily synthesized chemically and easily purified utilizing reagents free of contaminating bacteria or animal substances. The small size allows a clear focus on the mutated region of the protein and also reduces irrelevant antigenic competition from other components (unmutated protein or viral vector antigens).

[0092] In one embodiment the drug formulation is a multi-epitope vaccine or immunogenic composition of long peptides. Such "long" peptides undergo efficient internalization, processing and cross-presentation in professional antigen-presenting cells such as dendritic cells, and have been shown to induce CTLs in humans (Melief and van der Burg, Immunotherapy of established (pre) malignant disease by synthetic long peptide vaccines Nature Rev Cancer 8:351 (2008)). In one embodiment at least 2 peptides are prepared for immunization. In some embodiments 20 or more peptides are prepared for immunization. In one embodiment the neoantigenic peptide ranges from about 5 to about 50 amino acids in length. In another embodiment peptides from about 15 to about 35 amino acids in length is synthesized. In preferred embodiment the neoantigenic peptide ranges from about 20 to about 35 amino acids in length.

Production of Tumor Specific Neoantigens

[0093] The present invention is based, at least in part, on the ability to present the immune system of the patient with a pool of tumor specific neoantigens. One of skill in the art from this disclosure and the knowledge in the art will appreciate that there are a variety of ways in which to produce such tumor specific neoantigens. In general, such tumor specific neoantigens may be produced either in vitro or in vivo. Tumor specific neoantigens may be produced in vitro as peptides or polypeptides, which may then be formulated into a neoplasia vaccine or immunogenic composition and administered to a subject. As described in further detail herein,

such in vitro production may occur by a variety of methods known to one of skill in the art such as, for example, peptide synthesis or expression of a peptide/polypeptide from a DNA or RNA molecule in any of a variety of bacterial, eukaryotic, or viral recombinant expression systems, followed by purification of the expressed peptide/polypeptide. Alternatively, tumor specific neoantigens may be produced in vivo by introducing molecules (e.g., DNA, RNA, viral expression systems, and the like) that encode tumor specific neoantigens into a subject, whereupon the encoded tumor specific neoantigens are expressed. The methods of in vitro and in vivo production of neoantigens is also further described herein as it relates to pharmaceutical compositions and methods of delivery of the therapy.

[0094] In certain embodiments the present invention includes modified neoantigenic peptides. As used herein in reference to neoantigenic peptides, the terms "modified", "modification" and the like refer to one or more changes that enhance a desired property of the neoantigenic peptide, where the change does not alter the primary amino acid sequence of the neoantigenic peptide. "Modification" includes a covalent chemical modification that does not alter the primary amino acid sequence of the neoantigenic peptide itself. Such desired properties include, for example, prolonging the *in vivo* half-life, increasing the stability, reducing the clearance, altering the immunogenicity or allergenicity, enabling the raising of particular antibodies, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation. Changes to a neoantigenic peptide that may be carried out include, but are not limited to, conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids.

[0095] The clinical effectiveness of protein therapeutics is often limited by short plasma half-life and susceptibility to protease degradation. Studies of various therapeutic proteins (e.g., filgrastim) have shown that such difficulties may be overcome by various modifications, including conjugating or linking the polypeptide sequence to any of a variety of non-proteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes (see, for example, typically via a linking moiety covalently bound to both the

protein and the nonproteinaceous polymer, e.g., a PEG). Such PEG- conjugated biomolecules have been shown to possess clinically useful properties, including better physical and thermal stability, protection against susceptibility to enzymatic degradation, increased solubility, longer in vivo circulating half-life and decreased clearance, reduced immunogenicity and antigenicity, and reduced toxicity.

[0096] PEGs suitable for conjugation to a polypeptide sequence are generally soluble in water at room temperature, and have the general formula $R(O\text{-}CH_2\text{-}CH_2)_nO\text{-}R$, where R is hydrogen or a protective group such as an alkyl or an alkanol group, and where n is an integer from 1 to 1000. When R is a protective group, it generally has from 1 to 8 carbons. The PEG conjugated to the polypeptide sequence can be linear or branched. Branched PEG derivatives, "star-PEGs" and multi-armed PEGs are contemplated by the present disclosure. A molecular weight of the PEG used in the present disclosure is not restricted to any particular range, but certain embodiments have a molecular weight between 500 and 20,000 while other embodiments have a molecular weight between 4,000 and 10,000.

[0097] The present disclosure also contemplates compositions of conjugates wherein the PEGs have different n values and thus the various different PEGs are present in specific ratios. For example, some compositions comprise a mixture of conjugates where n=1, 2, 3 and 4. In some compositions, the percentage of conjugates where n=1 is 18-25%, the percentage of conjugates where n=2 is 50-66%, the percentage of conjugates where n=3 is 12-16%, and the percentage of conjugates where n=4 is up to 5%. Such compositions can be produced by reaction conditions and purification methods know in the art. For example, cation exchange chromatography may be used to separate conjugates, and a fraction is then identified which contains the conjugate having, for example, the desired number of PEGs attached, purified free from unmodified protein sequences and from conjugates having other numbers of PEGs attached.

[0098] PEG may be bound to a polypeptide of the present disclosure via a terminal reactive group (a "spacer"). The spacer is, for example, a terminal reactive group which mediates a bond between the free amino or carboxyl groups of one or more of the polypeptide sequences and polyethylene glycol. The PEG having the spacer which may be bound to the free amino group includes N-hydroxysuccinylimide polyethylene glycol which may be prepared by activating succinic acid ester of polyethylene glycol with N- hydroxy succinylimide. Another activated

polyethylene glycol which may be bound to a free amino group is 2,4-bis(0-methoxypolyethyleneglycol)-6-chloro-s-triazine which may be prepared by reacting polyethylene glycol monomethyl ether with cyanuric chloride. The activated polyethylene glycol which is bound to the free carboxyl group includes polyoxyethylenediamine.

[0099] Conjugation of one or more of the polypeptide sequences of the present disclosure to PEG having a spacer may be carried out by various conventional methods. For example, the conjugation reaction can be carried out in solution at a pH of from 5 to 10, at temperature from 4°C to room temperature, for 30 minutes to 20 hours, utilizing a molar ratio of reagent to protein of from 4: 1 to 30: 1. Reaction conditions may be selected to direct the reaction towards producing predominantly a desired degree of substitution. In general, low temperature, low pH (e.g., pH=5), and short reaction time tend to decrease the number of PEGs attached, whereas high temperature, neutral to high pH (e.g., pH>7), and longer reaction time tend to increase the number of PEGs attached. Various means known in the art may be used to terminate the reaction. In some embodiments the reaction is terminated by acidifying the reaction mixture and freezing at, e.g., -20°C.

[00100] The present disclosure also contemplates the use of PEG Mimetics. Recombinant PEG mimetics have been developed that retain the attributes of PEG (e.g., enhanced serum half-life) while conferring several additional advantageous properties. By way of example, simple polypeptide chains (comprising, for example, Ala, Glu, Gly, Pro, Ser and Thr) capable of forming an extended conformation similar to PEG can be produced recombinantly already fused to the peptide or protein drug of interest (e.g., Amunix' XTEN technology; Mountain View, CA). This obviates the need for an additional conjugation step during the manufacturing process. Moreover, established molecular biology techniques enable control of the side chain composition of the polypeptide chains, allowing optimization of immunogenicity and manufacturing properties.

[00101] For purposes of the present disclosure, "glycosylation" is meant to broadly refer to the enzymatic process that attaches glycans to proteins, lipids or other organic molecules. The use of the term "glycosylation" in conjunction with the present disclosure is generally intended to mean adding or deleting one or more carbohydrate moieties (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that may or may not be present in the native sequence. In

addition, the phrase includes qualitative changes in the glycosylation of the native proteins involving a change in the nature and proportions of the various carbohydrate moieties present. Glycosylation can dramatically affect the physical properties of proteins and can also be important in protein stability, secretion, and subcellular localization. Proper glycosylation can be essential for biological activity. In fact, some genes from eucaryotic organisms, when expressed in bacteria (e.g., E. coli) which lack cellular processes for glycosylating proteins, yield proteins that are recovered with little or no activity by virtue of their lack of glycosylation.

[00102] Addition of glycosylation sites can be accomplished by altering the amino acid sequence. The alteration to the polypeptide may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues (for O-linked glycosylation sites) or asparagine residues (for N-linked glycosylation sites). The structures of N-linked and O- linked oligosaccharides and the sugar residues found in each type may be different. One type of sugar that is commonly found on both is N-acetylneuraminic acid (hereafter referred to as sialic acid). Sialic acid is usually the terminal residue of both N-linked and O-linked oligosaccharides and, by virtue of its negative charge, may confer acidic properties to the glycoprotein. A particular embodiment of the present disclosure comprises the generation and use of N-glycosylation variants.

[00103] The polypeptide sequences of the present disclosure may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids. Another means of increasing the number of carbohydrate moieties on the polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

[00104] Removal of carbohydrates may be accomplished chemically or enzymatically, or by substitution of codons encoding amino acid residues that are glycosylated. Chemical deglycosylation techniques are known, and enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases.

[00105] Dihydrofolate reductase (DHFR) - deficient Chinese Hamster Ovary (CHO) cells are a commonly used host cell for the production of recombinant glycoproteins. These cells do not express the enzyme beta-galactoside alpha-2,6-sialyltransferase and therefore do not add sialic acid in the alpha-2,6 linkage to N-linked oligosaccharides of glycoproteins produced in these cells.

[00106] The present disclosure also contemplates the use of polysialylation, the conjugation of peptides and proteins to the naturally occurring, biodegradable a-(2→8) linked polysialic acid ("PSA") in order to improve their stability and in vivo pharmacokinetics. PSA is a biodegradable, non-toxic natural polymer that is highly hydrophilic, giving it a high apparent molecular weight in the blood which increases its serum half-life. In addition, polysialylation of a range of peptide and protein therapeutics has led to markedly reduced proteolysis, retention of activity in vivo activity, and reduction in immunogenicity and antigenicity (see, e.g., G. Gregoriadis et al., Int. J. Pharmaceutics 300(1-2): 125-30). As with modifications with other conjugates (e.g., PEG), various techniques for site-specific polysialylation are available (see, e.g., T. Lindhout et al., PNAS 108(18)7397-7402 (2011)).

[00107] Additional suitable components and molecules for conjugation include, for example, thyroglobulin; albumins such as human serum albumin (HAS); tetanus toxoid; Diphtheria toxoid; polyamino acids such as poly(D-lysine:D-glutamic acid); VP6 polypeptides of rotaviruses; influenza virus hemaglutinin, influenza virus nucleoprotein; Keyhole Limpet Hemocyanin (KLH); and hepatitis B virus core protein and surface antigen; or any combination of the foregoing.

[00108] Fusion of albumin to one or more polypeptides of the present disclosure can, for example, be achieved by genetic manipulation, such that the DNA coding for HSA, or a fragment thereof, is joined to the DNA coding for the one or more polypeptide sequences. Thereafter, a suitable host can be transformed or transfected with the fused nucleotide sequences in the form of, for example, a suitable plasmid, so as to express a fusion polypeptide. The expression may be effected in vitro from, for example, prokaryotic or eukaryotic cells, or in vivo from, for example, a transgenic organism. In some embodiments of the present disclosure, the expression of the fusion protein is performed in mammalian cell lines, for example, CHO cell lines. Transformation is used broadly herein to refer to the genetic alteration of a cell resulting from the direct uptake, incorporation and expression of exogenous genetic material (exogenous DNA) from its surroundings and taken up through the cell membrane(s). Transformation occurs naturally in some species of bacteria, but it can also be effected by artificial means in other cells.

[00109] Furthermore, albumin itself may be modified to extend its circulating half-life. Fusion of the modified albumin to one or more Polypeptides can be attained by the genetic manipulation

techniques described above or by chemical conjugation; the resulting fusion molecule has a half-life that exceeds that of fusions with non-modified albumin. (See WO2011/051489).

[00110] Several albumin - binding strategies have been developed as alternatives for direct fusion, including albumin binding through a conjugated fatty acid chain (acylation). Because serum albumin is a transport protein for fatty acids, these natural ligands with albumin - binding activity have been used for half-life extension of small protein therapeutics. For example, insulin determir (LEVEMIR), an approved product for diabetes, comprises a myristyl chain conjugated to a genetically-modified insulin, resulting in a long- acting insulin analog.

[00111] Another type of modification is to conjugate (e.g., link) one or more additional components or molecules at the N- and/or C-terminus of a polypeptide sequence, such as another protein (e.g., a protein having an amino acid sequence heterologous to the subject protein), or a carrier molecule. Thus, an exemplary polypeptide sequence can be provided as a conjugate with another component or molecule.

[00112] A conjugate modification may result in a polypeptide sequence that retains activity with an additional or complementary function or activity of the second molecule. For example, a polypeptide sequence may be conjugated to a molecule, e.g., to facilitate solubility, storage, in vivo or shelf half-life or stability, reduction in immunogenicity, delayed or controlled release in vivo, etc. Other functions or activities include a conjugate that reduces toxicity relative to an unconjugated polypeptide sequence, a conjugate that targets a type of cell or organ more efficiently than an unconjugated polypeptide sequence, or a drug to further counter the causes or effects associated with a disorder or disease as set forth herein (e.g., diabetes).

[00113] A Polypeptide may also be conjugated to large, slowly metabolized macromolecules such as proteins; polysaccharides, such as sepharose, agarose, cellulose, cellulose beads; polymeric amino acids such as polyglutamic acid, polylysine; amino acid copolymers; inactivated virus particles; inactivated bacterial toxins such as toxoid from diphtheria, tetanus, cholera, leukotoxin molecules; inactivated bacteria; and dendritic cells.

[00114] Additional candidate components and molecules for conjugation include those suitable for isolation or purification. Particular non-limiting examples include binding molecules, such as biotin (biotin-avidin specific binding pair), an antibody, a receptor, a ligand, a lectin, or molecules that comprise a solid support, including, for example, plastic or polystyrene beads, plates or beads, magnetic beads, test strips, and membranes.

[00115] Purification methods such as cation exchange chromatography may be used to separate conjugates by charge difference, which effectively separates conjugates into their various molecular weights. For example, the cation exchange column can be loaded and then washed with ~20 mM sodium acetate, pH ~4, and then eluted with a linear (0 M to 0.5 M) NaCl gradient buffered at a pH from about 3 to 5.5, e.g., at pH ~4.5. The content of the fractions obtained by cation exchange chromatography may be identified by molecular weight using conventional methods, for example, mass spectroscopy, SDS-PAGE, or other known methods for separating molecular entities by molecular weight.

[00116] In certain embodiments, the amino- or carboxyl- terminus of a polypeptide sequence of the present disclosure can be fused with an immunoglobulin Fc region (e.g., human Fc) to form a fusion conjugate (or fusion molecule). Fc fusion conjugates have been shown to increase the systemic half-life of biopharmaceuticals, and thus the biopharmaceutical product may require less frequent administration.

[00117] Fc binds to the neonatal Fc receptor (FcRn) in endothelial cells that line the blood vessels, and, upon binding, the Fc fusion molecule is protected from degradation and re- released into the circulation, keeping the molecule in circulation longer. This Fc binding is believed to be the mechanism by which endogenous IgG retains its long plasma half-life. More recent Fc-fusion technology links a single copy of a biopharmaceutical to the Fc region of an antibody to optimize the pharmacokinetic and pharmacodynamic properties of the biopharmaceutical as compared to traditional Fc-fusion conjugates.

[00118] The present disclosure contemplates the use of other modifications, currently known or developed in the future, of the Polypeptides to improve one or more properties. One such method for prolonging the circulation half-life, increasing the stability, reducing the clearance, or altering the immunogenicity or allergenicity of a polypeptide of the present disclosure involves modification of the polypeptide sequences by hesylation, which utilizes hydroxyethyl starch derivatives linked to other molecules in order to modify the molecule's characteristics. Various aspects of hesylation are described in, for example, U.S. Patent Appln. Nos. 2007/0134197 and 2006/0258607.

In Vitro Peptide/Polypeptide Synthesis

[00119] Proteins or peptides may be made by any technique known to those of skill in the art, including the expression of proteins, polypeptides or peptides through standard molecular biological techniques, the isolation of proteins or peptides from natural sources, in vitro translation, or the chemical synthesis of proteins or peptides. The nucleotide and protein, polypeptide and peptide sequences corresponding to various genes have been previously disclosed, and may be found at computerized databases known to those of ordinary skill in the art. One such database is the National Center for Biotechnology Information's Genbank and GenPept databases located at the National Institutes of Health website. The coding regions for known genes may be amplified and/or expressed using the techniques disclosed herein or as would be known to those of ordinary skill in the art. Alternatively, various commercial preparations of proteins, polypeptides and peptides are known to those of skill in the art.

[00120] Peptides can be readily synthesized chemically utilizing reagents that are free of contaminating bacterial or animal substances (Merrifield RB: Solid phase peptide synthesis. I. The synthesis of a tetrapeptide. J. Am. Chem. Soc. 85:2149-54, 1963). In certain embodiments, neoantigenic peptides are prepared by (1) parallel solid-phase synthesis on multi-channel instruments using uniform synthesis and cleavage conditions; (2) purification over a RP-HPLC column with column stripping; and re-washing, but not replacement, between peptides; followed by (3) analysis with a limited set of the most informative assays. The Good Manufacturing Practices (GMP) footprint can be defined around the set of peptides for an individual patient, thus requiring suite changeover procedures only between syntheses of peptides for different patients.

[00121] Alternatively, a nucleic acid (e.g., a polynucleotide) encoding a neoantigenic peptide of the invention may be used to produce the neoantigenic peptide in vitro. The polynucleotide may be, e.g., DNA, cDNA, PNA, CNA, RNA, either single- and/or double-stranded, or native or stabilized forms of polynucleotides, such as e.g. polynucleotides with a phosphorothiate backbone, or combinations thereof and it may or may not contain introns so long as it codes for the peptide. In one embodiment in vitro translation is used to produce the peptide. Many exemplary systems exist that one skilled in the art could utilize (e.g., Retic Lysate IVT Kit, Life Technologies, Waltham, MA).

[00122] An expression vector capable of expressing a polypeptide can also be prepared. Expression vectors for different cell types are well known in the art and can be selected without undue experimentation. Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognized by the desired host (e.g., bacteria), although such controls are generally available in the expression vector. The vector is then introduced into the host bacteria for cloning using standard techniques (see, e.g., Sambrook et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

[00123] Expression vectors comprising the isolated polynucleotides, as well as host cells containing the expression vectors, are also contemplated. The neoantigenic peptides may be provided in the form of RNA or cDNA molecules encoding the desired neoantigenic peptides. One or more neoantigenic peptides of the invention may be encoded by a single expression vector.

[00124] The term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequences for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequences. Polynucleotides can be in the form of RNA or in the form of DNA. DNA includes cDNA, genomic DNA, and synthetic DNA; and can be double-stranded or single-stranded, and if single stranded can be the coding strand or non-coding (anti-sense) strand.

[00125] In embodiments, the polynucleotides may comprise the coding sequence for the tumor specific neoantigenic peptide fused in the same reading frame to a polynucleotide which aids, for example, in expression and/or secretion of a polypeptide from a host cell (e.g., a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell). The polypeptide having a leader sequence is a preprotein and can have the leader sequence cleaved by the host cell to form the mature form of the polypeptide.

[00126] In embodiments, the polynucleotides can comprise the coding sequence for the tumor specific neoantigenic peptide fused in the same reading frame to a marker sequence that allows, for example, for purification of the encoded polypeptide, which may then be incorporated into the personalized neoplasia vaccine or immunogenic composition. For example, the marker sequence can be a hexa-histidine tag supplied by a pQE-9 vector to provide for purification of

the mature polypeptide fused to the marker in the case of a bacterial host, or the marker sequence can be a hemagglutinin (HA) tag derived from the influenza hemagglutinin protein when a mammalian host (e.g., COS-7 cells) is used. Additional tags include, but are not limited to, Calmodulin tags, FLAG tags, Myc tags, S tags, SBP tags, Softag 1, Softag 3, V5 tag, Xpress tag, Isopeptag, SpyTag, Biotin Carboxyl Carrier Protein (BCCP) tags, GST tags, fluorescent protein tags (e.g., green fluorescent protein tags), maltose binding protein tags, Nus tags, Strep-tag, thioredoxin tag, TC tag, Ty tag, and the like.

[00127] In embodiments, the polynucleotides may comprise the coding sequence for one or more of the tumor specific neoantigenic peptides fused in the same reading frame to create a single concatamerized neoantigenic peptide construct capable of producing multiple neoantigenic peptides.

[00128] In certain embodiments, isolated nucleic acid molecules having a nucleotide sequence at least 60% identical, at least 65% identical, at least 70% identical, at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 96%, 97%, 98% or 99% identical to a polynucleotide encoding a tumor specific neoantigenic peptide of the present invention, can be provided.

[00129] By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence can include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence can be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence can be inserted into the reference sequence. These mutations of the reference sequence can occur at the amino- or carboxy-terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

[00130] As a practical matter, whether any particular nucleic acid molecule is at least 80% identical, at least 85% identical, at least 90% identical, and in some embodiments, at least 95%, 96%, 97%, 98%, or 99% identical to a reference sequence can be determined conventionally

using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). Bestfit uses the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981), to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

[00131] The isolated tumor specific neoantigenic peptides described herein can be produced in vitro (e.g., in the laboratory) by any suitable method known in the art. Such methods range from direct protein synthetic methods to constructing a DNA sequence encoding isolated polypeptide sequences and expressing those sequences in a suitable transformed host. In some embodiments, a DNA sequence is constructed using recombinant technology by isolating or synthesizing a DNA sequence encoding a wild-type protein of interest. Optionally, the sequence can be mutagenized by site-specific mutagenesis to provide functional analogs thereof. See, e.g. Zoeller et al., Proc. Nat'l. Acad. Sci. USA 81:5662-5066 (1984) and U.S. Pat. No. 4,588,585.

[00132] In embodiments, a DNA sequence encoding a polypeptide of interest would be constructed by chemical synthesis using an oligonucleotide synthesizer. Such oligonucleotides can be designed based on the amino acid sequence of the desired polypeptide and selecting those codons that are favored in the host cell in which the recombinant polypeptide of interest is produced. Standard methods can be applied to synthesize an isolated polynucleotide sequence encoding an isolated polypeptide of interest. For example, a complete amino acid sequence can be used to construct a back-translated gene. Further, a DNA oligomer containing a nucleotide sequence coding for the particular isolated polypeptide can be synthesized. For example, several small oligonucleotides coding for portions of the desired polypeptide can be synthesized and then ligated. The individual oligonucleotides typically contain 5' or 3' overhangs for complementary assembly.

[00133] Once assembled (e.g., by synthesis, site-directed mutagenesis, or another method), the polynucleotide sequences encoding a particular isolated polypeptide of interest is inserted into an expression vector and optionally operatively linked to an expression control sequence

appropriate for expression of the protein in a desired host. Proper assembly can be confirmed by nucleotide sequencing, restriction mapping, and expression of a biologically active polypeptide in a suitable host. As well known in the art, in order to obtain high expression levels of a transfected gene in a host, the gene can be operatively linked to transcriptional and translational expression control sequences that are functional in the chosen expression host.

[00134] Recombinant expression vectors may be used to amplify and express DNA encoding the tumor specific neoantigenic peptides. Recombinant expression vectors are replicable DNA constructs which have synthetic or cDNA-derived DNA fragments encoding a tumor specific neoantigenic peptide or a bioequivalent analog operatively linked to suitable transcriptional or translational regulatory elements derived from mammalian, microbial, viral or insect genes. A transcriptional unit generally comprises an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, transcriptional promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription and translation initiation and termination sequences, as described in detail herein. Such regulatory elements can include an operator sequence to control transcription. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants can additionally be incorporated. DNA regions are operatively linked when they are functionally related to each other. For example, DNA for a signal peptide (secretory leader) is operatively linked to DNA for a polypeptide if it is expressed as a precursor which participates in the secretion of the polypeptide; a promoter is operatively linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operatively linked to a coding sequence if it is positioned so as to permit translation. Generally, operatively linked means contiguous, and in the case of secretory leaders, means contiguous and in reading frame. Structural elements intended for use in yeast expression systems include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it can include an N-terminal methionine residue. This residue can optionally be subsequently cleaved from the expressed recombinant protein to provide a final product.

[00135] Useful expression vectors for eukaryotic hosts, especially mammals or humans include, for example, vectors comprising expression control sequences from SV40, bovine papilloma virus, adenovirus and cytomegalovirus. Useful expression vectors for bacterial hosts

include known bacterial plasmids, such as plasmids from Escherichia coli, including pCR 1, pBR322, pMB9 and their derivatives, wider host range plasmids, such as M13 and filamentous single-stranded DNA phages.

[00136] Suitable host cells for expression of a polypeptide include prokaryotes, yeast, insect or higher eukaryotic cells under the control of appropriate promoters. Prokaryotes include gram negative or gram positive organisms, for example E. coli or bacilli. Higher eukaryotic cells include established cell lines of mammalian origin. Cell-free translation systems could also be employed. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are well known in the art (see Pouwels et al., Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., 1985).

[00137] Various mammalian or insect cell culture systems are also advantageously employed to express recombinant protein. Expression of recombinant proteins in mammalian cells can be performed because such proteins are generally correctly folded, appropriately modified and completely functional. Examples of suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, described by Gluzman (Cell 23:175, 1981), and other cell lines capable of expressing an appropriate vector including, for example, L cells, C127, 3T3, Chinese hamster ovary (CHO), 293, HeLa and BHK cell lines. Mammalian expression vectors can comprise nontranscribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, and other 5' or 3' flanking nontranscribed sequences, and 5' or 3' nontranslated sequences, such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, Bio/Technology 6:47 (1988).

[00138] The proteins produced by a transformed host can be purified according to any suitable method. Such standard methods include chromatography (e.g., ion exchange, affinity and sizing column chromatography, and the like), centrifugation, differential solubility, or by any other standard technique for protein purification. Affinity tags such as hexahistidine, maltose binding domain, influenza coat sequence, glutathione-S-transferase, and the like can be attached to the protein to allow easy purification by passage over an appropriate affinity column. Isolated proteins can also be physically characterized using such techniques as proteolysis, nuclear magnetic resonance and x-ray crystallography.

[00139] For example, supernatants from systems which secrete recombinant protein into culture media can be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate can be applied to a suitable purification matrix. Alternatively, an anion exchange resin can be employed, for example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Finally, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify a cancer stem cell protein-Fc composition. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a homogeneous recombinant protein.

[00140] Recombinant protein produced in bacterial culture can be isolated, for example, by initial extraction from cell pellets, followed by one or more concentration, salting-out, aqueous ion exchange or size exclusion chromatography steps. High performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of a recombinant protein can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

In Vivo Peptide/Polypeptide Synthesis

[00141] The present invention also contemplates the use of nucleic acid molecules as vehicles for delivering neoantigenic peptides/polypeptides to the subject in need thereof, in vivo, in the form of, e.g., DNA/RNA vaccines (see, e.g., WO2012/159643, and WO2012/159754, hereby incorporated by reference in their entirety).

[00142] In one embodiment neoantigens may be administered to a patient in need thereof by use of a plasmid. These are plasmids which usually consist of a strong viral promoter to drive the in vivo transcription and translation of the gene (or complementary DNA) of interest (Mor, et al., (1995). The Journal of Immunology 155 (4): 2039–2046). Intron A may sometimes be included to improve mRNA stability and hence increase protein expression (Leitner et al.

(1997).The Journal of Immunology 159 (12): 6112–6119). Plasmids also include a strong polyadenylation/transcriptional termination signal, such as bovine growth hormone or rabbit beta-globulin polyadenylation sequences (Alarcon et al., (1999). Adv. Parasitol. Advances in Parasitology 42: 343–410; Robinson et al., (2000). Adv. Virus Res. Advances in Virus Research 55: 1–74; Böhmet al., (1996). Journal of Immunological Methods 193 (1): 29–40.). Multicistronic vectors are sometimes constructed to express more than one immunogen, or to express an immunogen and an immunostimulatory protein (Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88).

[00143] Because the plasmid is the "vehicle" from which the immunogen is expressed, optimising vector design for maximal protein expression is essential (Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88). One way of enhancing protein expression is by optimising the codon usage of pathogenic mRNAs for eukaryotic cells. Another consideration is the choice of promoter. Such promoters may be the SV40 promoter or Rous Sarcoma Virus (RSV).

[00144] Plasmids may be introduced into animal tissues by a number of different methods. The two most popular approaches are injection of DNA in saline, using a standard hypodermic needle, and gene gun delivery. A schematic outline of the construction of a DNA vaccine plasmid and its subsequent delivery by these two methods into a host is illustrated at Scientific American (Weiner et al., (1999) Scientific American 281 (1): 34–41). Injection in saline is normally conducted intramuscularly (IM) in skeletal muscle, or intradermally (ID), with DNA being delivered to the extracellular spaces. This can be assisted by electroporation by temporarily damaging muscle fibres with myotoxins such as bupivacaine; or by using hypertonic solutions of saline or sucrose (Alarcon et al., (1999). Adv. Parasitol. Advances in Parasitology 42: 343–410). Immune responses to this method of delivery can be affected by many factors, including needle type, needle alignment, speed of injection, volume of injection, muscle type, and age, sex and physiological condition of the animal being injected(Alarcon et al., (1999). Adv. Parasitol. Advances in Parasitology 42: 343–410).

[00145] Gene gun delivery, the other commonly used method of delivery, ballistically accelerates plasmid DNA (pDNA) that has been adsorbed onto gold or tungsten microparticles into the target cells, using compressed helium as an accelerant (Alarcon et al., (1999). Adv.

Parasitol. Advances in Parasitology 42: 343–410; Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88).

[00146] Alternative delivery methods may include aerosol instillation of naked DNA on mucosal surfaces, such as the nasal and lung mucosa, (Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88) and topical administration of pDNA to the eye and vaginal mucosa (Lewis et al., (1999) Advances in Virus Research (Academic Press) 54: 129–88). Mucosal surface delivery has also been achieved using cationic liposome-DNA preparations, biodegradable microspheres, attenuated Shigella or Listeria vectors for oral administration to the intestinal mucosa, and recombinant adenovirus vectors. DNA or RNA may also be delivered to cells following mild mechanical disruption of the cell membrane, temporarily permeabilizing the cells. Such a mild mechanical disruption of the membrane can be accomplished by gently forcing cells through a small aperture (Ex Vivo Cytosolic Delivery of Functional Macromolecules to Immune Cells, Sharei et al, PLOS ONE | DOI:10.1371/journal.pone.0118803 April 13, 2015).

[00147] The method of delivery determines the dose of DNA required to raise an effective immune response. Saline injections require variable amounts of DNA, from 10 μg-1 mg, whereas gene gun deliveries require 100 to 1000 times less DNA than intramuscular saline injection to raise an effective immune response. Generally, 0.2 μg – 20 μg are required, although quantities as low as 16 ng have been reported. These quantities vary from species to species, with mice, for example, requiring approximately 10 times less DNA than primates. Saline injections require more DNA because the DNA is delivered to the extracellular spaces of the target tissue (normally muscle), where it has to overcome physical barriers (such as the basal lamina and large amounts of connective tissue, to mention a few) before it is taken up by the cells, while gene gun deliveries bombard DNA directly into the cells, resulting in less "wastage" (See e.g., Sedegah et al., (1994). Proceedings of the National Academy of Sciences of the United States of America 91 (21): 9866–9870; Daheshiaet al., (1997). The Journal of Immunology 159 (4): 1945–1952; Chen et al., (1998). The Journal of Immunology 160 (5): 2425–2432; Sizemore (1995) Science 270 (5234): 299–302; Fynan et al., (1993) Proc. Natl. Acad. Sci. U.S.A. 90 (24): 11478–82).

[00148] In one embodiment, a neoplasia vaccine or immunogenic composition may include separate DNA plasmids encoding, for example, one or more neoantigenic peptides/polypeptides as identified in according to the invention. As discussed herein, the exact choice of expression

vectors can depend upon the peptide/polypeptides to be expressed, and is well within the skill of the ordinary artisan. The expected persistence of the DNA constructs (e.g., in an episomal, non-replicating, non-integrated form in the muscle cells) is expected to provide an increased duration of protection.

[00149] One or more neoantigenic peptides of the invention may be encoded and expressed in vivo using a viral based system (e.g., an adenovirus system, an adeno associated virus (AAV) vector, a poxvirus, or a lentivirus). In one embodiment, the neoplasia vaccine or immunogenic composition may include a viral based vector for use in a human patient in need thereof, such as, for example, an adenovirus (see, e.g., Baden et al. First-in-human evaluation of the safety and immunogenicity of a recombinant adenovirus serotype 26 HIV-1 Env vaccine (IPCAVD 001). J Infect Dis. 2013 Jan 15;207(2):240-7, hereby incorporated by reference in its entirety). Plasmids that can be used for adeno associated virus, adenovirus, and lentivirus delivery have been described previously (see e.g., U.S. Patent Nos. 6,955,808 and 6,943,019, and U.S. Patent application No. 20080254008, hereby incorporated by reference).

[00150] The peptides and polypeptides of the invention can also be expressed by a vector, e.g., a nucleic acid molecule as herein-discussed, e.g., RNA or a DNA plasmid, a viral vector such as a poxvirus, e.g., orthopox virus, avipox virus, or adenovirus, AAV or lentivirus. This approach involves the use of a vector to express nucleotide sequences that encode the peptide of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the vector expresses the immunogenic peptide, and thereby elicits a host CTL response.

[00151] Among vectors that may be used in the practice of the invention, integration in the host genome of a cell is possible with retrovirus gene transfer methods, often resulting in long term expression of the inserted transgene. In a preferred embodiment the retrovirus is a lentivirus. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues. The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. A retrovirus can also be engineered to allow for conditional expression of the inserted transgene, such that only certain cell types are infected by the lentivirus. Cell type specific promoters can be used to target expression in specific cell types. Lentiviral vectors are retroviral vectors (and hence both lentiviral and retroviral vectors may be used in the practice of the invention). Moreover,

lentiviral vectors are preferred as they are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system may therefore depend on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the desired nucleic acid into the target cell to provide permanent expression. Widely used retroviral vectors that may be used in the practice of the invention include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., (1992) J. Virol. 66:2731-2739; Johann et al., (1992) J. Virol. 66:1635-1640; Sommnerfelt et al., (1990) Virol. 176:58-59; Wilson et al., (1998) J. Virol. 63:2374-2378; Miller et al., (1991) J. Virol. 65:2220-2224; PCT/US94/05700).

[00152] Also useful in the practice of the invention is a minimal non-primate lentiviral vector, such as a lentiviral vector based on the equine infectious anemia virus (EIAV) (see, e.g., Balagaan, (2006) J Gene Med; 8: 275 – 285, Published online 21 November 2005 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/jgm.845). The vectors may have cytomegalovirus (CMV) promoter driving expression of the target gene. Accordingly, the invention contemplates amongst vector(s) useful in the practice of the invention: viral vectors, including retroviral vectors and lentiviral vectors.

[00153] Lentiviral vectors have been disclosed as in the treatment for Parkinson's Disease, see, e.g., US Patent Publication No. 20120295960 and US Patent Nos. 7303910 and 7351585. Lentiviral vectors have also been disclosed for delivery to the Brain, see, e.g., US Patent Publication Nos. US20110293571; US20040013648, US20070025970, US20090111106 and US Patent No. US7259015. In another embodiment lentiviral vectors are used to deliver vectors to the brain of those being treated for a disease.

[00154] As to lentivirus vector systems useful in the practice of the invention, mention is made of US Patents Nos. 6428953, 6165782, 6013516, 5994136, 6312682, and 7,198,784, and documents cited therein.

[00155] In an embodiment herein the delivery is via an lentivirus. Zou et al. administered about 10 µl of a recombinant lentivirus having a titer of 1 x 10^9 transducing units (TU)/ml by an intrathecal catheter. These sort of dosages can be adapted or extrapolated to use of a retroviral or

lentiviral vector in the present invention. For transduction in tissues such as the brain, it is necessary to use very small volumes, so the viral preparation is concentrated by ultracentrifugation. The resulting preparation should have at least 10^8 TU/ml, preferably from 10^8 to 10^9 TU/ml, more preferably at least 10^9 TU/ml. Other methods of concentration such as ultrafiltration or binding to and elution from a matrix may be used.

[00156] In other embodiments the amount of lentivirus administered may be $1.x.10^5$ or about $1.x.10^5$ plaque forming units (PFU), $5.x.10^5$ or about $5.x.10^5$ PFU, $1.x.10^6$ or about $1.x10^6$ PFU, $5.x.10^6$ or about $5.x.10^6$ PFU, $1.x.10^7$ or about $1.x.10^7$ PFU, $5.x.10^7$ or about $5.x.10^7$ PFU, $1.x.10^8$ or about $1.x.10^8$ PFU, $5.x.10^8$ or about $5.x.10^8$ PFU, $1.x.10^9$ or about $1.x.10^9$ PFU, $5.x.10^9$ or about $5.x.10^9$ PFU, $1.x.10^{10}$ or about $1.x.10^{10}$ PFU or $5.x.10^{10}$ or about $5.x.10^{10}$ PFU as total single dosage for an average human of 75 kg or adjusted for the weight and size and species of the subject. One of skill in the art can determine suitable dosage. Suitable dosages for a virus can be determined empirically.

[00157] Also useful in the practice of the invention is an adenovirus vector. One advantage is the ability of recombinant adenoviruses to efficiently transfer and express recombinant genes in a variety of mammalian cells and tissues in vitro and in vivo, resulting in the high expression of the transferred nucleic acids. Further, the ability to productively infect quiescent cells, expands the utility of recombinant adenoviral vectors. In addition, high expression levels ensure that the products of the nucleic acids will be expressed to sufficient levels to generate an immune response (see e.g., U.S. Patent No. 7,029,848, hereby incorporated by reference).

[00158] As to adenovirus vectors useful in the practice of the invention, mention is made of US Patent No. 6,955,808. The adenovirus vector used can be selected from the group consisting of the Ad5, Ad35, Ad11, C6, and C7 vectors. The sequence of the Adenovirus 5 ("Ad5") genome has been published. (Chroboczek, J., Bieber, F., and Jacrot, B. (1992) The Sequence of the Genome of Adenovirus Type 5 and Its Comparison with the Genome of Adenovirus Type 2, Virology 186, 280-285; the contents if which is hereby incorporated by reference). Ad35 vectors are described in U.S. Pat. Nos. 6,974,695, 6,913,922, and 6,869,794. Ad11 vectors are described in U.S. Pat. No. 6,913,922. C6 adenovirus vectors are described in U.S. Pat. Nos. 6,780,407; 6,537,594; 6,309,647; 6,265,189; 6,156,567; 6,090,393; 5,942,235 and 5,833,975. C7 vectors are described in U.S. Pat. No. 6,277,558. Adenovirus vectors that are E1-defective or deleted, E3-defective or deleted, and/or E4-defective or deleted may also be used. Certain adenoviruses

having mutations in the E1 region have improved safety margin because E1-defective adenovirus mutants are replication-defective in non-permissive cells, or, at the very least, are highly attenuated. Adenoviruses having mutations in the E3 region may have enhanced the immunogenicity by disrupting the mechanism whereby adenovirus down-regulates MHC class I molecules. Adenoviruses having E4 mutations may have reduced immunogenicity of the adenovirus vector because of suppression of late gene expression. Such vectors may be particularly useful when repeated re-vaccination utilizing the same vector is desired. Adenovirus vectors that are deleted or mutated in E1, E3, E4, E1 and E3, and E1 and E4 can be used in accordance with the present invention. Furthermore, "gutless" adenovirus vectors, in which all viral genes are deleted, can also be used in accordance with the present invention. Such vectors require a helper virus for their replication and require a special human 293 cell line expressing both E1a and Cre, a condition that does not exist in natural environment. Such "gutless" vectors are non-immunogenic and thus the vectors may be inoculated multiple times for re-vaccination. The "gutless" adenovirus vectors can be used for insertion of heterologous inserts/genes such as the transgenes of the present invention, and can even be used for co-delivery of a large number of heterologous inserts/genes.

[00159] In an embodiment herein the delivery is via an adenovirus, which may be at a single booster dose containing at least 1 x 10^5 particles (also referred to as particle units, pu) of adenoviral vector. In an embodiment herein, the dose preferably is at least about 1 x 10^6 particles (for example, about 1 x 10^6-1 x 10^{12} particles), more preferably at least about 1 x 10^7 particles, more preferably at least about 1 x 10^8 particles (e.g., about 1 x 10^8-1 x 10^{11} particles or about 1 x 10^8-1 x 10^{12} particles), and most preferably at least about 1 x 10^9 particles (e.g., about 1 x 10^9-1 x 10^{10} particles or about 1 x 10^9-1 x 10^{12} particles), or even at least about 1 x 10^{10} particles (e.g., about 1 x 10^{10}-1 x 10^{12} particles) of the adenoviral vector. Alternatively, the dose comprises no more than about 1 x 10^{14} particles, preferably no more than about 1 x 10^{13} particles, even more preferably no more than about 1 x 10^{12} particles, even more preferably no more than about 1 x 10^{11} particles, and most preferably no more than about 1 x 10^{10} particles (e.g., no more than about 1 x 10^9 articles). Thus, the dose may contain a single dose of adenoviral vector with, for example, about 1 x 10^6 particle units (pu), about 2 x 10^6 pu, about 4 x 10^6 pu, about 1 x 10^7 pu, about 2 x 10^7 pu, about 4 x 10^7 pu, about 1 x 10^8 pu, about 2 x 10^8 pu, about 4 x 10^8 pu, about 1 x 10^9 pu, about 2 x 10^9 pu, about 4 x 10^9 pu, about 1 x 10^{10} pu, about 2 x 10^{10} pu, about 4 x 10^{10}

pu, about 1 x 10^{11} pu, about 2 x 10^{11} pu, about 4 x 10^{11} pu, about 1 x 10^{12} pu, about 2 x 10^{12} pu, or about 4 x 10^{12} pu of adenoviral vector. See, for example, the adenoviral vectors in U.S. Patent No. 8,454,972 B2 to Nabel, et. al., granted on June 4, 2013; incorporated by reference herein, and the dosages at col 29, lines 36-58 thereof. In an embodiment herein, the adenovirus is delivered via multiple doses.

[00160] In terms of in vivo delivery, AAV is advantageous over other viral vectors due to low toxicity and low probability of causing insertional mutagenesis because it doesn't integrate into the host genome. AAV has a packaging limit of 4.5 or 4.75 Kb. Constructs larger than 4.5 or 4.75 Kb result in significantly reduced virus production. There are many promoters that can be used to drive nucleic acid molecule expression. AAV ITR can serve as a promoter and is advantageous for eliminating the need for an additional promoter element. For ubiquitous expression, the following promoters can be used: CMV, CAG, CBh, PGK, SV40, Ferritin heavy or light chains, etc. For brain expression, the following promoters can be used: SynapsinI for all neurons, CaMKIIalpha for excitatory neurons, GAD67 or GAD65 or VGAT for GABAergic neurons, etc. Promoters used to drive RNA synthesis can include: Pol III promoters such as U6 or H1. The use of a Pol II promoter and intronic cassettes can be used to express guide RNA (gRNA).

[00161] With regard to AAV vectors useful in the practice of the invention, mention is made of US Patent Nos. 5658785, 7115391, 7172893, 6953690, 6936466, 6924128, 6893865, 6793926, 6537540, 6475769 and 6258595, and documents cited therein.

[00162] As to AAV, the AAV can be AAV1, AAV2, AAV5 or any combination thereof. One can select the AAV with regard to the cells to be targeted; e.g., one can select AAV serotypes 1, 2, 5 or a hybrid capsid AAV1, AAV2, AAV5 or any combination thereof for targeting brain or neuronal cells; and one can select AAV4 for targeting cardiac tissue. AAV8 is useful for delivery to the liver. The above promoters and vectors are preferred individually.

[00163] In an embodiment herein, the delivery is via an AAV. A therapeutically effective dosage for in vivo delivery of the AAV to a human is believed to be in the range of from about 20 to about 50 ml of saline solution containing from about 1 x 10^{10} to about 1 x 10^{50} functional AAV/ml solution. The dosage may be adjusted to balance the therapeutic benefit against any side effects. In an embodiment herein, the AAV dose is generally in the range of concentrations of from about 1 x 10^{5} to 1 x 10^{50} genomes AAV, from about 1 x 10^{8} to 1 x 10^{20} genomes AAV,

from about 1 x 10^{10} to about 1 x 10^{16} genomes, or about 1 x 10^{11} to about 1 x 10^{16} genomes AAV. A human dosage may be about 1 x 10^{13} genomes AAV. Such concentrations may be delivered in from about 0.001 ml to about 100 ml, about 0.05 to about 50 ml, or about 10 to about 25 ml of a carrier solution. In a preferred embodiment, AAV is used with a titer of about 2 x 10^{13} viral genomes/milliliter, and each of the striatal hemispheres of a mouse receives one 500 nanoliter injection. Other effective dosages can be readily established by one of ordinary skill in the art through routine trials establishing dose response curves. See, for example, U.S. Patent No. 8,404,658 B2 to Hajjar, et al., granted on March 26, 2013, at col. 27, lines 45-60.

[00164] In another embodiment effectively activating a cellular immune response for a neoplasia vaccine or immunogenic composition can be achieved by expressing the relevant neoantigens in a vaccine or immunogenic composition in a non-pathogenic microorganism. Well-known examples of such microorganisms are Mycobacterium bovis BCG, Salmonella and Pseudomona (See, U.S. Patent No. 6,991,797, hereby incorporated by reference in its entirety).

[00165] In another embodiment a Poxvirus is used in the neoplasia vaccine or immunogenic composition. These include orthopoxvirus, avipox, vaccinia, MVA, NYVAC, canarypox, ALVAC, fowlpox, TROVAC, etc. (see e.g., Verardiet al., Hum Vaccin Immunother. 2012 Jul;8(7):961-70; and Moss, Vaccine. 2013; 31(39): 4220–4222). Poxvirus expression vectors were described in 1982 and quickly became widely used for vaccine development as well as research in numerous fields. Advantages of the vectors include simple construction, ability to accommodate large amounts of foreign DNA and high expression levels.

[00166] Information concerning poxviruses that may be used in the practice of the invention, such as *Chordopoxvirinae* subfamily poxviruses (poxviruses of vertebrates), for instance, orthopoxviruses and avipoxviruses, e.g., vaccinia virus (e.g., Wyeth Strain, WR Strain (e.g., ATCC® VR-1354), Copenhagen Strain, NYVAC, NYVAC.1, NYVAC.2, MVA, MVA-BN), canarypox virus (e.g., Wheatley C93 Strain, ALVAC), fowlpox virus (e.g., FP9 Strain, Webster Strain, TROVAC), dovepox, pigeonpox, quailpox, and raccoon pox, *inter alia*, synthetic or non-naturally occurring recombinants thereof, uses thereof, and methods for making and using such recombinants may be found in scientific and patent literature, such as:

- US Patents Nos. 4,603,112, 4,769,330, 5,110,587, 5,174,993, 5,364,773, 5,762,938, 5,494,807, 5,766,597, 7,767,449, 6,780,407, 6,537,594, 6,265,189, 6,214,353, 6,130,066, 6,004,777, 5,990,091, 5,942,235, 5,833,975, 5,766,597, 5,756,101, 7,045,313, 6,780,417,

8,470,598, 8,372,622, 8,268,329, 8,268,325, 8,236,560, 8,163,293, 7,964,398, 7,964,396, 7,964,395, 7,939,086, 7,923,017, 7,897,156, 7,892,533, 7,628,980, 7,459,270, 7,445,924, 7,384,644, 7,335,364, 7,189,536, 7,097,842, 6,913,752, 6,761,893, 6,682,743, 5,770,212, 5,766,882, and 5,989,562, and

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each of which is incorporated herein by reference.

[00167] In another embodiment the vaccinia virus is used in the neoplasia vaccine or immunogenic composition to express a neoantigen. (Rolph et al., Recombinant viruses as vaccines and immunological tools. Curr Opin Immunol 9:517-524, 1997). The recombinant vaccinia virus is able to replicate within the cytoplasm of the infected host cell and the polypeptide of interest can therefore induce an immune response. Moreover, Poxviruses have been widely used as vaccine or immunogenic composition vectors because of their ability to target encoded antigens for processing by the major histocompatibility complex class I pathway by directly infecting immune cells, in particular antigen-presenting cells, but also due to their ability to self-adjuvant.

[00168] In another embodiment ALVAC is used as a vector in a neoplasia vaccine or immunogenic composition. ALVAC is a canarypox virus that can be modified to express foreign transgenes and has been used as a method for vaccination against both prokaryotic and eukaryotic antigens (Horig H, Lee DS, Conkright W, et al. Phase I clinical trial of a recombinant canarypoxvirus (ALVAC) vaccine expressing human carcinoembryonic antigen and the B7.1 co-stimulatory molecule. Cancer Immunol Immunother 2000;49:504–14; von Mehren M, Arlen P, Tsang KY, et al. Pilot study of a dual gene recombinant avipox vaccine containing both carcinoembryonic antigen (CEA) and B7.1 transgenes in patients with recurrent CEA-expressing adenocarcinomas. Clin Cancer Res 2000;6:2219–28; Musey L, Ding Y, Elizaga M, et al. HIV-1 vaccination administered intramuscularly can induce both systemic and mucosal T cell immunity

in HIV-1-uninfected individuals. J Immunol 2003;171:1094–101; Paoletti E. Applications of pox virus vectors to vaccination: an update. Proc Natl Acad Sci U S A 1996;93:11349–53; U.S. Patent No. 7,255,862). In a phase I clinical trial, an ALVAC virus expressing the tumor antigen CEA showed an excellent safety profile and resulted in increased CEA-specific T-cell responses in selected patients; objective clinical responses, however, were not observed (Marshall JL, Hawkins MJ, Tsang KY, et al. Phase I study in cancer patients of a replication-defective avipox recombinant vaccine that expresses human carcinoembryonic antigen. J Clin Oncol 1999;17:332–7).

[00169] In another embodiment a Modified Vaccinia Ankara (MVA) virus may be used as a viral vector for a neoantigen vaccine or immunogenic composition. MVA is a member of the Orthopoxvirus family and has been generated by about 570 serial passages on chicken embryo fibroblasts of the Ankara strain of Vaccinia virus (CVA) (for review see Mayr, A., et al., Infection 3, 6-14, 1975). As a consequence of these passages, the resulting MVA virus contains 31 kilobases less genomic information compared to CVA, and is highly host-cell restricted (Meyer, H. et al., J. Gen. Virol. 72, 1031-1038, 1991). MVA is characterized by its extreme attenuation, namely, by a diminished virulence or infectious ability, but still holds an excellent immunogenicity. When tested in a variety of animal models, MVA was proven to be avirulent, even in immuno-suppressed individuals. Moreover, MVA-BN®-HER2 is a candidate immunotherapy designed for the treatment of HER-2-positive breast cancer and is currently in clinical trials. (Mandl et al., Cancer Immunol Immunother. Jan 2012; 61(1): 19–29). Methods to make and use recombinant MVA has been described (e.g., see U.S. Patent Nos. 8,309,098 and 5,185,146 hereby incorporated in its entirety).

[00170] In another embodiment the modified Copenhagen strain of vaccinia virus, NYVAC and NYVAC variations are used as a vector (see U.S. Patent No. 7,255,862; PCT WO 95/30018; U.S. Pat. Nos. 5,364,773 and 5,494,807, hereby incorporated by reference in its entirety).

[00171] In one embodiment recombinant viral particles of the vaccine or immunogenic composition are administered to patients in need thereof. Dosages of expressed neoantigen can range from a few to a few hundred micrograms, e.g., 5 to 500 .mu.g. The vaccine or immunogenic composition can be administered in any suitable amount to achieve expression at these dosage levels. The viral particles can be administered to a patient in need thereof or transfected into cells in an amount of about at least $10^{3.5}$ pfu; thus, the viral particles are

preferably administered to a patient in need thereof or infected or transfected into cells in at least about 10^4 pfu to about 10^6 pfu; however, a patient in need thereof can be administered at least about 10^8 pfu such that a more preferred amount for administration can be at least about 10^7 pfu to about 10^9 pfu. Doses as to NYVAC are applicable as to ALVAC, MVA, MVA-BN, and avipoxes, such as canarypox and fowlpox.

Vaccine or Immunogenic Composition Adjuvant

[00172] Effective vaccine or immunogenic compositions advantageously include a strong adjuvant to initiate an immune response. As described herein, poly-ICLC, an agonist of TLR3 and the RNA helicase –domains of MDA5 and RIG3, has shown several desirable properties for a vaccine or immunogenic composition adjuvant. These properties include the induction of local and systemic activation of immune cells in vivo, production of stimulatory chemokines and cytokines, and stimulation of antigen-presentation by DCs. Furthermore, poly-ICLC can induce durable CD4+ and CD8+ responses in humans. Importantly, striking similarities in the upregulation of transcriptional and signal transduction pathways were seen in subjects vaccinated with poly-ICLC and in volunteers who had received the highly effective, replication-competent yellow fever vaccine. Furthermore, >90% of ovarian carcinoma patients immunized with poly-ICLC in combination with a NY-ESO-1 peptide vaccine (in addition to Montanide) showed induction of CD4+ and CD8+ T cell, as well as antibody responses to the peptide in a recent phase 1 study. At the same time, poly-ICLC has been extensively tested in more than 25 clinical trials to date and exhibited a relatively benign toxicity profile. In addition to a powerful and specific immunogen the neoantigen peptides may be combined with an adjuvant (e.g., poly-ICLC) or another anti-neoplastic agent. Without being bound by theory, these neoantigens are expected to bypass central thymic tolerance (thus allowing stronger anti-tumor T cell response), while reducing the potential for autoimmunity (e.g., by avoiding targeting of normal self-antigens). An effective immune response advantageously includes a strong adjuvant to activate the immune system (Speiser and Romero, Molecularly defined vaccines for cancer immunotherapy, and protective T cell immunity Seminars in Immunol 22:144 (2010)). For example, Toll-like receptors (TLRs) have emerged as powerful sensors of microbial and viral pathogen "danger signals", effectively inducing the innate immune system, and in turn, the adaptive immune system (Bhardwaj and Gnjatic, TLR AGONISTS: Are They Good Adjuvants?

Cancer J. 16:382-391 (2010)). Among the TLR agonists, poly-ICLC (a synthetic double-stranded RNA mimic) is one of the most potent activators of myeloid-derived dendritic cells. In a human volunteer study, poly-ICLC has been shown to be safe and to induce a gene expression profile in peripheral blood cells comparable to that induced by one of the most potent live attenuated viral vaccines, the yellow fever vaccine YF-17D (Caskey et al, Synthetic double-stranded RNA induces innate immune responses similar to a live viral vaccine in humans J Exp Med 208:2357 (2011)). In a preferred embodiment Hiltonol®, a GMP preparation of poly-ICLC prepared by Oncovir, Inc, is utilized as the adjuvant. In other embodiments, other adjuvants described herein are envisioned. For instance oil-in-water, water-in-oil or multiphasic W/O/W; see, e.g., US 7,608,279 and Aucouturier et al, Vaccine 19 (2001), 2666-2672, and documents cited therein.

Indications

[00173] Examples of cancers and cancer conditions that can be treated with the therapy of this document include, but are not limited to a patient in need thereof that has been diagnosed as having cancer, or at risk of developing cancer. The subject may have a solid tumor such as breast, ovarian, prostate, lung, kidney, gastric, colon, testicular, head and neck, pancreas, brain, melanoma, and other tumors of tissue organs and hematological tumors, such as lymphomas and leukemias, including acute myelogenous leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, T cell lymphocytic leukemia, and B cell lymphomas, tumors of the brain and central nervous system (e.g., tumors of the meninges, brain, spinal cord, cranial nerves and other parts of the CNS, such as glioblastomas or medulla blastomas); head and/or neck cancer, breast tumors, tumors of the circulatory system (e.g., heart, mediastinum and pleura, and other intrathoracic organs, vascular tumors, and tumor-associated vascular tissue); tumors of the blood and lymphatic system (e.g., Hodgkin's disease, Non-Hodgkin's disease lymphoma, Burkitt's lymphoma, AIDS-related lymphomas, malignant immunoproliferative diseases, multiple myeloma, and malignant plasma cell neoplasms, lymphoid leukemia, myeloid leukemia, acute or chronic lymphocytic leukemia, monocytic leukemia, other leukemias of specific cell type, leukemia of unspecified cell type, unspecified malignant neoplasms of lymphoid, hematopoietic and related tissues, such as diffuse large cell lymphoma, T-cell lymphoma or cutaneous T-cell lymphoma); tumors of the excretory system (e.g., kidney, renal pelvis, ureter, bladder, and other

urinary organs); tumors of the gastrointestinal tract (e.g., esophagus, stomach, small intestine, colon, colorectal, rectosigmoid junction, rectum, anus, and anal canal); tumors involving the liver and intrahepatic bile ducts, gall bladder, and other parts of the biliary tract, pancreas, and other digestive organs; tumors of the oral cavity (e.g., lip, tongue, gum, floor of mouth, palate, parotid gland, salivary glands, tonsil, oropharynx, nasopharynx, puriform sinus, hypopharynx, and other sites of the oral cavity); tumors of the reproductive system (e.g., vulva, vagina, Cervix uteri, uterus, ovary, and other sites associated with female genital organs, placenta, penis, prostate, testis, and other sites associated with male genital organs); tumors of the respiratory tract (e.g., nasal cavity, middle ear, accessory sinuses, larynx, trachea, bronchus and lung, such as small cell lung cancer and non-small cell lung cancer); tumors of the skeletal system (e.g., bone and articular cartilage of limbs, bone articular cartilage and other sites); tumors of the skin (e.g., malignant melanoma of the skin, non-melanoma skin cancer, basal cell carcinoma of skin, squamous cell carcinoma of skin, mesothelioma, Kaposi's sarcoma); and tumors involving other tissues including peripheral nerves and autonomic nervous system, connective and soft tissue, retroperitoneoum and peritoneum, eye, thyroid, adrenal gland, and other endocrine glands and related structures, secondary and unspecified malignant neoplasms of lymph nodes, secondary malignant neoplasm of respiratory and digestive systems and secondary malignant neoplasm of other sites. Thus the population of subjects described herein may be suffering from one of the above cancer types. In other embodiments, the population of subjects may be all subjects suffering from solid tumors, or all subjects suffering from liquid tumors.

[00174] Of special interest is the treatment of Non-Hodgkin's Lymphoma (NHL), clear cell Renal Cell Carcinoma (ccRCC), metastatic melanoma, sarcoma, leukemia or a cancer of the bladder, colon, brain, breast, head and neck, endometrium, lung, ovary, pancreas or prostate. In certain embodiments, the melanoma is high risk melanoma.

[00175] Cancers that can be treated using the therapy described herein may include among others cases which are refractory to treatment with other chemotherapeutics. The term "refractory, as used herein refers to a cancer (and/or metastases thereof), which shows no or only weak antiproliferative response (e.g., no or only weak inhibition of tumor growth) after treatment with another chemotherapeutic agent. These are cancers that cannot be treated satisfactorily with other chemotherapeutics. Refractory cancers encompass not only (i) cancers where one or more chemotherapeutics have already failed during treatment of a patient, but also (ii) cancers that can

be shown to be refractory by other means, e.g., biopsy and culture in the presence of chemotherapeutics.

[00176] The therapy described herein is also applicable to the treatment of patients in need thereof who have not been previously treated.

[00177] The therapy described herein is also applicable where the subject has no detectable neoplasia but is at high risk for disease recurrence.

[00178] Also of special interest is the treatment of patients in need thereof who have undergone Autologous Hematopoietic Stem Cell Transplant (AHSCT), and in particular patients who demonstrate residual disease after undergoing AHSCT. The post-AHSCT setting is characterized by a low volume of residual disease, the infusion of immune cells to a situation of homeostatic expansion, and the absence of any standard relapse-delaying therapy. These features provide a unique opportunity to use the claimed neoplastic vaccine or immunogenic composition compositions to delay disease relapse.

Pharmaceutical Compositions/Methods of Delivery

[00179] The present invention is also directed to pharmaceutical compositions comprising an effective amount of one or more neoantigenic peptides as described herein (including a pharmaceutically acceptable salt, thereof), optionally in combination with a pharmaceutically acceptable carrier, excipient or additive.

[00180] When administered as a combination, the therapeutic agents (i.e. the neoantigenic peptides) can be formulated as separate compositions that are given at the same time or different times, or the therapeutic agents can be given as a single composition.

[00181] The compositions may be administered once daily, twice daily, once every two days, once every three days, once every four days, once every five days, once every six days, once every seven days, once every two weeks, once every three weeks, once every four weeks, once every two months, once every six months, or once per year. The dosing interval can be adjusted according to the needs of individual patients. For longer intervals of administration, extended release or depot formulations can be used.

[00182] The compositions of the invention can be used to treat diseases and disease conditions that are acute, and may also be used for treatment of chronic conditions. In particular, the compositions of the invention are used in methods to treat or prevent a neoplasia. In certain

embodiments, the compounds of the invention are administered for time periods exceeding two weeks, three weeks, one month, two months, three months, four months, five months, six months, one year, two years, three years, four years, or five years, ten years, or fifteen years; or for example, any time period range in days, months or years in which the low end of the range is any time period between 14 days and 15 years and the upper end of the range is between 15 days and 20 years (e.g., 4 weeks and 15 years, 6 months and 20 years). In some cases, it may be advantageous for the compounds of the invention to be administered for the remainder of the patient's life. In preferred embodiments, the patient is monitored to check the progression of the disease or disorder, and the dose is adjusted accordingly. In preferred embodiments, treatment according to the invention is effective for at least two weeks, three weeks, one month, two months, three months, four months, five months, six months, one year, two years, three years, four years, or five years, ten years, fifteen years, twenty years, or for the remainder of the subject's life.

[00183] Surgical resection uses surgery to remove abnormal tissue in cancer, such as mediastinal, neurogenic, or germ cell tumors, or thymoma. In certain embodiments, administration of the composition is initiated following tumor resection. In other embodiments, administration of the neoplasia vaccine or immunogenic composition is initiated 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more weeks after tumor resection. Preferably, administration of the neoplasia vaccine or immunogenic composition is initiated 4, 5, 6, 7, 8, 9, 10, 11 or 12 weeks after tumor resection.

[00184] Prime/ boost regimens refer to the successive administrations of a vaccine or immunogenic or immunological compositions. In certain embodiments, administration of the neoplasia vaccine or immunogenic composition is in a prime/ boost dosing regimen, for example administration of the neoplasia vaccine or immunogenic composition at weeks 1, 2, 3 or 4 as a prime and administration of the neoplasia vaccine or immunogenic composition is at months 2, 3 or 4 as a boost. In another embodiment heterologous prime-boost strategies are used to ellicit a greater cytotoxic T-cell response (see Schneider et al., Induction of CD8+ T cells using heterologous prime-boost immunisation strategies, Immunological Reviews Volume 170, Issue 1, pages 29–38, August 1999). In another embodiment DNA encoding neoantigens is used to prime followed by a protein boost. In another embodiment protein is used to prime followed by boosting with a virus encoding the neoantigen. In another embodiment a virus encoding the

neoantigen is used to prime and another virus is used to boost. In another embodiment protein is used to prime and DNA is used to boost. In a preferred embodiment a DNA vaccine or immunogenic composition is used to prime a T-cell response and a recombinant viral vaccine or immunogenic composition is used to boost the response. In another preferred embodiment a viral vaccine or immunogenic composition is coadministered with a protein or DNA vaccine or immunogenic composition to act as an adjuvant for the protein or DNA vaccine or immunogenic composition. The patient can then be boosted with either the viral vaccine or immunogenic composition, protein, or DNA vaccine or immunogenic composition (see Hutchings et al., Combination of protein and viral vaccines induces potent cellular and humoral immune responses and enhanced protection from murine malaria challenge. Infect Immun. 2007 Dec;75(12):5819-26. Epub 2007 Oct 1).

[00185] The pharmaceutical compositions can be processed in accordance with conventional methods of pharmacy to produce medicinal agents for administration to patients in need thereof, including humans and other mammals.

[00186] Modifications of the neoantigenic peptides can affect the solubility, bioavailability and rate of metabolism of the peptides, thus providing control over the delivery of the active species. Solubility can be assessed by preparing the neoantigenic peptide and testing according to known methods well within the routine practitioner's skill in the art.

[00187] In certain embodiments of the pharmaceutical composition the pharmaceutically acceptable carrier comprises water. In certain embodiments, the pharmaceutically acceptable carrier further comprises dextrose. In certain embodiments, the pharmaceutically acceptable carrier further comprises dimethylsulfoxide. In certain embodiments, the pharmaceutical composition further comprises an immunomodulator or adjuvant. In certain embodiments, the immunodulator or adjuvant is selected from the group consisting of poly-ICLC, STING agonist, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PEPTEL, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon. In certain embodiments, the immunomodulator or adjuvant comprises poly-ICLC.

[00188] Xanthenone derivatives such as, for example, Vadimezan or AsA404 (also known as 5,6-dimethylaxanthenone-4-acetic acid (DMXAA)), may also be used as adjuvants according to embodiments of the invention. Alternatively, such derivatives may also be administered in parallel to the vaccine or immunogenic composition of the invention, for example via systemic or intratumoral delivery, to stimulate immunity at the tumor site. Without being bound by theory, it is believed that such xanthenone derivatives act by stimulating interferon (IFN) production via the stimulator of IFN gene ISTING) receptor (see e.g., Conlon et al. (2013) Mouse, but not Human STING, Binds and Signals in Response to the Vascular Disrupting Agent 5,6-Dimethylxanthenone-4-Acetic Acid, Journal of Immunology, 190:5216-25 and Kim et al. (2013) Anticancer Flavonoids are Mouse-Selective STING Agonists, 8:1396-1401).

[00189] The vaccine or immunological composition may also include an adjuvant compound chosen from the acrylic or methacrylic polymers and the copolymers of maleic anhydride and an alkenyl derivative. It is in particular a polymer of acrylic or methacrylic acid cross-linked with a polyalkenyl ether of a sugar or polyalcohol (carbomer), in particular cross-linked with an allyl sucrose or with allylpentaerythritol. It may also be a copolymer of maleic anhydride and ethylene cross-linked, for example, with divinyl ether (see U.S. Patent No. 6,713,068 hereby incorporated by reference in its entirety)..

[00190] In certain embodiments, the pH modifier can stabilize the adjuvant or immunomodulator as described herein.

[00191] In certain embodiments, a pharmaceutical composition comprises: one to five peptides, dimethylsulfoxide (DMSO), dextrose, water, succinate, poly I: poly C, poly-L-lysine, carboxymethylcellulose, and chloride. In certain embodiments, each of the one to five peptides is present at a concentration of 300 μg/ml. In certain embodiments, the pharmaceutical composition comprises ≤ 3% DMSO by volume. In certain embodiments, the pharmaceutical composition comprises 3.6 – 3.7 % dextrose in water. In certain embodiments, the pharmaceutical composition comprises 3.6 – 3.7 mM succinate (e.g., as sodium succinate) or a salt thereof. In certain embodiments, the pharmaceutical composition comprises 0.5 mg/ml poly I: poly C. In certain embodiments, the pharmaceutical composition comprises 0.375 mg/ml poly-L-Lysine. In certain embodiments, the pharmaceutical composition comprises 1.25 mg/ml sodium carboxymethylcellulose. In certain embodiments, the pharmaceutical composition comprises 0.225% sodium chloride.

[00192] Pharmaceutical compositions comprise the herein-described tumor specific neoantigenic peptides in a therapeutically effective amount for treating diseases and conditions (e.g., a neoplasia/tumor), which have been described herein, optionally in combination with a pharmaceutically acceptable additive, carrier and/or excipient. One of ordinary skill in the art from this disclosure and the knowledge in the art will recognize that a therapeutically effective amount of one of more compounds according to the present invention may vary with the condition to be treated, its severity, the treatment regimen to be employed, the pharmacokinetics of the agent used, as well as the patient (animal or human) treated.

[00193] To prepare the pharmaceutical compositions according to the present invention, a therapeutically effective amount of one or more of the compounds according to the present invention is preferably intimately admixed with a pharmaceutically acceptable carrier according to conventional pharmaceutical compounding techniques to produce a dose. A carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., ocular, oral, topical or parenteral, including gels, creams ointments, lotions and time released implantable preparations, among numerous others. In preparing pharmaceutical compositions in oral dosage form, any of the usual pharmaceutical media may be used. Thus, for liquid oral preparations such as suspensions, elixirs and solutions, suitable carriers and additives including water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents and the like may be used. For solid oral preparations such as powders, tablets, capsules, and for solid preparations such as suppositories, suitable carriers and additives including starches, sugar carriers, such as dextrose, mannitol, lactose and related carriers, diluents, granulating agents, lubricants, binders, disintegrating agents and the like may be used. If desired, the tablets or capsules may be enteric-coated or sustained release by standard techniques.

[00194] The active compound is included in the pharmaceutically acceptable carrier or diluent in an amount sufficient to deliver to a patient a therapeutically effective amount for the desired indication, without causing serious toxic effects in the patient treated.

[00195] Oral compositions generally include an inert diluent or an edible carrier. They may be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound or its prodrug derivative can be incorporated with excipients and used in the form of tablets, troches, or capsules. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition.

[00196] The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a dispersing agent such as alginic acid or corn starch; a lubricant such as magnesium stearate; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring. When the dosage unit form is a capsule, it can contain, in addition to material herein discussed, a liquid carrier such as a fatty oil. In addition, dosage unit forms can contain various other materials which modify the physical form of the dosage unit, for example, coatings of sugar, shellac, or enteric agents.

[00197] Formulations of the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets each containing a predetermined amount of the active ingredient; as a powder or granules; as a solution or a suspension in an aqueous liquid or a non-aqueous liquid; or as an oil-in-water liquid emulsion or a water-in-oil emulsion and as a bolus, etc.

[00198] A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared by compressing in a suitable machine the active ingredient in a free-flowing form such as a powder or granules, optionally mixed with a binder, lubricant, inert diluent, preservative, surface-active or dispersing agent. Molded tablets may be made by molding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent. The tablets optionally may be coated or scored and may be formulated so as to provide slow or controlled release of the active ingredient therein.

[00199] Methods of formulating such slow or controlled release compositions of pharmaceutically active ingredients, are known in the art and described in several issued US Patents, some of which include, but are not limited to, US Patent Nos. 3,870,790; 4,226,859; 4,369,172; 4,842,866 and 5,705,190, the disclosures of which are incorporated herein by reference in their entireties. Coatings can be used for delivery of compounds to the intestine (see, e.g., U.S. Patent Nos. 6,638,534, 5,541,171, 5,217,720, and 6,569,457, and references cited therein).

[00200] The active compound or pharmaceutically acceptable salt thereof may also be administered as a component of an elixir, suspension, syrup, wafer, chewing gum or the like. A

syrup may contain, in addition to the active compounds, sucrose or fructose as a sweetening agent and certain preservatives, dyes and colorings and flavors.

[00201] Solutions or suspensions used for ocular, parenteral, intradermal, subcutaneous, or topical application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose.

[00202] In certain embodiments, the pharmaceutically acceptable carrier is an aqueous solvent, i.e., a solvent comprising water, optionally with additional co-solvents. Exemplary pharmaceutically acceptable carriers include water, buffer solutions in water (such as phosphate-buffered saline (PBS), and 5% dextrose in water (D5W). In certain embodiments, the aqueous solvent further comprises dimethyl sulfoxide (DMSO), e.g., in an amount of about 1-4%, or 1-3%. In certain embodiments, the pharmaceutically acceptable carrier is isotonic (i.e., has substantially the same osmotic pressure as a body fluid such as plasma).

[00203] In one embodiment, the active compounds are prepared with carriers that protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid, and polylactic-co-glycolic acid (PLGA). Methods for preparation of such formulations are within the ambit of the skilled artisan in view of this disclosure and the knowledge in the art.

[00204] A skilled artisan from this disclosure and the knowledge in the art recognizes that in addition to tablets, other dosage forms can be formulated to provide slow or controlled release of the active ingredient. Such dosage forms include, but are not limited to, capsules, granulations and gel-caps.

[00205] Liposomal suspensions may also be pharmaceutically acceptable carriers. These may be prepared according to methods known to those skilled in the art. For example, liposomal formulations may be prepared by dissolving appropriate lipid(s) in an inorganic solvent that is then evaporated, leaving behind a thin film of dried lipid on the surface of the container. An

aqueous solution of the active compound are then introduced into the container. The container is then swirled by hand to free lipid material from the sides of the container and to disperse lipid aggregates, thereby forming the liposomal suspension. Other methods of preparation well known by those of ordinary skill may also be used in this aspect of the present invention.

[00206] The formulations may conveniently be presented in unit dosage form and may be prepared by conventional pharmaceutical techniques. Such techniques include the step of bringing into association the active ingredient and the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

[00207] Formulations and compositions suitable for topical administration in the mouth include lozenges comprising the ingredients in a flavored basis, usually sucrose and acacia or tragacanth; pastilles comprising the active ingredient in an inert basis such as gelatin and glycerin, or sucrose and acacia; and mouthwashes comprising the ingredient to be administered in a suitable liquid carrier.

[00208] Formulations suitable for topical administration to the skin may be presented as ointments, creams, gels and pastes comprising the ingredient to be administered in a pharmaceutical acceptable carrier. A preferred topical delivery system is a transdermal patch containing the ingredient to be administered.

[00209] Formulations for rectal administration may be presented as a suppository with a suitable base comprising, for example, cocoa butter or a salicylate.

[00210] Formulations suitable for nasal administration, wherein the carrier is a solid, include a coarse powder having a particle size, for example, in the range of 20 to 500 microns which is administered in the manner in which snuff is administered, i.e., by rapid inhalation through the nasal passage from a container of the powder held close up to the nose. Suitable formulations, wherein the carrier is a liquid, for administration, as for example, a nasal spray or as nasal drops, include aqueous or oily solutions of the active ingredient.

[00211] Formulations suitable for vaginal administration may be presented as pessaries, tampons, creams, gels, pastes, foams or spray formulations containing in addition to the active ingredient such carriers as are known in the art to be appropriate.

[00212] The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic. If administered intravenously, preferred carriers include, for example, physiological saline or phosphate buffered saline (PBS).

[00213] For parenteral formulations, the carrier usually comprises sterile water or aqueous sodium chloride solution, though other ingredients including those which aid dispersion may be included. Of course, where sterile water is to be used and maintained as sterile, the compositions and carriers are also sterilized. Injectable suspensions may also be prepared, in which case appropriate liquid carriers, suspending agents and the like may be employed.

[00214] Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain antioxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example, water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described.

[00215] Administration of the active compound may range from continuous (intravenous drip) to several oral administrations per day (for example, Q.I.D.) and may include oral, topical, eye or ocular, parenteral, intramuscular, intravenous, sub-cutaneous, transdermal (which may include a penetration enhancement agent), buccal and suppository administration, among other routes of administration, including through an eye or ocular route.

[00216] The neoplasia vaccine or immunogenic composition, and any additional agents, may be administered by injection, orally, parenterally, by inhalation spray, rectally, vaginally, or topically in dosage unit formulations containing conventional pharmaceutically acceptable carriers, adjuvants, and vehicles. The term parenteral as used herein includes, into a lymph node or nodes, subcutaneous, intravenous, intramuscular, intrasternal, infusion techniques, intraperitoneally, eye or ocular, intravitreal, intrabuccal, transdermal, intranasal, into the brain, including intracranial and intradural, into the joints, including ankles, knees, hips, shoulders, elbows, wrists, directly into tumors, and the like, and in suppository form.

[00217] In certain embodiments, the vaccine or immunogenic composition is administered intravenously or subcutaneously. Various techniques can be used for providing the subject compositions at the site of interest, such as injection, use of catheters, trocars, projectiles, pluronic gel, stents, sustained drug release polymers or other device which provides for internal access. Where an organ or tissue is accessible because of removal from the patient, such organ or tissue may be bathed in a medium containing the subject compositions, the subject compositions may be painted onto the organ, or may be applied in any convenient way.

[00218] The tumor specific neoantigenic peptides may be administered through a device suitable for the controlled and sustained release of a composition effective in obtaining a desired local or systemic physiological or pharmacological effect. The method includes positioning the sustained released drug delivery system at an area wherein release of the agent is desired and allowing the agent to pass through the device to the desired area of treatment.

[00219] The tumor specific neoantigenic peptides may be utilized in combination with at least one known other therapeutic agent, or a pharmaceutically acceptable salt of said agent. Examples of known therapeutic agents which can be used for combination therapy include, but are not limited to, corticosteroids (e.g., cortisone, prednisone, dexamethasone), non-steroidal anti-inflammatory drugs (NSAIDS) (e.g., ibuprofen, celecoxib, aspirin, indomethicin, naproxen), alkylating agents such as busulfan, cis-platin, mitomycin C, and carboplatin; antimitotic agents such as colchicine, vinblastine, paclitaxel, and docetaxel; topo I inhibitors such as camptothecin and topotecan; topo II inhibitors such as doxorubicin and etoposide; and/or RNA/DNA antimetabolites such as 5-azacytidine, 5-fluorouracil and methotrexate; DNA antimetabolites such as 5-fluoro-2′-deoxy-uridine, ara-C, hydroxyurea and thioguanine; antibodies such as HERCEPTIN and RITUXAN.

[00220] It should be understood that in addition to the ingredients particularly mentioned herein, the formulations of the present invention may include other agents conventional in the art having regard to the type of formulation in question, for example, those suitable for oral administration may include flavoring agents.

[00221] Pharmaceutically acceptable salt forms may be the preferred chemical form of compounds according to the present invention for inclusion in pharmaceutical compositions according to the present invention.

[00222] The present compounds or their derivatives, including prodrug forms of these agents, can be provided in the form of pharmaceutically acceptable salts. As used herein, the term pharmaceutically acceptable salts or complexes refers to appropriate salts or complexes of the active compounds according to the present invention which retain the desired biological activity of the parent compound and exhibit limited toxicological effects to normal cells. Nonlimiting examples of such salts are (a) acid addition salts formed with inorganic acids (for example, hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid, and the like), and salts formed with organic acids such as acetic acid, oxalic acid, tartaric acid, succinic acid, malic acid, ascorbic acid, benzoic acid, tannic acid, pamoic acid, alginic acid, and polyglutamic acid, among others; (b) base addition salts formed with metal cations such as zinc, calcium, sodium, potassium, and the like, among numerous others.

[00223] The compounds herein are commercially available or can be synthesized. As can be appreciated by the skilled artisan, further methods of synthesizing the compounds of the formulae herein is evident to those of ordinary skill in the art. Additionally, the various synthetic steps may be performed in an alternate sequence or order to give the desired compounds. Synthetic chemistry transformations and protecting group methodologies (protection and deprotection) useful in synthesizing the compounds described herein are known in the art and include, for example, those such as described in R. Larock, Comprehensive Organic Transformations, 2nd. Ed., Wiley-VCH Publishers (1999); T.W. Greene and P.G.M. Wuts, Protective Groups in Organic Synthesis, 3rd. Ed., John Wiley and Sons (1999); L. Fieser and M. Fieser, Fieser and Fieser's Reagents for Organic Synthesis, John Wiley and Sons (1999); and L. Paquette, ed., Encyclopedia of Reagents for Organic Synthesis, John Wiley and Sons (1995), and subsequent editions thereof.

[00224] The additional agents that may be included with the tumor specific neo-antigenic peptides of this invention may contain one or more asymmetric centers and thus occur as racemates and racemic mixtures, single enantiomers, individual diastereomers and diastereomeric mixtures. All such isomeric forms of these compounds are expressly included in the present invention. The compounds of this invention may also be represented in multiple tautomeric forms, in such instances, the invention expressly includes all tautomeric forms of the compounds described herein (e.g., alkylation of a ring system may result in alkylation at multiple sites, the invention expressly includes all such reaction products). All such isomeric forms of

such compounds are expressly included in the present invention. All crystal forms of the compounds described herein are expressly included in the present invention.

Dosage

[00225] When the agents described herein are administered as pharmaceuticals to humans or animals, they can be given per se or as a pharmaceutical composition containing active ingredient in combination with a pharmaceutically acceptable carrier, excipient, or diluent.

[00226] Actual dosage levels and time course of administration of the active ingredients in the pharmaceutical compositions of the invention can be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. Generally, agents or pharmaceutical compositions of the invention are administered in an amount sufficient to reduce or eliminate symptoms associated with neoplasia, e.g. cancer or tumors.

[00227] A preferred dose of an agent is the maximum that a patient can tolerate and not develop serious or unacceptable side effects. Exemplary dose ranges include 0.01 mg to 250 mg per day, 0.01 mg to 100 mg per day, 1 mg to 100 mg per day, 10 mg to 100 mg per day, 1 mg to 10 mg per day, and 0.01 mg to 10 mg per day. A preferred dose of an agent is the maximum that a patient can tolerate and not develop serious or unacceptable side effects. In embodiments, the agent is administered at a concentration of about 10 micrograms to about 100 mg per kilogram of body weight per day, about 0.1 to about 10 mg/kg per day, or about 1.0 mg to about 10 mg/kg of body weight per day.

[00228] In embodiments, the pharmaceutical composition comprises an agent in an amount ranging between 1 and 10 mg, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 mg.

[00229] In embodiments, the therapeutically effective dosage produces a serum concentration of an agent of from about 0.1 ng/ml to about 50-100 mg/ml. The pharmaceutical compositions 5 typically should provide a dosage of from about 0.001 mg to about 2000 mg of compound per kilogram of body weight per day. For example, dosages for systemic administration to a human patient can range from 1-10 mglkg, 20-80 mglkg, 5-50 mg/kg, 75-150 mg/kg, 100-500 mg/kg, 250-750 mg/kg, 500-1000 mg/kg, 1-10 mg/kg, 5-50 mg/kg, 25-75 mg/kg, 50-100 mg/kg, 100-250 mg/kg, 50-100 mg/kg, 250-500 mg/kg, 500-750 mg/kg, 750-1000 mg/kg, 1000-1500 mg/kg, 10 1500-2000 mg/kg, 5 mg/kg, 20 mg/kg, 50 mg/kg, 100 mg/kg, 500 mg/kg, 1000 mg/kg, 1500

mg/kg, or 2000 mg/kg. Pharmaceutical dosage unit forms are prepared to provide from about 1 mg to about 5000 mg, for example from about 100 to about 2500 mg of the compound or a combination of essential ingredients per dosage unit form.

[00230] In embodiments, about 50 nM to about 1μM of an agent is administered to a subject. In related embodiments, about 50-100 nM, 50-250 nM, 100-500 nM, 250-500 nM, 250-750 nM, 500-750 nM, 500 nM to 1μM, or 750 nM to 1μM of an agent is administered to a subject.

[00231] Determination of an effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. Generally, an efficacious or effective amount of an agent is determined by first administering a low dose of the agent(s) and then incrementally increasing the administered dose or dosages until a desired effect (e.g., reduce or eliminate symptoms associated with viral infection or autoimmune disease) is observed in the treated subject, with minimal or acceptable toxic side effects. Applicable methods for determining an appropriate dose and dosing schedule for administration of a pharmaceutical composition of the present invention are described, for example, in Goodman and Gilman's The Pharmacological Basis of Therapeutics, Goodman et al., eds., 11th Edition, McGraw-Hill 2005, and Remington: The Science and Practice of Pharmacy, 20th and 21st Editions, Gennaro and University of the Sciences in Philadelphia, Eds., Lippencott Williams & Wilkins (2003 and 2005), each of which is hereby incorporated by reference.

[00232] Preferred unit dosage formulations are those containing a daily dose or unit, daily sub-dose, as herein discussed, or an appropriate fraction thereof, of the administered ingredient.

[00233] The dosage regimen for treating a disorder or a disease with the tumor specific neoantigenic peptides of this invention and/or compositions of this invention is based on a variety of factors, including the type of disease, the age, weight, sex, medical condition of the patient, the severity of the condition, the route of administration, and the particular compound employed. Thus, the dosage regimen may vary widely, but can be determined routinely using standard methods.

[00234] The amounts and dosage regimens administered to a subject can depend on a number of factors, such as the mode of administration, the nature of the condition being treated, the body weight of the subject being treated and the judgment of the prescribing physician; all such factors being within the ambit of the skilled artisan from this disclosure and the knowledge in the art.

[00235] The amount of compound included within therapeutically active formulations according to the present invention is an effective amount for treating the disease or condition. In general, a therapeutically effective amount of the present preferred compound in dosage form usually ranges from slightly less than about 0.025 mg/kg/day to about 2.5 g/kg/day, preferably about 0.1 mg/kg/day to about 100 mg/kg/day of the patient or considerably more, depending upon the compound used, the condition or infection treated and the route of administration, although exceptions to this dosage range may be contemplated by the present invention. In its most preferred form, compounds according to the present invention are administered in amounts ranging from about 1 mg/kg/day to about 100 mg/kg/day. The dosage of the compound can depend on the condition being treated, the particular compound, and other clinical factors such as weight and condition of the patient and the route of administration of the compound. It is to be understood that the present invention has application for both human and veterinary use.

[00236] For oral administration to humans, a dosage of between approximately 0.1 to 100 mg/kg/day, preferably between approximately 1 and 100 mg/kg/day, is generally sufficient.

[00237] Where drug delivery is systemic rather than topical, this dosage range generally produces effective blood level concentrations of active compound ranging from less than about 0.04 to about 400 micrograms/cc or more of blood in the patient. The compound is conveniently administered in any suitable unit dosage form, including but not limited to one containing 0.001 to 3000 mg, preferably 0.05 to 500 mg of active ingredient per unit dosage form. An oral dosage of 10-250 mg is usually convenient.

[00238] According to certain exemplary embodiments, the vaccine or immunogenic composition is administered at a dose of about 10 μg to 1 mg per neoantigenic peptide. According to certain exemplary embodiments, the vaccine or immunogenic composition is administered at an average weekly dose level of about 10 μg to 2000 μg per neoantigenic peptide.

[00239] The concentration of active compound in the drug composition will depend on absorption, distribution, inactivation, and excretion rates of the drug as well as other factors known to those of skill in the art. It is to be noted that dosage values will also vary with the severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of

the compositions, and that the concentration ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition. The active ingredient may be administered at once, or may be divided into a number of smaller doses to be administered at varying intervals of time.

[00240] The invention provides for pharmaceutical compositions containing at least one tumor specific neoantigen described herein. In embodiments, the pharmaceutical compositions contain a pharmaceutically acceptable carrier, excipient, or diluent, which includes any pharmaceutical agent that does not itself induce the production of an immune response harmful to a subject receiving the composition, and which may be administered without undue toxicity. As used herein, the term "pharmaceutically acceptable" means being approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopia, European Pharmacopia or other generally recognized pharmacopia for use in mammals, and more particularly in humans. These compositions can be useful for treating and/or preventing viral infection and/or autoimmune disease.

[00241] A thorough discussion of pharmaceutically acceptable carriers, diluents, and other excipients is presented in Remington's Pharmaceutical Sciences (17th ed., Mack Publishing Company) and Remington: The Science and Practice of Pharmacy (21st ed., Lippincott Williams & Wilkins), which are hereby incorporated by reference. The formulation of the pharmaceutical composition should suit the mode of administration. In embodiments, the pharmaceutical composition is suitable for administration to humans, and can be sterile, non-particulate and/or non-pyrogenic.

[00242] Pharmaceutically acceptable carriers, excipients, or diluents include, but are not limited, to saline, buffered saline, dextrose, water, glycerol, ethanol, sterile isotonic aqueous buffer, and combinations thereof.

[00243] Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives, and antioxidants can also be present in the compositions.

[00244] Examples of pharmaceutically-acceptable antioxidants include, but are not limited to: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl

palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[00245] In embodiments, the pharmaceutical composition is provided in a solid form, such as a lyophilized powder suitable for reconstitution, a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder.

[00246] In embodiments, the pharmaceutical composition is supplied in liquid form, for example, in a sealed container indicating the quantity and concentration of the active ingredient in the pharmaceutical composition. In related embodiments, the liquid form of the pharmaceutical composition is supplied in a hermetically sealed container.

[00247] Methods for formulating the pharmaceutical compositions of the present invention are conventional and well known in the art (see Remington and Remington's). One of skill in the art can readily formulate a pharmaceutical composition having the desired characteristics (e.g., route of administration, biosafety, and release profile).

[00248] Methods for preparing the pharmaceutical compositions include the step of bringing into association the active ingredient with a pharmaceutically acceptable carrier and, optionally, one or more accessory ingredients. The pharmaceutical compositions can be prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers, or finely divided solid carriers, or both, and then, if necessary, shaping the product. Additional methodology for preparing the pharmaceutical compositions, including the preparation of multilayer dosage forms, are described in Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems (9th ed., Lippincott Williams & Wilkins), which is hereby incorporated by reference.

[00249] Pharmaceutical compositions suitable for oral administration can be in the form of capsules, cachets, pills, tablets, lozenges (using a flavored basis, usually sucrose and acacia or tragacanth), powders, granules, or as a solution or a suspension in an aqueous or non-aqueous liquid, or as an oil-in-water or water-in-oil liquid emulsion, or as an elixir or syrup, or as pastilles (using an inert base, such as gelatin and glycerin, or sucrose and acacia) and/or as mouth washes and the like, each containing a predetermined amount of a compound(s) described herein, a derivative thereof, or a pharmaceutically acceptable salt or prodrug thereof as the active ingredient(s). The active ingredient can also be administered as a bolus, electuary, or paste.

[00250] In solid dosage forms for oral administration (e.g., capsules, tablets, pills, dragees, powders, granules and the like), the active ingredient is mixed with one or more pharmaceutically acceptable carriers, excipients, or diluents, such as sodium citrate or dicalcium phosphate, and/or any of the following: (1) fillers or extenders, such as starches, lactose, sucrose, glucose, mannitol, and/or silicic acid; (2) binders, such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinyl pyrrolidone, sucrose and/or acacia; (3) humectants, such as glycerol; (4) disintegrating agents, such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate; (5) solution retarding agents, such as paraffin; (6) absorption accelerators, such as quaternary ammonium compounds; (7) wetting agents, such as, for example, acetyl alcohol and glycerol monostearate; (8) absorbents, such as kaolin and bentonite clay; (9) lubricants, such a talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof; and (10) coloring agents. In the case of capsules, tablets, and pills, the pharmaceutical compositions can also comprise buffering agents. Solid compositions of a similar type can also be prepared using fillers in soft and hard-filled gelatin capsules, and excipients such as lactose or milk sugars, as well as high molecular weight polyethylene glycols and the like.

[00251] A tablet can be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets can be prepared using binders (for example, gelatin or hydroxypropylmethyl cellulose), lubricants, inert diluents, preservatives, disintegrants (for example, sodium starch glycolate or cross-linked sodium carboxymethyl cellulose), surface-actives, and/ or dispersing agents. Molded tablets can be made by molding in a suitable machine a mixture of the powdered active ingredient moistened with an inert liquid diluent.

[00252] The tablets and other solid dosage forms, such as dragees, capsules, pills, and granules, can optionally be scored or prepared with coatings and shells, such as enteric coatings and other coatings well known in the art.

[00253] In some embodiments, in order to prolong the effect of an active ingredient, it is desirable to slow the absorption of the compound from subcutaneous or intramuscular injection. This can be accomplished by the use of a liquid suspension of crystalline or amorphous material having poor water solubility. The rate of absorption of the active ingredient then depends upon its rate of dissolution which, in turn, can depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally-administered active ingredient is

accomplished by dissolving or suspending the compound in an oil vehicle. In addition, prolonged absorption of the injectable pharmaceutical form can be brought about by the inclusion of agents that delay absorption such as aluminum monostearate and gelatin.

[00254] Controlled release parenteral compositions can be in form of aqueous suspensions, microspheres, microcapsules, magnetic microspheres, oil solutions, oil suspensions, emulsions, or the active ingredient can be incorporated in biocompatible carrier(s), liposomes, nanoparticles, implants or infusion devices.

[00255] Materials for use in the preparation of microspheres and/or microcapsules include biodegradable/bioerodible polymers such as polyglactin, poly-(isobutyl cyanoacrylate), poly(2-hydroxyethyl-L-glutamine) and poly(lactic acid).

[00256] Biocompatible carriers which can be used when formulating a controlled release parenteral formulation include carbohydrates such as dextrans, proteins such as albumin, lipoproteins or antibodies.

[00257] Materials for use in implants can be non-biodegradable, e.g., polydimethylsiloxane, or biodegradable such as, e.g., poly(caprolactone), poly(lactic acid), poly(glycolic acid) or poly(ortho esters).

[00258] In embodiments, the active ingredient(s) are administered by aerosol. This is accomplished by preparing an aqueous aerosol, liposomal preparation, or solid particles containing the compound. A nonaqueous (e.g., fluorocarbon propellant) suspension can be used. The pharmaceutical composition can also be administered using a sonic nebulizer, which would minimize exposing the agent to shear, which can result in degradation of the compound.

[00259] Ordinarily, an aqueous aerosol is made by formulating an aqueous solution or suspension of the active ingredient(s) together with conventional pharmaceutically-acceptable carriers and stabilizers. The carriers and stabilizers vary with the requirements of the particular compound, but typically include nonionic surfactants (Tweens, Pluronics, or polyethylene glycol), innocuous proteins like serum albumin, sorbitan esters, oleic acid, lecithin, amino acids such as glycine, buffers, salts, sugars or sugar alcohols. Aerosols generally are prepared from isotonic solutions.

[00260] Dosage forms for topical or transdermal administration of an active ingredient(s) includes powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and

inhalants. The active ingredient(s) can be mixed under sterile conditions with a pharmaceutically acceptable carrier, and with any preservatives, buffers, or propellants as appropriate.

[00261] Transdermal patches suitable for use in the present invention are disclosed in Transdermal Drug Delivery: Developmental Issues and Research Initiatives (Marcel Dekker Inc., 1989) and U.S. Pat. Nos. 4,743,249, 4,906,169, 5,198,223, 4,816,540, 5,422,119, 5,023,084, which are hereby incorporated by reference. The transdermal patch can also be any transdermal patch well known in the art, including transscrotal patches. Pharmaceutical compositions in such transdermal patches can contain one or more absorption enhancers or skin permeation enhancers well known in the art (see, e.g., U.S. Pat. Nos. 4,379,454 and 4,973,468, which are hereby incorporated by reference). Transdermal therapeutic systems for use in the present invention can be based on iontophoresis, diffusion, or a combination of these two effects.

[00262] Transdermal patches have the added advantage of providing controlled delivery of active ingredient(s) to the body. Such dosage forms can be made by dissolving or dispersing the active ingredient(s) in a proper medium. Absorption enhancers can also be used to increase the flux of the active ingredient across the skin. The rate of such flux can be controlled by either providing a rate controlling membrane or dispersing the active ingredient(s) in a polymer matrix or gel.

[00263] Such pharmaceutical compositions can be in the form of creams, ointments, lotions, liniments, gels, hydrogels, solutions, suspensions, sticks, sprays, pastes, plasters and other kinds of transdermal drug delivery systems. The compositions can also include pharmaceutically acceptable carriers or excipients such as emulsifying agents, antioxidants, buffering agents, preservatives, humectants, penetration enhancers, chelating agents, gel-forming agents, ointment bases, perfumes, and skin protective agents.

[00264] Examples of emulsifying agents include, but are not limited to, naturally occurring gums, e.g. gum acacia or gum tragacanth, naturally occurring phosphatides, e.g. soybean lecithin and sorbitan monooleate derivatives.

[00265] Examples of antioxidants include, but are not limited to, butylated hydroxy anisole (BHA), ascorbic acid and derivatives thereof, tocopherol and derivatives thereof, and cysteine.

[00266] Examples of preservatives include, but are not limited to, parabens, such as methyl or propyl p-hydroxybenzoate and benzalkonium chloride.

[00267] Examples of humectants include, but are not limited to, glycerin, propylene glycol, sorbitol and urea.

[00268] Examples of penetration enhancers include, but are not limited to, propylene glycol, DMSO, triethanolamine, N,N-dimethylacetamide, N,N-dimethylformamide, 2-pyrrolidone and derivatives thereof, tetrahydrofurfuryl alcohol, propylene glycol, diethylene glycol monoethyl or monomethyl ether with propylene glycol monolaurate or methyl laurate, eucalyptol, lecithin, TRANSCUTOL, and AZONE.

[00269] Examples of chelating agents include, but are not limited to, sodium EDTA, citric acid and phosphoric acid.

[00270] Examples of gel forming agents include, but are not limited to, Carbopol, cellulose derivatives, bentonite, alginates, gelatin and polyvinylpyrrolidone.

[00271] In addition to the active ingredient(s), the ointments, pastes, creams, and gels of the present invention can contain excipients, such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or mixtures thereof.

[00272] Powders and sprays can contain excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants, such as chlorofluorohydrocarbons, and volatile unsubstituted hydrocarbons, such as butane and propane.

[00273] Injectable depot forms are made by forming microencapsule matrices of compound(s) of the invention in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of compound to polymer, and the nature of the particular polymer employed, the rate of compound release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are also prepared by entrapping the drug in liposomes or microemulsions which are compatible with body tissue.

[00274] Subcutaneous implants are well known in the art and are suitable for use in the present invention. Subcutaneous implantation methods are preferably non-irritating and mechanically resilient. The implants can be of matrix type, of reservoir type, or hybrids thereof. In matrix type devices, the carrier material can be porous or non-porous, solid or semi-solid, and permeable or impermeable to the active compound or compounds. The carrier material can be biodegradable or may slowly erode after administration. In some instances, the matrix is non-

degradable but instead relies on the diffusion of the active compound through the matrix for the carrier material to degrade. Alternative subcutaneous implant methods utilize reservoir devices where the active compound or compounds are surrounded by a rate controlling membrane, e.g., a membrane independent of component concentration (possessing zero-order kinetics). Devices consisting of a matrix surrounded by a rate controlling membrane also suitable for use.

[00275] Both reservoir and matrix type devices can contain materials such as polydimethylsiloxane, such as SILASTIC, or other silicone rubbers. Matrix materials can be insoluble polypropylene, polyethylene, polyvinyl chloride, ethylvinyl acetate, polystyrene and polymethacrylate, as well as glycerol esters of the glycerol palmitostearate, glycerol stearate, and glycerol behenate type. Materials can be hydrophobic or hydrophilic polymers and optionally contain solubilizing agents.

[00276] Subcutaneous implant devices can be slow-release capsules made with any suitable polymer, e.g., as described in U.S. Pat. Nos. 5,035,891 and 4,210,644, which are hereby incorporated by reference.

[00277] In general, at least four different approaches are applicable in order to provide rate control over the release and transdermal permeation of a drug compound. These approaches are: membrane-moderated systems, adhesive diffusion-controlled systems, matrix dispersion-type systems and microreservoir systems. It is appreciated that a controlled release percutaneous and/or topical composition can be obtained by using a suitable mixture of these approaches.

[00278] In a membrane-moderated system, the active ingredient is present in a reservoir which is totally encapsulated in a shallow compartment molded from a drug-impermeable laminate, such as a metallic plastic laminate, and a rate-controlling polymeric membrane such as a microporous or a non-porous polymeric membrane, e.g., ethylene-vinyl acetate copolymer. The active ingredient is released through the rate controlling polymeric membrane. In the drug reservoir, the active ingredient can either be dispersed in a solid polymer matrix or suspended in an unleachable, viscous liquid medium such as silicone fluid. On the external surface of the polymeric membrane, a thin layer of an adhesive polymer is applied to achieve an intimate contact of the transdermal system with the skin surface. The adhesive polymer is preferably a polymer which is hypoallergenic and compatible with the active drug substance.

[00279] In an adhesive diffusion-controlled system, a reservoir of the active ingredient is formed by directly dispersing the active ingredient in an adhesive polymer and then by, e.g.,

solvent casting, spreading the adhesive containing the active ingredient onto a flat sheet of substantially drug-impermeable metallic plastic backing to form a thin drug reservoir layer.

[00280] A matrix dispersion-type system is characterized in that a reservoir of the active ingredient is formed by substantially homogeneously dispersing the active ingredient in a hydrophilic or lipophilic polymer matrix. The drug-containing polymer is then molded into disc with a substantially well-defined surface area and controlled thickness. The adhesive polymer is spread along the circumference to form a strip of adhesive around the disc.

[00281] A microreservoir system can be considered as a combination of the reservoir and matrix dispersion type systems. In this case, the reservoir of the active substance is formed by first suspending the drug solids in an aqueous solution of water-soluble polymer and then dispersing the drug suspension in a lipophilic polymer to form a multiplicity of unleachable, microscopic spheres of drug reservoirs.

[00282] Any of the herein-described controlled release, extended release, and sustained release compositions can be formulated to release the active ingredient in about 30 minutes to about 1 week, in about 30 minutes to about 72 hours, in about 30 minutes to 24 hours, in about 30 minutes to 12 hours, in about 30 minutes to 6 hours, in about 30 minutes to 4 hours, and in about 3 hours to 10 hours. In embodiments, an effective concentration of the active ingredient(s) is sustained in a subject for 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 16 hours, 24 hours, 48 hours, 72 hours, or more after administration of the pharmaceutical compositions to the subject.

Vaccine or immunogenic compositions

[00283] The present invention is directed in some aspects to pharmaceutical compositions suitable for the prevention or treatment of cancer. In one embodiment, the composition comprises at least an immunogenic composition, e.g., a neoplasia vaccine or immunogenic composition capable of raising a specific T-cell response. The neoplasia vaccine or immunogenic composition comprises neoantigenic peptides and/or neoantigenic polypeptides corresponding to tumor specific neoantigens as described herein.

[00284] A suitable neoplasia vaccine or immunogenic composition can preferably contain a plurality of tumor specific neoantigenic peptides. In an embodiment, the vaccine or immunogenic composition can include between 1 and 100 sets of peptides, more preferably between 1 and 50 such peptides, even more preferably between 10 and 30 sets peptides, even

more preferably between 15 and 25 peptides. According to another preferred embodiment, the vaccine or immunogenic composition can include at least one peptides, more preferably 2, 3, 4, or 5 peptides, In certain embodiments, the vaccine or immunogenic composition can comprise 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 different peptides.

[00285] The optimum amount of each peptide to be included in the vaccine or immunogenic composition and the optimum dosing regimen can be determined by one skilled in the art without undue experimentation. For example, the peptide or its variant may be prepared for intravenous (i.v.) injection, sub-cutaneous (s.c.) injection, intradermal (i.d.) injection, intraperitoneal (i.p.) injection, intramuscular (i.m.) injection. Preferred methods of peptide injection include s.c, i.d., i.p., i.m., and i.v. Preferred methods of DNA injection include i.d., i.m., s.c, i.p. and i.v. For example, doses of between 1 and 500 mg 50 μg and 1.5 mg, preferably 10 μg to 500 μg, of peptide or DNA may be given and can depend from the respective peptide or DNA. Doses of this range were successfully used in previous trials (Brunsvig P F, et al., Cancer Immunol Immunother. 2006; 55(12): 1553- 1564; M. Staehler, et al., ASCO meeting 2007; Abstract No 3017). Other methods of administration of the vaccine or immunogenic composition are known to those skilled in the art.

[00286] In one embodiment of the present invention the different tumor specific neoantigenic peptides and/or polypeptides are selected for use in the neoplasia vaccine or immunogenic composition so as to maximize the likelihood of generating an immune attack against the neoplasias/tumors in a high proportion of subjects in the population. Without being bound by theory, it is believed that the inclusion of a diversity of tumor specific neoantigenic peptides can generate a broad scale immune attack against a neoplasia/tumor. In one embodiment, the selected tumor specific neoantigenic peptides/polypeptides are encoded by missense mutations. In a second embodiment, the selected tumor specific neoantigenic peptides/polypeptides are encoded by a combination of missense mutations and neoORF mutations. In a third embodiment, the selected tumor specific neoantigenic peptides/polypeptides are encoded by neoORF mutations.

[00287] In one embodiment in which the selected tumor specific neoantigenic peptides/polypeptides are encoded by missense mutations, the peptides and/or polypeptides are chosen based on their capability to associate with the MHC molecules of a high proportion of

subjects in the population. Peptides/polypeptides derived from neoORF mutations can also be selected on the basis of their capability to associate with the MHC molecules of the patient population.

[00288] The vaccine or immunogenic composition is capable of raising a specific cytotoxic T-cells response and/or a specific helper T-cell response.

[00289] The vaccine or immunogenic composition can further comprise an adjuvant and/or a carrier. Examples of useful adjuvants and carriers are given herein herein. The peptides and/or polypeptides in the composition can be associated with a carrier such as, e.g., a protein or an antigen-presenting cell such as e.g. a dendritic cell (DC) capable of presenting the peptide to a T-cell.

[00290] Adjuvants are any substance whose admixture into the vaccine or immunogenic composition increases or otherwise modifies the immune response to the mutant peptide. Carriers are scaffold structures, for example a polypeptide or a polysaccharide, to which the neoantigenic peptides, is capable of being associated. Optionally, adjuvants are conjugated covalently or non-covalently to the peptides or polypeptides of the invention.

[00291] The ability of an adjuvant to increase the immune response to an antigen is typically manifested by a significant increase in immune-mediated reaction, or reduction in disease symptoms. For example, an increase in humoral immunity is typically manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T-cell activity is typically manifested in increased cell proliferation, or cellular cytotoxicity, or cytokine secretion. An adjuvant may also alter an immune response, for example, by changing a primarily humoral or Th2 response into a primarily cellular, or Th1 response.

[00292] Suitable adjuvants include, but are not limited to 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PEPTEL. vector system, PLG microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon (Aquila Biotech, Worcester, Mass., USA) which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall mimics, and other proprietary adjuvants such as Ribi's Detox. Quil or Superfos. Several

immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Dupuis M, et al., Cell Immunol. 1998; 186(1): 18-27; Allison A C; Dev Biol Stand. 1998; 92:3-11). Also cytokines may be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-alpha), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, IL-1 and IL-4) (U.S. Pat. No. 5,849,589, specifically incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12) (Gabrilovich D I, et al., J Immunother Emphasis Tumor Immunol. 1996 (6):414-418).

[00293] Toll like receptors (TLRs) may also be used as adjuvants, and are important members of the family of pattern recognition receptors (PRRs) which recognize conserved motifs shared by many micro-organisms, termed "pathogen-associated molecular patterns" (PAMPS). Recognition of these "danger signals" activates multiple elements of the innate and adaptive immune system. TLRs are expressed by cells of the innate and adaptive immune systems such as dendritic cells (DCs), macrophages, T and B cells, mast cells, and granulocytes and are localized in different cellular compartments, such as the plasma membrane, lysosomes, endosomes, and endolysosomes. Different TLRs recognize distinct PAMPS. For example, TLR4 is activated by LPS contained in bacterial cell walls, TLR9 is activated by unmethylated bacterial or viral CpG DNA, and TLR3 is activated by double stranded RNA. TLR ligand binding leads to the activation of one or more intracellular signaling pathways, ultimately resulting in the production of many key molecules associated with inflammation and immunity (particularly the transcription factor NF-κB and the Type-I interferons). TLR mediated DC activation leads to enhanced DC activation, phagocytosis, upregulation of activation and co-stimulation markers such as CD80, CD83, and CD86, expression of CCR7 allowing migration of DC to draining lymph nodes and facilitating antigen presentation to T cells, as well as increased secretion of cytokines such as type I interferons, IL-12, and IL-6. All of these downstream events are critical for the induction of an adaptive immune response.

[00294] Among the most promising cancer vaccine or immunogenic composition adjuvants currently in clinical development are the TLR9 agonist CpG and the synthetic double-stranded RNA (dsRNA) TLR3 ligand poly-ICLC. In preclinical studies poly-ICLC appears to be the most potent TLR adjuvant when compared to LPS and CpG due to its induction of pro-inflammatory cytokines and lack of stimulation of IL-10, as well as maintenance of high levels of co-

stimulatory molecules in DCs1. Furthermore, poly-ICLC was recently directly compared to CpG in non-human primates (rhesus macaques) as adjuvant for a protein vaccine or immunogenic composition consisting of human papillomavirus (HPV)16 capsomers (Stahl-Hennig C, Eisenblatter M, Jasny E, et al. Synthetic double-stranded RNAs are adjuvants for the induction of T helper 1 and humoral immune responses to human papillomavirus in rhesus macaques. PLoS pathogens. Apr 2009;5(4)).

[00295] CpG immuno stimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a vaccine or immunogenic composition setting. Without being bound by theory, CpG oligonucleotides act by activating the innate (non- adaptive) immune system via Toll-like receptors (TLR), mainly TLR9. CpG triggered TLR9 activation enhances antigen-specific humoral and cellular responses to a wide variety of antigens, including peptide or protein antigens, live or killed viruses, dendritic cell vaccines, autologous cellular vaccines and polysaccharide conjugates in both prophylactic and therapeutic vaccines. More importantly, it enhances dendritic cell maturation and differentiation, resulting in enhanced activation of Thl cells and strong cytotoxic T- lymphocyte (CTL) generation, even in the absence of CD4 T-cell help. The Thl bias induced by TLR9 stimulation is maintained even in the presence of vaccine adjuvants such as alum or incomplete Freund's adjuvant (IFA) that normally promote a Th2 bias. CpG oligonucleotides show even greater adjuvant activity when formulated or co-administered with other adjuvants or in formulations such as microparticles, nano particles, lipid emulsions or similar formulations, which are especially necessary for inducing a strong response when the antigen is relatively weak. They also accelerate the immune response and enabled the antigen doses to be reduced by approximately two orders of magnitude, with comparable antibody responses to the full-dose vaccine without CpG in some experiments (Arthur M. Krieg, Nature Reviews, Drug Discovery, 5, Jun. 2006, 471-484). U.S. Pat. No. 6,406,705 Bl describes the combined use of CpG oligonucleotides, non-nucleic acid adjuvants and an antigen to induce an antigen- specific immune response. A commercially available CpG TLR9 antagonist is dSLIM (double Stem Loop Immunomodulator) by Mologen (Berlin, GERMANY), which is a preferred component of the pharmaceutical composition of the present invention. Other TLR binding molecules such as RNA binding TLR 7, TLR 8 and/or TLR 9 may also be used.

[00296] Other examples of useful adjuvants include, but are not limited to, chemically modified CpGs (e.g. CpR, Idera), Poly(I:C)(e.g. polyi:CI2U), non-CpG bacterial DNA or RNA

as well as immunoactive small molecules and antibodies such as cyclophosphamide, sunitinib, bevacizumab, celebrex, NCX-4016, sildenafil, tadalafil, vardenafil, sorafinib, XL-999, CP-547632, pazopanib, ZD2171, AZD2171, ipilimumab, tremelimumab, and SC58175, which may act therapeutically and/or as an adjuvant. The amounts and concentrations of adjuvants and additives useful in the context of the present invention can readily be determined by the skilled artisan without undue experimentation. Additional adjuvants include colony- stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim).

[00297] Poly-ICLC is a synthetically prepared double-stranded RNA consisting of polyI and polyC strands of average length of about 5000 nucleotides, which has been stabilized to thermal denaturation and hydrolysis by serum nucleases by the addition of polylysine and carboxymethylcellulose. The compound activates TLR3 and the RNA helicase-domain of MDA5, both members of the PAMP family, leading to DC and natural killer (NK) cell activation and production of a "natural mix" of type I interferons, cytokines, and chemokines. Furthermore, poly-ICLC exerts a more direct, broad host-targeted anti-infectious and possibly antitumor effect mediated by the two IFN-inducible nuclear enzyme systems, the 2'5'-OAS and the P1/eIF2a kinase, also known as the PKR (4-6), as well as RIG-I helicase and MDA5.

[00298] In rodents and non-human primates, poly-ICLC was shown to enhance T cell responses to viral antigens, cross-priming, and the induction of tumor-, virus-, and autoantigen-specific CD8+ T-cells. In a recent study in non-human primates, poly-ICLC was found to be essential for the generation of antibody responses and T-cell immunity to DC targeted or non-targeted HIV Gag p24 protein, emphasizing its effectiveness as a vaccine adjuvant.

[00299] In human subjects, transcriptional analysis of serial whole blood samples revealed similar gene expression profiles among the 8 healthy human volunteers receiving one single s.c. administration of poly-ICLC and differential expression of up to 212 genes between these 8 subjects versus 4 subjects receiving placebo. Remarkably, comparison of the poly-ICLC gene expression data to previous data from volunteers immunized with the highly effective yellow fever vaccine YF17D showed that a large number of transcriptional and signal transduction canonical pathways, including those of the innate immune system, were similarly upregulated at peak time points.

[00300] More recently, an immunologic analysis was reported on patients with ovarian, fallopian tube, and primary peritoneal cancer in second or third complete clinical remission who

were treated on a phase 1 study of subcutaneous vaccination with synthetic overlapping long peptides (OLP) from the cancer testis antigen NY-ESO-1 alone or with Montanide-ISA-51, or with 1.4 mg poly-ICLC and Montanide. The generation of NY-ESO-1-specific CD4+ and CD8+ T-cell and antibody responses were markedly enhanced with the addition of poly-ICLC and Montanide compared to OLP alone or OLP and Montanide.

[00301] A vaccine or immunogenic composition according to the present invention may comprise more than one different adjuvant. Furthermore, the invention encompasses a therapeutic composition comprising any adjuvant substance including any of those herein discussed. It is also contemplated that the peptide or polypeptide, and the adjuvant can be administered separately in any appropriate sequence.

[00302] A carrier may be present independently of an adjuvant. The carrier may be covalently linked to the antigen. A carrier can also be added to the antigen by inserting DNA encoding the carrier in frame with DNA encoding the antigen. The function of a carrier can for example be to confer stability, to increase the biological activity, or to increase serum half-life. Extension of the half-life can help to reduce the number of applications and to lower doses, thus are beneficial for therapeutic but also economic reasons. Furthermore, a carrier may aid presenting peptides to T-cells. The carrier may be any suitable carrier known to the person skilled in the art, for example a protein or an antigen presenting cell. A carrier protein could be but is not limited to keyhole limpet hemocyanin, serum proteins such as transferrin, bovine serum albumin, human serum albumin, thyroglobulin or ovalbumin, immunoglobulins, or hormones, such as insulin or palmitic acid. For immunization of humans, the carrier may be a physiologically acceptable carrier acceptable to humans and safe. However, tetanus toxoid and/or diptheria toxoid are suitable carriers in one embodiment of the invention. Alternatively, the carrier may be dextrans for example sepharose.

[00303] Cytotoxic T-cells (CTLs) recognize an antigen in the form of a peptide bound to an MHC molecule rather than the intact foreign antigen itself. The MHC molecule itself is located at the cell surface of an antigen presenting cell. Thus, an activation of CTLs is only possible if a trimeric complex of peptide antigen, MHC molecule, and APC is present. Correspondingly, it may enhance the immune response if not only the peptide is used for activation of CTLs, but if additionally APCs with the respective MHC molecule are added. Therefore, in some

embodiments the vaccine or immunogenic composition according to the present invention additionally contains at least one antigen presenting cell.

[00304] The antigen-presenting cell (or stimulator cell) typically has an MHC class I or II molecule on its surface, and in one embodiment is substantially incapable of itself loading the MHC class I or II molecule with the selected antigen. As is described in more detail herein, the MHC class I or II molecule may readily be loaded with the selected antigen in vitro.

[00305] CD8+ cell activity may be augmented through the use of CD4+ cells. The identification of CD4 T+ cell epitopes for tumor antigens has attracted interest because many immune based therapies against cancer may be more effective if both CD8+ and CD4+ T lymphocytes are used to target a patient's tumor. CD4+ cells are capable of enhancing CD8 T cell responses. Many studies in animal models have clearly demonstrated better results when both CD4+ and CD8+ T cells participate in anti-tumor responses (see e.g., Nishimura et al. (1999) Distinct role of antigen-specific T helper type 1 (TH1) and Th2 cells in tumor eradication in vivo. J Ex Med 190:617-27). Universal CD4+ T cell epitopes have been identified that are applicable to developing therapies against different types of cancer (see e.g., Kobayashi et al. (2008) Current Opinion in Immunology 20:221-27). For example, an HLA-DR restricted helper peptide from tetanus toxoid was used in melanoma vaccines to activate CD4+ T cells non-specifically (see e.g., Slingluff et al. (2007) Immunologic and Clinical Outcomes of a Randomized Phase II Trial of Two Multipeptide Vaccines for Melanoma in the Adjuvant Setting, Clinical Cancer Research 13(21):6386-95). It is contemplated within the scope of the invention that such CD4+ cells may be applicable at three levels that vary in their tumor specificity: 1) a broad level in which universal CD4+ epitopes (e.g., tetanus toxoid) may be used to augment CD8+ cells; 2) an intermediate level in which native, tumor-associated CD4+ epitopes may be used to augment CD8+ cells; and 3) a patient specific level in which neoantigen CD4+ epitopes may be used to augment CD8+ cells in a patient specific manner. Although current algorithms for predicting CD4 epitopes are limited in accuracy, it is a reasonable expectation that many long peptides containing predicted CD8 neoepitopes will also include CD4 epitopes. CD4 epitopes are longer than CD8 epitopes and typically are 10 -12 amino acids in length although some can be longer (Kreiter et al, Mutant MHC Class II epitopes drive therapeutic immune responses to cancer, Nature (2015). Thus the neoantigenic epitopes described herein, either in the form of

long peptides (>25 amino acids) or nucleic acids encoding such long peptides, may also boost CD4 responses in a tumor and patient-specific manner (level (3) above).

[00306] CD8+ cell immunity may also be generated with neoantigen loaded dendritic cell (DC) vaccine. DCs are potent antigen-presenting cells that initiate T cell immunity and can be used as cancer vaccines when loaded with one or more peptides of interest, for example, by direct peptide injection. For example, patients that were newly diagnosed with metastatic melanoma were shown to be immunized against 3 HLA-A*0201-restricted gp100 melanoma antigen-derived peptides with autologous peptide pulsed CD40L/IFN-g-activated mature DCs via an IL-12p70-producing patient DC vaccine (see e.g., Carreno et al (2013) L-12p70-producing patient DC vaccine elicits Tc1-polarized immunity, Journal of Clinical Investigation, 123(8):3383-94 and Ali et al. (2009) In situ regulation of DC subsets and T cells mediates tumor regression in mice, Cancer Immunotherapy, 1(8):1-10). It is contemplated within the scope of the invention that neoantigen loaded DCs may be prepared using the synthetic TLR 3 agonist Polyinosinic-Polycytidylic Acid-poly-L-lysine Carboxymethylcellulose (Poly-ICLC) to stimulate the DCs. Poly-ICLC is a potent individual maturation stimulus for human DCs as assessed by an upregulation of CD83 and CD86, induction of interleukin-12 (IL-12), tumor necrosis factor (TNF), interferon gamma-induced protein 10 (IP-10), interleukin 1 (IL-1), and type I interferons (IFN), and minimal interleukin 10 (IL-10) production. DCs may be differentiated from frozen peripheral blood mononuclear cells (PBMCs) obtained by leukapheresis, while PBMCs may be isolated by Ficoll gradient centrifugation and frozen in aliquots.

[00307] Illustratively, the following 7 day activation protocol may be used. Day 1—PBMCs are thawed and plated onto tissue culture flasks to select for monocytes which adhere to the plastic surface after 1-2 hr incubation at 37°C in the tissue culture incubator. After incubation, the lymphocytes are washed off and the adherent monocytes are cultured for 5 days in the presence of interleukin-4 (IL-4) and granulocyte macrophage-colony stimulating factor (GM-CSF) to differentiate to immature DCs. On Day 6, immature DCs are pulsed with the keyhole limpet hemocyanin (KLH) protein which serves as a control for the quality of the vaccine and may boost the immunogenicity of the vaccine. The DCs are stimulated to mature, loaded with peptide antigens, and incubated overnight. On Day 7, the cells are washed, and frozen in 1 ml aliquots containing 4-20 x 10(6) cells using a controlled-rate freezer. Lot release testing for the batches of DCs may be performed to meet minimum specifications before the DCs are injected

into patients (see e.g., Sabado et al. (2013) Preparation of tumor antigen-loaded mature dendritic cells for immunotherapy, J. Vis Exp. Aug 1;(78). doi: 10.3791/50085).

[00308] A DC vaccine may be incorporated into a scaffold system to facilitate delivery to a patient. Therapeutic treatment of a patients neoplasia with a DC vaccine may utilize a biomaterial system that releases factors that recruit host dendritic cells into the device, differentiates the resident, immature DCs by locally presenting adjuvants (e.g., danger signals) while releasing antigen, and promotes the release of activated, antigen loaded DCs to the lymph nodes (or desired site of action) where the DCs may interact with T cells to generate a potent cytotoxic T lymphocyte response to the cancer neoantigens. Implantable biomaterials may be used to generate a potent cytotoxic T lymphocyte response against a neoplasia in a patient specific manner. The biomaterial-resident dendritic cells may then be activated by exposing them to danger signals mimicking infection, in concert with release of antigen from the biomaterial. The activated dendritic cells then migrate from the biomaterials to lymph nodes to induce a cytotoxic T effector response. This approach has previously been demonstrated to lead to regression of established melanoma in preclinical studies using a lysate prepared from tumor biopsies (see e.g., Ali et al. (2209) In situ regulation of DC subsets and T cells mediates tumor regression in mice, Cancer Immunotherapy 1(8):1-10; Ali et al. (2009) Infection-mimicking materials to program dendritic cells in situ. Nat Mater 8:151-8), and such a vaccine is currently being tested in a Phase I clinical trial recently initiated at the Dana-Farber Cancer Institute. This approach has also been shown to lead to regression of glioblastoma, as well as the induction of a potent memory response to prevent relapse, using the C6 rat glioma model.24 in the current proposal. The ability of such an implantable, biomatrix vaccine delivery scaffold to amplify and sustain tumor specific dendritic cell activation may lead to more robust anti-tumor immunosensitization than can be achieved by traditional subcutaneous or intra-nodal vaccine administrations.

[00309] The present invention may include any method for loading a neoantigenic peptide onto a dendritic cell. One such method applicable to the present invention is a microfluidic intracellular delivery system. Such systems cause temporary membrane disruption by rapid mechanical deformation of human and mouse immune cells, thus allowing the intracellular delivery of biomolecules (Sharei et al., 2015, PLOS ONE).

[00310] Preferably, the antigen presenting cells are dendritic cells. Suitably, the dendritic cells are autologous dendritic cells that are pulsed with the neoantigenic peptide. The peptide may be any suitable peptide that gives rise to an appropriate T-cell response. T-cell therapy using autologous dendritic cells pulsed with peptides from a tumor associated antigen is disclosed in Murphy et al. (1996) The Prostate 29, 371-380 and Tjua et al. (1997) The Prostate 32, 272-278. In certain embodiments the dendritic cells are targeted using CD141, DEC205, or XCR1 markers. CD141+XCR1+ DC's were identified as a subset that may be better suited to the induction of anti-tumor responses (Bachem et al., J. Exp. Med. 207, 1273-1281 (2010); Crozat et al., J. Exp. Med. 207, 1283-1292 (2010); and Gallois & Bhardwaj, Nature Med. 16, 854-856 (2010)).

[00311] Thus, in one embodiment of the present invention the vaccine or immunogenic composition containing at least one antigen presenting cell is pulsed or loaded with one or more peptides of the present invention. Alternatively, peripheral blood mononuclear cells (PBMCs) isolated from a patient may be loaded with peptides ex vivo and injected back into the patient. As an alternative the antigen presenting cell comprises an expression construct encoding a peptide of the present invention. The polynucleotide may be any suitable polynucleotide and it is preferred that it is capable of transducing the dendritic cell, thus resulting in the presentation of a peptide and induction of immunity.

[00312] The inventive pharmaceutical composition may be compiled so that the selection, number and/or amount of peptides present in the composition covers a high proportion of subjects in the population. The selection may be dependent on the specific type of cancer, the status of the disease, earlier treatment regimens, and, of course, the HLA-haplotypes present in the patient population.

[00313] Pharmaceutical compositions comprising the peptide of the invention may be administered to an individual already suffering from cancer. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use can depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the

initial immunization (that is for therapeutic or prophylactic administration) from about 1.0 μg to about 50,000 μg of peptide for a 70 kg patient, followed by boosting dosages or from about 1.0 μg to about 10,000 μg of peptide pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition and possibly by measuring specific CTL activity in the patient's blood. It should be kept in mind that the peptide and compositions of the present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations, especially when the cancer has metastasized. For therapeutic use, administration should begin as soon as possible after the detection or surgical removal of tumors. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter.

[00314] The pharmaceutical compositions (e.g., vaccine compositions) for therapeutic treatment are intended for parenteral, topical, nasal, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. The compositions may be administered at the site of surgical excision to induce a local immune response to the tumor. The invention provides compositions for parenteral administration which comprise a solution of the peptides and vaccine or immunogenic compositions are dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.9% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

[00315] A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated. For targeting to the immune cells, a ligand, such as, e.g., antibodies or fragments thereof specific for

cell surface determinants of the desired immune system cells, can be incorporated into the liposome.

[00316] For solid compositions, conventional or nanoparticle nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

[00317] For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01 %-20% by weight, preferably 1%-10%. The surfactant can, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included as desired, as with, e.g., lecithin for intranasal delivery.

[00318] The peptides and polypeptides of the invention can be readily synthesized chemically utilizing reagents that are free of contaminating bacterial or animal substances (Merrifield RB: Solid phase peptide synthesis. I. The synthesis of a tetrapeptide. J. Am. Chem. Soc. 85:2149-54, 1963).

[00319] The peptides and polypeptides of the invention can also be expressed by a vector, e.g., a nucleic acid molecule as herein-discussed, e.g., RNA or a DNA plasmid, a viral vector such as a poxvirus, e.g., orthopox virus, avipox virus, or adenovirus, AAV or lentivirus. This approach involves the use of a vector to express nucleotide sequences that encode the peptide of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the vector expresses the immunogenic peptide, and thereby elicits a host CTL response.

[00320] For therapeutic or immunization purposes, nucleic acids encoding the peptide of the invention and optionally one or more of the peptides described herein can also be administered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nucleic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff et al., Science 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. Generally, a plasmid for a vaccine or immunological composition can comprise DNA encoding an antigen (e.g., one or more neoantigens) operatively linked to regulatory sequences which control expression or expression and secretion of the antigen from a host cell, e.g., a mammalian cell; for instance, from upstream to downstream, DNA for a promoter, such as a mammalian virus promoter (e.g., a CMV promoter such as an hCMV or mCMV promoter, e.g., an early-intermediate promoter, or an SV40 promoter--see documents cited or incorporated herein for useful promoters), DNA for a eukaryotic leader peptide for secretion (e.g., tissue plasminogen activator), DNA for the neoantigen(s), and DNA encoding a terminator (e.g., the 3' UTR transcriptional terminator from the gene encoding Bovine Growth Hormone or bGH polyA). A composition can contain more than one plasmid or vector, whereby each vector contains and expresses a different neoantigen. Mention is also made of Wasmoen U.S. Pat. No. 5,849,303, and Dale U.S. Pat. No. 5,811,104, whose text may be useful. DNA or DNA plasmid formulations can be formulated with or inside cationic lipids; and, as to cationic lipids, as well as adjuvants, mention is also made of Loosmore U.S. Patent Application 2003/0104008. Also, teachings in Audonnet U.S. Pat. Nos. 6,228,846 and 6,159,477 may be relied upon for DNA plasmid teachings that can be employed in constructing and using DNA plasmids that contain and express in vivo.

[00321] The nucleic acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO1996/18372; WO 1993/24640; Mannino & Gould-Fogerite , BioTechniques 6(7): 682-691 (1988); U.S. Patent No. 5,279,833; WO 1991/06309; and Feigner et al., Proc. Natl. Acad. Sci. USA 84: 7413-7414 (1987).

[00322] RNA encoding the peptide of interest (e.g., mRNA) can also be used for delivery (see, e.g., Kiken et al, 2011; Su et al , 2011; see also US 8278036; Halabi et al. J Clin Oncol (2003) 21:1232-1237; Petsch et al, Nature Biotechnology 2012 Dec 7;30(12):1210-6).

[00323] Viral vectors as described herein can also be used to deliver the neoantigenic peptides of the invention. Vectors can be administered so as to have in vivo expression and response akin to doses and/or responses elicited by antigen administration.

[00324] A preferred means of administering nucleic acids encoding the peptide of the invention uses minigene constructs encoding multiple epitopes. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte, epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally- occurring flanking sequences adjacent to the CTL epitopes.

[00325] The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then cloned into a desired expression vector.

[00326] Standard regulatory sequences well known to those of skill in the art are included in the vector to ensure expression in the target cells. Several vector elements are required: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an E. coli origin of replication; and an E. coli selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human cytomegalovirus (hCMV) promoter. See, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

[00327] Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences can also be considered for increasing minigene expression. It has recently been proposed that immuno stimulatory sequences (ISSs or CpGs) play a role in the immunogenicity of DNA' vaccines. These sequences could be included in the vector, outside the minigene coding sequence, if found to enhance immunogenicity.

[00328] In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (e.g., IL2, IL12, GM-CSF), cytokine-inducing molecules (e.g. LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF-β) may be beneficial in certain diseases.

[00329] Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate E. coli strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

[00330] Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques may become available. As noted herein, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to

influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00331] Target cell sensitization can be used as a functional assay for expression and MHC class I presentation of minigene-encoded CTL epitopes. The plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used is dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct in vitro transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 labeled and used as target cells for epitope- specific CTL lines. Cytolysis, detected by 51 Cr release, indicates production of MHC presentation of mini gene-encoded CTL epitopes.

[00332] In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human MHC molecules are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g. IM for DNA in PBS, IP for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for 1 week in the presence of peptides encoding each epitope being tested. These effector cells (CTLs) are assayed for cytolysis of peptide-loaded, chromium-51 labeled target cells using standard techniques. Lysis of target cells sensitized by MHC loading of peptides corresponding to minigene-encoded epitopes demonstrates DNA vaccine function for in vivo induction of CTLs.

[00333] Peptides may be used to elicit CTL ex vivo, as well. The resulting CTL, can be used to treat chronic tumors in patients in need thereof that do not respond to other conventional forms of therapy, or does not respond to a peptide vaccine approach of therapy. Ex vivo CTL responses to a particular tumor antigen are induced by incubating in tissue culture the patient's CTL precursor cells (CTLp) together with a source of antigen-presenting cells (APC) and the appropriate peptide. After an appropriate incubation time (typically 1-4 weeks), in which the CTLp are activated and mature and expand into effector CTL, the cells are infused back into the patient, where they destroy their specific target cell (i.e., a tumor cell). In order to optimize the in vitro conditions for the generation of specific cytotoxic T cells, the culture of stimulator cells are maintained in an appropriate serum-free medium.

[00334] Prior to incubation of the stimulator cells with the cells to be activated, e.g., precursor CD8+ cells, an amount of antigenic peptide is added to the stimulator cell culture, of sufficient quantity to become loaded onto the human Class I molecules to be expressed on the surface of the stimulator cells. In the present invention, a sufficient amount of peptide is an amount that allows about 200, and preferably 200 or more, human Class I MHC molecules loaded with peptide to be expressed on the surface of each stimulator cell. Preferably, the stimulator cells are incubated with >2μg/ml peptide. For example, the stimulator cells are incubates with > 3, 4, 5, 10, 15, or more μg/ml peptide.

[00335] Resting or precursor CD8+ cells are then incubated in culture with the appropriate stimulator cells for a time period sufficient to activate the CD8+ cells. Preferably, the CD8+ cells are activated in an antigen- specific manner. The ratio of resting or precursor CD8+ (effector) cells to stimulator cells may vary from individual to individual and may further depend upon variables such as the amenability of an individual's lymphocytes to culturing conditions and the nature and severity of the disease condition or other condition for which the within-described treatment modality is used. Preferably, however, the lymphocyte: stimulator cell ratio is in the range of about 30: 1 to 300: 1. The effector/stimulator culture may be maintained for as long a time as is necessary to stimulate a therapeutically useable or effective number of CD8+ cells.

[00336] The induction of CTL in vitro requires the specific recognition of peptides that are bound to allele specific MHC class I molecules on APC. The number of specific MHC/peptide complexes per APC is crucial for the stimulation of CTL, particularly in primary immune responses. While small amounts of peptide/MHC complexes per cell are sufficient to render a cell susceptible to lysis by CTL, or to stimulate a secondary CTL response, the successful activation of a CTL precursor (pCTL) during primary response requires a significantly higher number of MHC/peptide complexes. Peptide loading of empty major histocompatability complex molecules on cells allows the induction of primary cytotoxic T lymphocyte responses.

[00337] Since mutant cell lines do not exist for every human MHC allele, it is advantageous to use a technique to remove endogenous MHC- associated peptides from the surface of APC, followed by loading the resulting empty MHC molecules with the immunogenic peptides of interest. The use of non-transformed (non-tumorigenic), noninfected cells, and preferably, autologous cells of patients as APC is desirable for the design of CTL induction protocols

directed towards development of ex vivo CTL therapies. This application discloses methods for stripping the endogenous MHC-associated peptides from the surface of APC followed by the loading of desired peptides.

[00338] A stable MHC class I molecule is a trimeric complex formed of the following elements: 1) a peptide usually of 8 - 10 residues, 2) a transmembrane heavy polymorphic protein chain which bears the peptide-binding site in its al and a2 domains, and 3) a non-covalently associated non-polymorphic light chain, p2microglobuiin. Removing the bound peptides and/or dissociating the p2microglobulin from the complex renders the MHC class I molecules nonfunctional and unstable, resulting in rapid degradation. All MHC class I molecules isolated from PBMCs have endogenous peptides bound to them. Therefore, the first step is to remove all endogenous peptides bound to MHC class I molecules on the APC without causing their degradation before exogenous peptides can be added to them.

[00339] Two possible ways to free up MHC class I molecules of bound peptides include lowering the culture temperature from 37°C to 26°C overnight to destablize p2microglobulin and stripping the endogenous peptides from the cell using a mild acid treatment. The methods release previously bound peptides into the extracellular environment allowing new exogenous peptides to bind to the empty class I molecules. The cold-temperature incubation method enables exogenous peptides to bind efficiently to the MHC complex, but requires an overnight incubation at 26°C which may slow the cell's metabolic rate. It is also likely that cells not actively synthesizing MHC molecules (e.g., resting PBMC) would not produce high amounts of empty surface MHC molecules by the cold temperature procedure.

[00340] Harsh acid stripping involves extraction of the peptides with trifluoroacetic acid, pH 2, or acid denaturation of the immunoaffinity purified class I-peptide complexes. These methods are not feasible for CTL induction, since it is important to remove the endogenous peptides while preserving APC viability and an optimal metabolic state which is critical for antigen presentation. Mild acid solutions of pH 3 such as glycine or citrate -phosphate buffers have been used to identify endogenous peptides and to identify tumor associated T cell epitopes. The treatment is especially effective, in that only the MHC class I molecules are destabilized (and associated peptides released), while other surface antigens remain intact, including MHC class II molecules. Most importantly, treatment of cells with the mild acid solutions do not affect the cell's viability or metabolic state. The mild acid treatment is rapid since the stripping of the

endogenous peptides occurs in two minutes at 4°C and the APC is ready to perform its function after the appropriate peptides are loaded. The technique is utilized herein to make peptide-specific APCs for the generation of primary antigen- specific CTL. The resulting APC are efficient in inducing peptide- specific CD8+ CTL.

[00341] Activated CD8+ cells may be effectively separated from the stimulator cells using one of a variety of known methods. For example, monoclonal antibodies specific for the stimulator cells, for the peptides loaded onto the stimulator cells, or for the CD8+ cells (or a segment thereof) may be utilized to bind their appropriate complementary ligand. Antibody-tagged molecules may then be extracted from the stimulator-effector cell admixture via appropriate means, e.g., via well-known immunoprecipitation or immunoassay methods.

[00342] Effective, cytotoxic amounts of the activated CD8+ cells can vary between in vitro and in vivo uses, as well as with the amount and type of cells that are the ultimate target of these killer cells. The amount can also vary depending on the condition of the patient and should be determined via consideration of all appropriate factors by the practitioner. Preferably, however, about 1 X 10^6 to about 1 X 10^{12}, more preferably about 1 X 10^8 to about 1 X 10^{11}, and even more preferably, about 1 X 10^9 to about 1 X 10^{10} activated CD8+ cells are utilized for adult humans, compared to about 5 X 10^6 - 5 X 10^7 cells used in mice.

[00343] Preferably, as discussed herein, the activated CD8+ cells are harvested from the cell culture prior to administration of the CD8+ cells to the individual being treated. It is important to note, however, that unlike other present and proposed treatment modalities, the present method uses a cell culture system that is not tumorigenic. Therefore, if complete separation of stimulator cells and activated CD8+ cells are not achieved, there is no inherent danger known to be associated with the administration of a small number of stimulator cells, whereas administration of mammalian tumor-promoting cells may be extremely hazardous.

[00344] Methods of re-introducing cellular components are known in the art and include procedures such as those exemplified in U.S. Patent No. 4,844,893 to Honsik, et al. and U.S. Patent No. 4,690,915 to Rosenberg. For example, administration of activated CD8+ cells via intravenous infusion is appropriate.

[00345] The practice of the present invention employs, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are well within the purview of the skilled

artisan. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", second edition (Sambrook, 1989); "Oligonucleotide Synthesis" (Gait, 1984); "Animal Cell Culture" (Freshney, 1987); "Methods in Enzymology" "Handbook of Experimental Immunology" (Wei, 1996); "Gene Transfer Vectors for Mammalian Cells" (Miller and Calos, 1987); "Current Protocols in Molecular Biology" (Ausubel, 1987); "PCR: The Polymerase Chain Reaction", (Mullis, 1994); "Current Protocols in Immunology" (Coligan, 1991). These techniques are applicable to the production of the polynucleotides and polypeptides of the invention, and, as such, may be considered in making and practicing the invention. Particularly useful techniques for particular embodiments are discussed in the sections that follow.

Therapeutic Methods

[00346] The present invention provides methods of inducing a neoplasia/tumor specific immune response in a subject, vaccinating against a neoplasia/tumor, treating and or alleviating a symptom of cancer in a subject by administering the subject a plurality of neoantigenic peptides or composition of the invention.

[00347] According to the invention, the herein-described neoplasia vaccine or immunogenic composition may be used for a patient that has been diagnosed as having cancer, or at risk of developing cancer.

[00348] The claimed combination of the invention is administered in an amount sufficient to induce a CTL response.

Additional Therapies

[00349] The tumor specific neoantigen peptides and pharmaceutical compositions described herein can also be administered in a combination therapy with another agent, for example a therapeutic agent. In certain embodiments, the additional agents can be, but are not limited to, chemotherapeutic agents, anti-angiogenesis agents and agents that reduce immune-suppression.

[00350] The neoplasia vaccine or immunogenic composition can be administered before, during, or after administration of the additional agent. In embodiments, the neoplasia vaccine or immunogenic composition is administered before the first administration of the additional agent. In other embodiments, the neoplasia vaccine or immunogenic composition is administered after the first administration of the additional therapeutic agent (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12,

13, 14 days or more). In embodiments, the neoplasia vaccine or immunogenic composition is administered simultaneously with the first administration of the additional therapeutic agent.

[00351] The therapeutic agent is for example, a chemotherapeutic or biotherapeutic agent, radiation, or immunotherapy. Any suitable therapeutic treatment for a particular cancer may be administered. Examples of chemotherapeutic and biotherapeutic agents include, but are not limited to, an angiogenesis inhibitor, such ashydroxy angiostatin K1-3, DL-α-Difluoromethyl-ornithine, endostatin, fumagillin, genistein, minocycline, staurosporine, and thalidomide; a DNA intercaltor/cross-linker, such as Bleomycin, Carboplatin, Carmustine, Chlorambucil, Cyclophosphamide, cis-Diammineplatinum(II) dichloride (Cisplatin), Melphalan, Mitoxantrone, and Oxaliplatin; a DNA synthesis inhibitor, such as (±)-Amethopterin (Methotrexate), 3-Amino-1,2,4-benzotriazine 1,4-dioxide, Aminopterin, Cytosine β-D-arabinofuranoside, 5-Fluoro-5'-deoxyuridine, 5-Fluorouracil, Ganciclovir, Hydroxyurea, and Mitomycin C; a DNA-RNA transcription regulator, such as Actinomycin D, Daunorubicin, Doxorubicin, Homoharringtonine, and Idarubicin; an enzyme inhibitor, such as S(+)-Camptothecin, Curcumin, (-)-Deguelin, 5,6-Dichlorobenzimidazole 1-β-D-ribofuranoside, Etoposide, Formestane, Fostriecin, Hispidin, 2-Imino-1-imidazoli-dineacetic acid (Cyclocreatine), Mevinolin, Trichostatin A, Tyrphostin AG 34, and Tyrphostin AG 879; a gene regulator, such as 5-Aza-2'-deoxycytidine, 5-Azacytidine, Cholecalciferol (Vitamin D3), 4-Hydroxytamoxifen, Melatonin, Mifepristone, Raloxifene, all trans-Retinal (Vitamin A aldehyde), Retinoic acid all trans (Vitamin A acid), 9-cis-Retinoic Acid, 13-cis-Retinoic acid, Retinol (Vitamin A), Tamoxifen, and Troglitazone; a microtubule inhibitor, such as Colchicine, docetaxel, Dolastatin 15, Nocodazole, Paclitaxel, Podophyllotoxin, Rhizoxin, Vinblastine, Vincristine, Vindesine, and Vinorelbine (Navelbine); and an unclassified therapeutic agent, such as 17-(Allylamino)-17-demethoxygeldanamycin, 4-Amino-1,8-naphthalimide, Apigenin, Brefeldin A, Cimetidine, Dichloromethylene-diphosphonic acid, Leuprolide (Leuprorelin), Luteinizing Hormone-Releasing Hormone, Pifithrin-α, Rapamycin, Sex hormone-binding globulin, Thapsigargin, and Urinary trypsin inhibitor fragment (Bikunin). The therapeutic agent may be altretamine, amifostine, asparaginase, capecitabine, cladribine, cisapride, cytarabine, dacarbazine (DTIC), dactinomycin, dronabinol, epoetin alpha, filgrastim, fludarabine, gemcitabine, granisetron, ifosfamide, irinotecan, lansoprazole, levamisole, leucovorin, megestrol, mesna, metoclopramide, mitotane, omeprazole, ondansetron, pilocarpine, prochloroperazine, or topotecan hydrochloride. The therapeutic agent may be a monoclonal

antibody or small molecule such as rituximab (Rituxan®), alemtuzumab (Campath®), Bevacizumab (Avastin®), Cetuximab (Erbitux®), panitumumab (Vectibix®), and trastuzumab (Herceptin®), Vemurafenib (Zelboraf®) imatinib mesylate (Gleevec®), erlotinib (Tarceva®), gefitinib (Iressa®), Vismodegib (Erivedge™), 90Y-ibritumomab tiuxetan, 131I-tositumomab, ado-trastuzumab emtansine, lapatinib (Tykerb®), pertuzumab (Perjeta™), ado-trastuzumab emtansine (Kadcyla™), regorafenib (Stivarga®), sunitinib (Sutent®), Denosumab (Xgeva®), sorafenib (Nexavar®), pazopanib (Votrient®), axitinib (Inlyta®), dasatinib (Sprycel®), nilotinib (Tasigna®), bosutinib (Bosulif®), ofatumumab (Arzerra®), obinutuzumab (Gazyva™), ibrutinib (Imbruvica™), idelalisib (Zydelig®), crizotinib (Xalkori®), erlotinib (Tarceva®), afatinib dimaleate (Gilotrif®), ceritinib (LDK378/Zykadia), Tositumomab and 131I-tositumomab (Bexxar®), ibritumomab tiuxetan (Zevalin®), brentuximab vedotin (Adcetris®), bortezomib (Velcade®), siltuximab (Sylvant™), trametinib (Mekinist®), dabrafenib (Tafinlar®), pembrolizumab (Keytruda®), carfilzomib (Kyprolis®), Ramucirumab (Cyramza™), Cabozantinib (Cometriq™), vandetanib (Caprelsa®), Optionally, the therapeutic agent is a neoantigen. The therapeutic agent may be a cytokine such as interferons (INFs), interleukins (ILs), or hematopoietic growth factors. The therapeutic agent may be INF-α, IL-2, Aldesleukin, IL-2, Erythropoietin, Granulocyte-macrophage colony-stimulating factor (GM-CSF) or granulocyte colony-stimulating factor. The therapeutic agent may be a targeted therapy such as toremifene (Fareston®), fulvestrant (Faslodex®), anastrozole (Arimidex®), exemestane (Aromasin®), letrozole (Femara®), ziv-aflibercept (Zaltrap®), Alitretinoin (Panretin®), temsirolimus (Torisel®), Tretinoin (Vesanoid®), denileukin diftitox (Ontak®), vorinostat (Zolinza®), romidepsin (Istodax®), bexarotene (Targretin®), pralatrexate (Folotyn®), lenaliomide (Revlimid®), belinostat (Beleodaq™), lenaliomide (Revlimid®), pomalidomide (Pomalyst®), Cabazitaxel (Jevtana®), enzalutamide (Xtandi®), abiraterone acetate (Zytiga®), radium 223 chloride (Xofigo®), or everolimus (Afinitor®). Aditionally, the therapeutic agent may be an epigenetic targeted drug such as HDAC inhibitors, kinase inhibitors, DNA methyltransferase inhibitors, histone demethylase inhibitors, or histone methylation inhibitors. The epigenetic drugs may be Azacitidine (Vidaza), Decitabine (Dacogen), Vorinostat (Zolinza), Romidepsin (Istodax), or Ruxolitinib (Jakafi). For prostate cancer treatment, a preferred chemotherapeutic agent with which anti- CTLA-4 can be combined is paclitaxel (TAXOL).

[00352] In certain embodiments, the one or more additional agents are one or more anti-glucocorticoid-induced tumor necrosis factor family receptor (GITR) agonistic antibodies. GITR is a costimulatory molecule for T lymphocytes, modulates innate and adaptive immune system and has been found to participate in a variety of immune responses and inflammatory processes. GITR was originally described by Nocentini et al. after being cloned from dexamethasone-treated murine T cell hybridomas (Nocentini et al. Proc Natl Acad Sci USA 94:6216–6221.1997). Unlike CD28 and CTLA-4, GITR has a very low basal expression on naive CD4+ and CD8+ T cells (Ronchetti et al. Eur J Immunol 34:613–622. 2004). The observation that GITR stimulation has immunostimulatory effects in vitro and induced autoimmunity in vivo prompted the investigation of the antitumor potency of triggering this pathway. A review of Modulation Of Ctla 4 And Gitr For Cancer Immunotherapy can be found in Cancer Immunology and Immunotherapy (Avogadri et al. Current Topics in Microbiology and Immunology 344. 2011). Other agents that can contribute to relief of immune suppression include checkpoint inhibitors targeted at another member of the CD28/CTLA4 Ig superfamily such as BTLA, LAG3, ICOS, PDL1 or KIR (Page et a, Annual Review of Medicine 65:27 (2014)). In further additional embodiments, the checkpoint inhibitor is targeted at a member of the TNFR superfamily such as CD40, OX40, CD137, GITR, CD27 or TIM-3. In some cases targeting a checkpoint inhibitor is accomplished with an inhibitory antibody or similar molecule. In other cases, it is accomplished with an agonist for the target; examples of this class include the stimulatory targets OX40 and GITR.

[00353] In certain embodiments, the one or more additional agents are synergistic in that they increase immunogenicity after treatment. In one embodiment the additional agent allows for lower toxicity and/or lower discomfort due to lower doses of the additional therapeutic agents or any components of the combination therapy described herein. In another embodiment the additional agent results in longer lifespan due to increased effectiveness of the combination therapy described herein. Chemotherapeutic treatments that enhance the immunological response in a patient have been reviewed (Zitvogel et al., Immunological aspects of cancer chemotherapy. Nat Rev Immunol. 2008 Jan;8(1):59-73). Aditionally, chemotherapeutic agents can be administered safely with immunotherapy without inhibiting vaccine specific T-cell responses (Perez et al., A new era in anticancer peptide vaccines. Cancer May 2010). In one embodiment the additional agent is administered to increase the efficacy of the therapy described herein. In

one embodiment the additional agent is a chemotherapy treatment. In one embodiment low doses of chemotherapy potentiate delayed-type hypersensitivity (DTH) responses. In one embodiment the chemotheray agent targets regulatory T-cells. In one embodiment cyclophosphamide is the therapeutic agent. In one embodiment cyclophosphamide is administered prior to vaccination. In one embodiment cyclophosphamide is administered as a single dose before vaccination (Walter et al., Multipeptide immune response to cancer vaccine IMA901 after single-dose cyclophosphamide associates with longer patient survival. Nature Medicine; 18:8 2012). In another embodiment, cyclophosphamide is administered according to a metronomic program, where a daily dose is administered for one month (Ghiringhelli et al., Metronomic cyclophosphamide regimen selectively depletes CD4+CD25+ regulatory T cells and restores T and NK effector functions in end stage cancer patients. Cancer Immunol Immunother 2007 56:641–648). In another embodiment taxanes are administered before vaccination to enhance T-cell and NK-cell functions (Zitvogel et al., 2008). In another embodiment a low dose of a chemotherapeutic agent is administered with the therapy described herein. In one embodiment the chemotherapeutic agent is estramustine. In one embodiment the cancer is hormone resistant prostate cancer. A ≥50% decrease in serum prostate specific antigen (PSA) was seen in 8.7% of advanced hormone refractory prostate cancer patients by personalized vaccination alone, whereas such a decrease was seen in 54% of patients when the personalized vaccination was combined with a low dose of estramustine (Itoh et al., Personalized peptide vaccines: A new therapeutic modality for cancer. Cancer Sci 2006; 97: 970–976). In another embodiment glucocorticoids are administered with or before the therapy described herein (Zitvogel et al., 2008). In another embodiment glucocorticoids are administered after the therapy described herein. In another embodiment Gemcitabine is administered before, simultaneously, or after the therapy described herein to enhance the frequency of tumor specific CTL precursors (Zitvogel et al., 2008). In another embodiment 5-fluorouracil is administered with the therapy described herein as synergistic effects were seen with a peptide based vaccine (Zitvogel et al., 2008). In another embodiment an inhibitor of Braf, such as Vemurafenib, is used as an additional agent. Braf inhibition has been shown to be associated with an increase in melanoma antigen expression and T-cell infiltrate and a decrease in immunosuppressive cytokines in tumors of treated patients (Frederick et al., BRAF inhibition is associated with enhanced melanoma antigen expression and a more favorable tumor microenvironment in patients with metastatic melanoma. Clin Cancer

Res. 2013; 19:1225-1231). In another embodiment an inhibitor of tyrosine kinases is used as an additional agent. In one embodiment the tyrosine kinase inhibitor is used before vaccination with the therapy described herein. In one embodiment the tyrosine kinase inhibitor is used simultaneously with the therapy described herein. In another embodiment the tyrosine kinase inhibitor is used to create a more immune permissive environment. In another embodiment the tyrosine kinase inhibitor is sunitinib or imatinib mesylate. It has previously been shown that favorable outcomes could be achieved with sequential administration of continuous daily dosing of sunitinib and recombinant vaccine (Farsaci et al., Consequence of dose scheduling of sunitinib on host immune response elements and vaccine combination therapy. Int J Cancer; 130: 1948-1959). Sunitinib has also been shown to reverse type-1 immune suppression using a daily dose of 50 mg/day (Finke et al., Sunitinib Reverses Type-1 Immune Suppression and Decreases T-Regulatory Cells in Renal Cell Carcinoma Patients. Clin Cancer Res 2008;14(20)). In another embodiment targeted therapies are administered in combination with the therapy described herein. Doses of targeted therapies has been described previously (Alvarez, Present and future evolution of advanced breast cancer therapy. Breast Cancer Research 2010, 12(Suppl 2):S1). In another embodiment temozolomide is administered with the therapy described herein. In one embodiment temozolomide is administered at 200 mg/day for 5 days every fourth week of a combination therapy with the therapy described herein. Results of a similar strategy have been shown to have low toxicity (Kyte et al., Telomerase Peptide Vaccination Combined with Temozolomide: A Clinical Trial in Stage IV Melanoma Patients. Clin Cancer Res; 17(13) 2011). In another embodiment the therapy is administered with an additional therapeutic agent that results in lymphopenia. In one embodiment the additional agent is temozolomide. An immune response can still be induced under these conditions (Sampson et al., Greater chemotherapy-induced lymphopenia enhances tumor-specific immune responses that eliminate EGFRvIII-expressing tumor cells in patients with glioblastoma. Neuro-Oncology 13(3):324–333, 2011).

[00354] Patients in need thereof may receive a series of priming vaccinations with a mixture of tumor-specific peptides. Additionally, over a 4 week period the priming may be followed by two boosts during a maintenance phase. All vaccinations are subcutaneously delivered. The vaccine or immunogenic composition is evaluated for safety, tolerability, immune response and clinical effect in patients and for feasibility of producing vaccine or immunogenic composition and successfully initiating vaccination within an appropriate time frame. The first cohort can

consist of 5 patients, and after safety is adequately demonstrated, an additional cohort of 10 patients may be enrolled. Peripheral blood is extensively monitored for peptide-specific T-cell responses and patients are followed for up to two years to assess disease recurrence.

Administering a combination therapy consistent with standard of care

[00355] In another aspect, the therapy described herein provides selecting the appropriate point to administer a combination therapy in relation to and within the standard of care for the cancer being treated for a patient in need thereof. The studies described herein show that the combination therapy can be effectively administered even within the standard of care that includes surgery, radiation, or chemotherapy. The standards of care for the most common cancers can be found on the website of National Cancer Institute (www.cancer.gov/cancertopics). The standard of care is the current treatment that is accepted by medical experts as a proper treatment for a certain type of disease and that is widely used by healthcare professionals. Standard or care is also called best practice, standard medical care, and standard therapy. Standards of Care for cancer generally include surgery, lymph node removal, radiation, chemotherapy, targeted therapies, antibodies targeting the tumor, and immunotherapy. Immunotherapy can include checkpoint blockers (CBP), chimeric antigen receptors (CARs), and adoptive T-cell therapy. The combination therapy described herein can be incorporated within the standard of care. The combination therapy described herein may also be administered where the standard of care has changed due to advances in medicine.

[00356] Incorporation of the combination therapy described herein may depend on a treatment step in the standard of care that can lead to activation of the immune system. Treatment steps that can activate and function synergistically with the combination therapy have been described herein. The therapy can be advantageously administered simultaneously or after a treatment that activates the immune system.

[00357] Incorporation of the combination therapy described herein may depend on a treatment step in the standard of care that causes the immune system to be suppressed. Such treatment steps may include irradiation, high doses of alkylating agents and/or methotrexate, steroids such as glucosteroids, surgery, such as to remove the lymph nodes, imatinib mesylate, high doses of TNF, and taxanes (Zitvogel et al., 2008). The combination therapy may be administered before such steps or may be administered after.

[00358] In one embodiment the combination therapy may be administered after bone marrow transplants and peripheral blood stem cell transplantation. Bone marrow transplantation and peripheral blood stem cell transplantation are procedures that restore stem cells that were destroyed by high doses of chemotherapy and/or radiation therapy. After being treated with high-dose anticancer drugs and/or radiation, the patient receives harvested stem cells, which travel to the bone marrow and begin to produce new blood cells. A "mini-transplant" uses lower, less toxic doses of chemotherapy and/or radiation to prepare the patient for transplant. A "tandem transplant" involves two sequential courses of high-dose chemotherapy and stem cell transplant. In autologous transplants, patients receive their own stem cells. In syngeneic transplants, patients receive stem cells from their identical twin. In allogeneic transplants, patients receive stem cells from their brother, sister, or parent. A person who is not related to the patient (an unrelated donor) also may be used. In some types of leukemia, the graft-versus-tumor (GVT) effect that occurs after allogeneic BMT and PBSCT is crucial to the effectiveness of the treatment. GVT occurs when white blood cells from the donor (the graft) identify the cancer cells that remain in the patient's body after the chemotherapy and/or radiation therapy (the tumor) as foreign and attack them. Immunotherapy with the combination therapy described herein can take advantage of this by vaccinating after a transplant. Additionally, the transferred cells may be presented with neoantigens of the combination therapy described herein before transplantation.

[00359] In one embodiment the combination therapy is administered to a patient in need thereof with a cancer that requires surgery. In one embodiment the combination therapy described herein is administered to a patient in need thereof in a cancer where the standard of care is primarily surgery followed by treatment to remove possible micro-metastases, such as breast cancer. Breast cancer is commonly treated by various combinations of surgery, radiation therapy, chemotherapy, and hormone therapy based on the stage and grade of the cancer. Adjuvant therapy for breast cancer is any treatment given after primary therapy to increase the chance of long-term survival. Neoadjuvant therapy is treatment given before primary therapy. Adjuvant therapy for breast cancer is any treatment given after primary therapy to increase the chance of long-term disease-free survival. Primary therapy is the main treatment used to reduce or eliminate the cancer. Primary therapy for breast cancer usually includes surgery, a mastectomy (removal of the breast) or a lumpectomy (surgery to remove the tumor and a small amount of normal tissue around it; a type of breast-conserving surgery). During either type of

surgery, one or more nearby lymph nodes are also removed to see if cancer cells have spread to the lymphatic system. When a woman has breast-conserving surgery, primary therapy almost always includes radiation therapy. Even in early-stage breast cancer, cells may break away from the primary tumor and spread to other parts of the body (metastasize). Therefore, doctors give adjuvant therapy to kill any cancer cells that may have spread, even if they cannot be detected by imaging or laboratory tests.

[00360] In one embodiment the combination therapy is administered consistent with the standard of care for Ductal carcinoma *in situ* (DCIS). The standard of care for this breast cancer type is:

1. Breast-conserving surgery and radiation therapy with or without tamoxifen.
2. Total mastectomy with or without tamoxifen.
3. Breast-conserving surgery without radiation therapy.

[00361] The combination therapy may be administered before breast conserving surgery or total mastectomy to shrink the tumor before surgery. In another embodiment the combination therapy can be administered as an adjuvant therapy to remove any remaining cancer cells.

In another embodiment patients diagnosed with stage I, II, IIIA, and Operable IIIC breast cancer are treated with the combination therapy as described herein. The standard of care for this breast cancer type is:

1. Local-regional treatment:

- Breast-conserving therapy (lumpectomy, breast radiation, and surgical staging of the axilla).
- Modified radical mastectomy (removal of the entire breast with level I–II axillary dissection) with or without breast reconstruction.
- Sentinel node biopsy.

2. Adjuvant radiation therapy postmastectomy in axillary node-positive tumors:

- For one to three nodes: unclear role for regional radiation (infra/supraclavicular nodes, internal mammary nodes, axillary nodes, and chest wall).
- For more than four nodes or extranodal involvement: regional radiation is advised.

3. Adjuvant systemic therapy

[00362] In one embodiment the combination therapy is administered as a neoadjuvant therapy to shrink the tumor. In another embodiment the combination is administered as an adjuvant systemic therapy.

[00363] In another embodiment patients diagnosed with inoperable stage IIIB or IIIC or inflammatory breast cancer are treated with the combination therapy as described herein. The standard of care for this breast cancer type is:

1. Multimodality therapy delivered with curative intent is the standard of care for patients with clinical stage IIIB disease.

2. Initial surgery is generally limited to biopsy to permit the determination of histology, estrogen-receptor (ER) and progesterone-receptor (PR) levels, and human epidermal growth factor receptor 2 (HER2/neu) overexpression. Initial treatment with anthracycline-based chemotherapy and/or taxane-based therapy is standard. For patients who respond to neoadjuvant chemotherapy, local therapy may consist of total mastectomy with axillary lymph node dissection followed by postoperative radiation therapy to the chest wall and regional lymphatics. Breast-conserving therapy can be considered in patients with a good partial or complete response to neoadjuvant chemotherapy. Subsequent systemic therapy may consist of further chemotherapy. Hormone therapy should be administered to patients whose tumors are ER-positive or unknown. All patients should be considered candidates for clinical trials to evaluate the most appropriate fashion in which to administer the various components of multimodality regimens.

[00364] In one embodiment the combination therapy is administered as part of the various components of multimodality regimens. In another embodiment the combination therapy is administered before, simultaneously with, or after the multimodality regimens. In another embodiment the combination therapy is administered based on synergism between the modalities. In another embodiment the combination therapy is administered after treatment with anthracycline-based chemotherapy and/or taxane-based therapy (Zitvogel et al., 2008). Treatment after administering the combination therapy may negatively affect dividing effector T-cells. The combination therapy may also be administered after radiation.

[00365] In another embodiment the combination therapy described herein is used in the treatment in a cancer where the standard of care is primarily not surgery and is primarily based on systemic treatments, such as Chronic Lymphocytic Leukemia (CLL).

[00366] In another embodiment patients diagnosed with stage I, II, III, and IV Chronic Lymphocytic Leukemia are treated with the combination therapy as described herein. The standard of care for this cancer type is:

1. Observation in asymptomatic or minimally affected patients
2. Rituximab
3. Ofatumomab
4. Oral alkylating agents with or without corticosteroids
5. Fludarabine, 2-chlorodeoxyadenosine, or pentostatin
6. Bendamustine
7. Lenalidomide
8. Combination chemotherapy.

   combination chemotherapy regimens include the following:

   - Fludarabine plus cyclophosphamide plus rituximab.
   - Fludarabine plus rituximab as seen in the CLB-9712 and CLB-9011 trials.
   - Fludarabine plus cyclophosphamide versus fludarabine plus cyclophosphamide plus rituximab.
   - Pentostatin plus cyclophosphamide plus rituximab as seen in the MAYO-MC0183 trial, for example.
   - Ofatumumab plus fludarabine plus cyclophosphamide.
   - CVP: cyclophosphamide plus vincristine plus prednisone.
   - CHOP: cyclophosphamide plus doxorubicin plus vincristine plus prednisone.
   - Fludarabine plus cyclophosphamide versus fludarabine as seen in the E2997 trial [NCT00003764] and the LRF-CLL4 trial, for example.
   - Fludarabine plus chlorambucil as seen in the CLB-9011 trial, for example.
9. Involved-field radiation therapy.
10. Alemtuzumab
11. Bone marrow and peripheral stem cell transplantations are under clinical evaluation.
12. Ibrutinib

[00367] In one embodiment the combination therapy is administered before, simultaneously with or after treatment with Rituximab or Ofatumomab. As these are monoclonal antibodies that target B-cells, treatment with the combination therapy may be synergistic. In another

embodiment the combination therapy is administered after treatment with oral alkylating agents with or without corticosteroids, and Fludarabine, 2-chlorodeoxyadenosine, or pentostatin, as these treatments may negatively affect the immune system if administered before. In one embodiment bendamustine is administered with the combination therapy in low doses based on the results for prostate cancer described herein. In one embodiment the combination therapy is administered after treatment with bendamustine.

[00368] In another embodiment, therapies targeted to specific recurrent mutations in genes that include extracellular domains are used in the treatment of a patient in need thereof suffering from cancer. The genes may advantageously be well-expressed genes. Well expressed may be expressed in "transcripts per million" (TPM). A TPM greater than 100 is considered well expressed. Well expressed genes may be FGFR3, ERBB3, EGFR, MUC4, PDGFRA, MMP12, TMEM52, and PODXL. The therapies may be a ligand capable of binding to an extracellular neoantigen epitope. Such ligands are well known in the art and may include therapeutic antibodies or fragments thereof, antibody-drug conjugates, engineered T cells, or aptamers. Engineered T cells may be chimeric antigen receptors (CARs). Antibodies may be fully humanized, humanized, or chimeric. The antibody fragments may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment. Antibodies may be developed against tumor-specific neoepitopes using known methods in the art.

Adoptive cell transfer (ACT)

[00369] Aspects of the invention involve the adoptive transfer of immune system cells, such as T cells, specific for selected antigens, such as tumor associated antigens (see Maus et al., 2014, Adoptive Immunotherapy for Cancer or Viruses, Annual Review of Immunology, Vol. 32: 189-225; Rosenberg and Restifo, 2015, Adoptive cell transfer as personalized immunotherapy for human cancer, Science Vol. 348 no. 6230 pp. 62-68; Restifo et al., 2015, Adoptive immunotherapy for cancer: harnessing the T cell response. Nat. Rev. Immunol. 12(4): 269-281; and Jenson and Riddell, 2014, Design and implementation of adoptive therapy with chimeric antigen receptor-modified T cells. Immunol Rev. 257(1): 127–144). Various strategies may for example be employed to genetically modify T cells by altering the specificity of the T cell receptor (TCR) for example by introducing new TCR α and β chains with selected peptide

specificity (see U.S. Patent No. 8,697,854; PCT Patent Publications: WO2003020763, WO2004033685, WO2004044004, WO2005114215, WO2006000830, WO2008038002, WO2008039818, WO2004074322, WO2005113595, WO2006125962, WO2013166321, WO2013039889, WO2014018863, WO2014083173; U.S. Patent No. 8,088,379).

[00370] As an alternative to, or addition to, TCR modifications, chimeric antigen receptors (CARs) may be used in order to generate immunoresponsive cells, such as T cells, specific for selected targets, such as malignant cells, with a wide variety of receptor chimera constructs having been described (see U.S. Patent Nos. 5,843,728; 5,851,828; 5,912,170; 6,004,811; 6,284,240; 6,392,013; 6,410,014; 6,753,162; 8,211,422; and, PCT Publication WO9215322). Alternative CAR constructs may be characterized as belonging to successive generations. First-generation CARs typically consist of a single-chain variable fragment of an antibody specific for an antigen, for example comprising a V_L linked to a V_H of a specific antibody, linked by a flexible linker, for example by a CD8α hinge domain and a CD8α transmembrane domain, to the transmembrane and intracellular signaling domains of either CD3ζ or FcRγ (scFv-CD3ζ or scFv-FcRγ; see U.S. Patent No. 7,741,465; U.S. Patent No. 5,912,172; U.S. Patent No. 5,906,936). Second-generation CARs incorporate the intracellular domains of one or more costimulatory molecules, such as CD28, OX40 (CD134), or 4-1BB (CD137) within the endodomain (for example scFv-CD28/OX40/4-1BB-CD3ζ; see U.S. Patent Nos. 8,911,993; 8,916,381; 8,975,071; 9,101,584; 9,102,760; 9,102,761). Third-generation CARs include a combination of costimulatory endodomains, such a CD3ζ-chain, CD97, GDI la-CD18, CD2, ICOS, CD27, CD154, CDS, OX40, 4-1BB, or CD28 signaling domains (for example scFv-CD28-4-1BB-CD3ζ or scFv-CD28-OX40-CD3ζ; see U.S. Patent No. 8,906,682; U.S. Patent No. 8,399,645; U.S. Pat. No. 5,686,281; PCT Publication No. WO2014134165; PCT Publication No. WO2012079000). Alternatively, costimulation may be orchestrated by expressing CARs in antigen-specific T cells, chosen so as to be activated and expanded following engagement of their native αβTCR, for example by antigen on professional antigen-presenting cells, with attendant costimulation. In addition, additional engineered receptors may be provided on the immunoresponsive cells, for example to improve targeting of a T-cell attack and/or minimize side effects.

[00371] Alternative techniques may be used to transform target immunoresponsive cells, such as protoplast fusion, lipofection, transfection or electroporation. A wide variety of vectors may be used, such as retroviral vectors, lentiviral vectors, adenoviral vectors, adeno-associated viral

vectors, plasmids or transposons, such as a Sleeping Beauty transposon (see U.S. Patent Nos. 6,489,458; 7,148,203; 7,160,682; 7,985,739; 8,227,432), may be used to introduce CARs, for example using 2nd generation antigen-specific CARs signaling through CD3ζ and either CD28 or CD137. Viral vectors may for example include vectors based on HIV, SV40, EBV, HSV or BPV.

[00372] Cells that are targeted for transformation may for example include T cells, Natural Killer (NK) cells, cytotoxic T lymphocytes (CTL), regulatory T cells, human embryonic stem cells, tumor-infiltrating lymphocytes (TIL) or a pluripotent stem cell from which lymphoid cells may be differentiated. T cells expressing a desired CAR may for example be selected through co-culture with γ-irradiated activating and propagating cells (AaPC), which co-express the cancer antigen and co-stimulatory molecules. The engineered CAR T-cells may be expanded, for example by co-culture on AaPC in presence of soluble factors, such as IL-2 and IL-21. This expansion may for example be carried out so as to provide memory CAR+ T cells (which may for example be assayed by non-enzymatic digital array and/or multi-panel flow cytometry). In this way, CAR T cells may be provided that have specific cytotoxic activity against antigen-bearing tumors (optionally in conjunction with production of desired chemokines such as interferon-γ). CAR T cells of this kind may for example be used in animal models, for example to treat tumor xenografts.

[00373] Approaches such as the foregoing may be adapted to provide methods of treating and/or increasing survival of a subject having a disease, such as a neoplasia, for example by administering an effective amount of an immunoresponsive cell comprising an antigen recognizing receptor that binds a selected antigen, wherein the binding activates the immunoreponsive cell, thereby treating or preventing the disease (such as a neoplasia, a pathogen infection, an autoimmune disorder, or an allogeneic transplant reaction).

[00374] In one embodiment, the treatment can be administrated into patients undergoing an immunosuppressive treatment. The cells or population of cells, may be made resistant to at least one immunosuppressive agent due to the inactivation of a gene encoding a receptor for such immunosuppressive agent. Not being bound by a theory, the immunosuppressive treatment should help the selection and expansion of the immunoresponsive or T cells according to the invention within the patient.

[00375] The administration of the cells or population of cells according to the present invention may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The cells or population of cells may be administered to a patient subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous or intralymphatic injection, or intraperitoneally. In one embodiment, the cell compositions of the present invention are preferably administered by intravenous injection.

[00376] The administration of the cells or population of cells can consist of the administration of 10^4- 10^9 cells per kg body weight, preferably 10^5 to 10^6 cells/kg body weight including all integer values of cell numbers within those ranges. Dosing in CAR T cell therapies may for example involve administration of from 10^6 to 10^9 cells/kg, with or without a course of lymphodepletion, for example with cyclophosphamide. The cells or population of cells can be administrated in one or more doses. In another embodiment, the effective amount of cells are administrated as a single dose. In another embodiment, the effective amount of cells are administrated as more than one dose over a period time. Timing of administration is within the judgment of managing physician and depends on the clinical condition of the patient. The cells or population of cells may be obtained from any source, such as a blood bank or a donor. While individual needs vary, determination of optimal ranges of effective amounts of a given cell type for a particular disease or conditions are within the skill of one in the art. An effective amount means an amount which provides a therapeutic or prophylactic benefit. The dosage administrated will be dependent upon the age, health and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment and the nature of the effect desired.

[00377] In another embodiment, the effective amount of cells or composition comprising those cells are administrated parenterally. The administration can be an intravenous administration. The administration can be directly done by injection within a tumor.

[00378] To guard against possible adverse reactions, engineered immunoresponsive cells may be equipped with a transgenic safety switch, in the form of a transgene that renders the cells vulnerable to exposure to a specific signal. For example, the herpes simplex viral thymidine kinase (TK) gene may be used in this way, for example by introduction into allogeneic T lymphocytes used as donor lymphocyte infusions following stem cell transplantation (Greco, et al., Improving the safety of cell therapy with the TK-suicide gene. Front. Pharmacol. 2015; 6:

95). In such cells, administration of a nucleoside prodrug such as ganciclovir or acyclovir causes cell death. Alternative safety switch constructs include inducible caspase 9, for example triggered by administration of a small-molecule dimerizer that brings together two nonfunctional icasp9 molecules to form the active enzyme. A wide variety of alternative approaches to implementing cellular proliferation controls have been described (see U.S. Patent Publication No. 20130071414; PCT Patent Publication WO2011146862; PCT Patent Publication WO2014011987; PCT Patent Publication WO2013040371; Zhou et al. BLOOD, 2014, 123/25:3895 – 3905; Di Stasi et al., The New England Journal of Medicine 2011; 365:1673-1683; Sadelain M, The New England Journal of Medicine 2011; 365:1735-173; Ramos et al., Stem Cells 28(6):1107-15 (2010)).

[00379] In a further refinement of adoptive therapies, genome editing may be used to tailor immunoresponsive cells to alternative implementations, for example providing edited CAR T cells (see Poirot et al., 2015, Multiplex genome edited T-cell manufacturing platform for "off-the-shelf" adoptive T-cell immunotherapies, Cancer Res 75 (18): 3853). Cells may be edited using any DNA targeting protein, including, but not limited to a CRISPR system, Zinc Finger binding protein, TALE or TALEN as known in the art. DNA targeting proteins may be delivered to an immune cell by any method known in the art. In preferred embodiments, cells are edited *ex vivo* and transferred to a subject in need thereof. Immunoresponsive cells, CAR T cells or any cells used for adoptive cell transfer may be edited. Editing may be performed to eliminate potential alloreactive T-cell receptors (TCR), disrupt the target of a chemotherapeutic agent, block an immune checkpoint, activate a T cell, and/or increase the differentiation and/or proliferation of functionally exhausted or dysfunctional CD8+ T-cells (see PCT Patent Publications: WO2013176915, WO2014059173, WO2014172606, WO2014184744, and WO2014191128). Editing may result in inactivation of a gene.

[00380] By inactivating a gene it is intended that the gene of interest is not expressed in a functional protein form. In a particular embodiment, the CRISPR system specifically catalyzes cleavage in one targeted gene thereby inactivating said targeted gene. The nucleic acid strand breaks caused are commonly repaired through the distinct mechanisms of homologous recombination or non-homologous end joining (NHEJ). However, NHEJ is an imperfect repair process that often results in changes to the DNA sequence at the site of the cleavage. Repair via non-homologous end joining (NHEJ) often results in small insertions or deletions (Indel) and can

be used for the creation of specific gene knockouts. Cells in which a cleavage induced mutagenesis event has occurred can be identified and/or selected by well-known methods in the art.

[00381] T cell receptors (TCR) are cell surface receptors that participate in the activation of T cells in response to the presentation of antigen. The TCR is generally made from two chains, α and β, which assemble to form a heterodimer and associates with the CD3-transducing subunits to form the T cell receptor complex present on the cell surface. Each α and β chain of the TCR consists of an immunoglobulin-like N-terminal variable (V) and constant (C) region, a hydrophobic transmembrane domain, and a short cytoplasmic region. As for immunoglobulin molecules, the variable region of the α and β chains are generated by V(D)J recombination, creating a large diversity of antigen specificities within the population of T cells. However, in contrast to immunoglobulins that recognize intact antigen, T cells are activated by processed peptide fragments in association with an MHC molecule, introducing an extra dimension to antigen recognition by T cells, known as MHC restriction. Recognition of MHC disparities between the donor and recipient through the T cell receptor leads to T cell proliferation and the potential development of graft versus host disease (GVHD). The inactivation of TCRα or TCRβ can result in the elimination of the TCR from the surface of T cells preventing recognition of alloantigen and thus GVHD. However, TCR disruption generally results in the elimination of the CD3 signaling component and alters the means of further T cell expansion.

[00382] Allogeneic cells are rapidly rejected by the host immune system. It has been demonstrated that, allogeneic leukocytes present in non-irradiated blood products will persist for no more than 5 to 6 days (Boni, Muranski et al. 2008 Blood 1;112(12):4746-54). Thus, to prevent rejection of allogeneic cells, the host's immune system usually has to be suppressed to some extent. However, in the case of adoptive cell transfer the use of immunosuppressive drugs also have a detrimental effect on the introduced therapeutic T cells. Therefore, to effectively use an adoptive immunotherapy approach in these conditions, the introduced cells would need to be resistant to the immunosuppressive treatment. Thus, in a particular embodiment, the present invention further comprises a step of modifying T cells to make them resistant to an immunosuppressive agent, preferably by inactivating at least one gene encoding a target for an immunosuppressive agent. An immunosuppressive agent is an agent that suppresses immune function by one of several mechanisms of action. An immunosuppressive agent can be, but is not

limited to a calcineurin inhibitor, a target of rapamycin, an interleukin-2 receptor α-chain blocker, an inhibitor of inosine monophosphate dehydrogenase, an inhibitor of dihydrofolic acid reductase, a corticosteroid or an immunosuppressive antimetabolite. The present invention allows conferring immunosuppressive resistance to T cells for immunotherapy by inactivating the target of the immunosuppressive agent in T cells. As non-limiting examples, targets for an immunosuppressive agent can be a receptor for an immunosuppressive agent such as: CD52, glucocorticoid receptor (GR), a FKBP family gene member and a cyclophilin family gene member.

[00383] Immune checkpoints are inhibitory pathways that slow down or stop immune reactions and prevent excessive tissue damage from uncontrolled activity of immune cells. In certain embodiments, the immune checkpoint targeted is the programmed death-1 (PD-1 or CD279) gene (*PDCD1*). In other embodiments, the immune checkpoint targeted is cytotoxic T-lymphocyte-associated antigen (CTLA-4). In additional embodiments, the immune checkpoint targeted is another member of the CD28 and CTLA4 Ig superfamily such as BTLA, LAG3, ICOS, PDL1 or KIR. In further additional embodiments, the immune checkpoint targeted is a member of the TNFR superfamily such as CD40, OX40, CD137, GITR, CD27 or TIM-3.

[00384] Additional immune checkpoints include Src homology 2 domain-containing protein tyrosine phosphatase 1 (SHP-1) (Watson HA, et al., SHP-1: the next checkpoint target for cancer immunotherapy? Biochem Soc Trans. 2016 Apr 15;44(2):356-62). SHP-1 is a widely expressed inhibitory protein tyrosine phosphatase (PTP). In T-cells, it is a negative regulator of antigen-dependent activation and proliferation. It is a cytosolic protein, and therefore not amenable to antibody-mediated therapies, but its role in activation and proliferation makes it an attractive target for genetic manipulation in adoptive transfer strategies, such as chimeric antigen receptor (CAR) T cells. Immune checkpoints may also include T cell immunoreceptor with Ig and ITIM domains (TIGIT/Vstm3/WUCAM/VSIG9) and VISTA (Le Mercier I, et al., (2015) Beyond CTLA-4 and PD-1, the generation Z of negative checkpoint regulators. Front. Immunol. 6:418).

[00385] WO2014172606 relates to the use of MT1 and/or MT1 inhibitors to increase proliferation and/or activity of exhausted CD8+ T-cells and to decrease CD8+ T-cell exhaustion (e.g., decrease functionally exhausted or unresponsive CD8+ immune cells). In certain embodiments, metallothioneins are targeted by gene editing in adoptively transferred T cells.

[00386] In certain embodiments, targets of gene editing may be at least one targeted locus involved in the expression of an immune checkpoint protein. Such targets may include, but are not limited to CTLA4, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, ICOS (CD278), PDL1, KIR, LAG3, HAVCR2, BTLA, CD160, TIGIT, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244 (2B4), TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, TGFBRII, TGFRBRI, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, VISTA, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, MT1, MT2, CD40, OX40, CD137, GITR, CD27, SHP-1 or TIM-3. In preferred embodiments, the gene locus involved in the expression of PD-1 or CTLA-4 genes is targeted. In other preferred embodiments, combinations of genes are targeted, such as but not limited to PD-1 and TIGIT.

[00387] In other embodiments, at least two genes are edited. Pairs of genes may include, but are not limited to PD1 and TCRα, PD1 and TCRβ, CTLA-4 and TCRα, CTLA-4 and TCRβ, LAG3 and TCRα, LAG3 and TCRβ, Tim3 and TCRα, Tim3 and TCRβ, BTLA and TCRα, BTLA and TCRβ, BY55 and TCRα, BY55 and TCRβ, TIGIT and TCRα, TIGIT and TCRβ, B7H5 and TCRα, B7H5 and TCRβ, LAIR1 and TCRα, LAIR1 and TCRβ, SIGLEC10 and TCRα, SIGLEC10 and TCRβ, 2B4 and TCRα, 2B4 and TCRβ.

[00388] Whether prior to or after genetic modification of the T cells, the T cells can be activated and expanded generally using methods as described, for example, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and 7,572,631. T cells can be expanded *in vitro* or *in vivo*.

Selecting the patient population most likely to benefit from the therapy

[00389] In another aspect, the invention provides selecting for the patients in need thereof most likely to benefit from the therapy of the present invention. Although the compositions and methods of the present invention are typically applicable in a high proportion of subjects suffering from cancer, the method may still comprise one or more steps of selecting patients from the patient population who are likely to benefit. For instance, the method may comprise selecting subjects whose tumors contain one or more of the mutations represented in the neoantigenic peptides in the composition. In another embodiment, the method may comprise

selecting subjects having at least one HLA allele which binds to one or more neoepitopes represented in the neoantigenic peptides in the composition.

Vaccine or Immunogenic Composition Kits and Co-Packaging

[00390] In an aspect, the invention provides kits containing any one or more of the elements discussed herein to allow administration of the therapy. Elements may be provided individually or in combinations, and may be provided in any suitable container, such as a vial, a bottle, or a tube. In some embodiments, the kit includes instructions in one or more languages, for example in more than one language. In some embodiments, a kit comprises one or more reagents for use in a process utilizing one or more of the elements described herein. Reagents may be provided in any suitable container. For example, a kit may provide one or more delivery or storage buffers. Reagents may be provided in a form that is usable in a particular process, or in a form that requires addition of one or more other components before use (e.g. in concentrate or lyophilized form). A buffer can be any buffer, including but not limited to a sodium carbonate buffer, a sodium bicarbonate buffer, a borate buffer, a Tris buffer, a MOPS buffer, a HEPES buffer, and combinations thereof. In some embodiments, the buffer is alkaline. In some embodiments, the buffer has a pH from about 7 to about 10. In some embodiments, the kit comprises one or more of the vectors, proteins and/or one or more of the polynucleotides described herein. The kit may advantageously allow the provision of all elements of the systems of the invention. Kits can involve vector(s) and/or particle(s) and/or nanoparticle(s) containing or encoding RNA(s) for 1-50 or more neoantigen mutations to be administered to an animal, mammal, primate, rodent, etc., with such a kit including instructions for administering to such a eukaryote; and such a kit can optionally include any of the anti-cancer agents described herein. The kit may include any of the components above (e.g. vector(s) and/or particle(s) and/or nanoparticle(s) containing or encoding RNA(s) for 1-50 or more neoantigen mutations, neoantigen proteins or peptides) as well as instructions for use with any of the methods of the present invention.

[00391] In one embodiment the kit contains at least one vial with an immunogenic composition or vaccine. In one embodiment the kit contains at least one vial with an immunogenic composition or vaccine and at least one vial with an anticancer agent. In one embodiment kits may comprise ready to use components that are mixed and ready to administer.

In one aspect a kit contains a ready to use immunogenic or vaccine composition and a ready to use anti-cancer agent. The ready to use immunogenic or vaccine composition may comprise separate vials containing different pools of immunogenic compositions. The immunogenic compositions may comprise one vial containing a viral vector or DNA plasmid and the other vial may comprise immunogenic protein. The ready to use anticancer agent may comprise a cocktail of anticancer agents or a single anticancer agent. Separate vials may contain different anti-cancer agents. In another embodiment a kit may contain a ready to use anti-cancer agent and an immunogenic composition or vaccine in a ready to be reconstituted form. The immunogenic or vaccine composition may be freeze dried or lyophilized. The kit may comprise a separate vial with a reconstitution buffer that can be added to the lyophilized composition so that it is ready to administer. The buffer may advantageously comprise an adjuvant or emulsion according to the present invention. In another embodiment the kit may comprise a ready to reconstitute anti-cancer agent and a ready to reconstitute immunogenic composition or vaccine. In this aspect both may be lyophilized. In this aspect separate reconstitution buffers for each may be included in the kit. The buffer may advantageously comprise an adjuvant or emulsion according to the present invention. In another embodiment the kit may comprise single vials containing a dose of immunogenic composition and anti-cancer agent that are administered together. In another aspect multiple vials are included so that one vial is administered according to a treatment timeline. One vial may only contain the anti-cancer agent for one dose of treatment, another may contain both the anti-cancer agent and immunogenic composition for another dose of treatment, and one vial may only contain the immunogenic composition for yet another dose. In a further aspect the vials are labeled for their proper administration to a patient in need thereof. The immunogen or anti-cancer agents of any embodiment may be in a lyophilized form, a dried form or in aqueous solution as described herein. The immunogen may be a live attenuated virus, protein, or nucleic acid as described herein.

[00392] In one embodiment the anticancer agent is one that enhances the immune system to enhance the effectiveness of the immunogenic composition or vaccine. In a preferred embodiment the anti-cancer agent is a checkpoint inhibitor. In another embodiment the kit contains multiple vials of immunogenic compositions and anti-cancer agents to be administered at different time intervals along a treatment plan. In another embodiment the kit may comprise separate vials for an immunogenic composition for use in priming an immune response and

another immunogenic composition to be used for boosting. In one aspect the priming immunogenic composition could be DNA or a viral vector and the boosting immunogenic composition may be protein. Either composition may be lyophilized or ready for administering. In another embodiment different cocktails of anti-cancer agents containing at least one anti-cancer agent are included in different vials for administration in a treatment plan.

[00393] Although the present invention and its advantages have been described in detail, it should be understood that various changes, substitutions and alterations can be made herein without departing from the spirit and scope of the invention as defined in the appended claims.

[00394] The present invention will be further illustrated in the following Examples which are given for illustration purposes only and are not intended to limit the invention in any way.

Examples

Example 1

[00395] **sPDL1 generates immunogenic epitopes across a variety of HLA alleles.** PDL1 (CD274) is a trans- membrane protein which interacts with PD1 (CD279; *PDCD1*) on T cells and may be involved in multiple forms of natural immune suppression (such as during gestation). Expression of PDL1is also utilized by tumor cells as a way to evade host immune response. sPDL1 is an alternate spliced form of the PDL1 gene. This alternate spliced form is caused by a lack of splicing at the end of Exon 4, reading into the 4th intron. The transcript terminates within intron 4. The translation product is in frame for 18 amino acids before a stop codon is encountered.

[00396] The translated product lacks the transmembrane domain typically found in PDL1 and thus is secreted. It also contains a cysteine within the neoORF translated from the intron and appears to dimerize in the media. The secreted form appears to block binding between PDL1 and PD1.

[00397] Applicants analyzed the predicted binding possibilities for 9 and 10mer peptides containing the neoORF region encoded by the intron. The analysis is shown for predicted 9mer peptides Table 1. The values highlighted in yellow are alleles that are present at a frequency >5% in the indicated population. Notably, the common HLA allele A0210 in the Caucasian population is predicted to have a reasonably tight binding peptide. A similar analysis shows that 10mer peptides are also predicted to be potentially immunogenic, including for the A0201 allele

(85 nM). Tumor cells expressing the alternate form of the PDL1 message would be thus rendered as targets of the immune system.

[00398] These peptides could be utilized across multiple patients (either HLA-restricted or more broadly if the patient is expected to have some probability to contain a relevant HLA allele) as a "Shared Neoantigen". Note that given the relatively short size of the neoORF region of sPDL1, two or three long overlapping peptides could be used as a mixture, allowing targeting of any HLA allele, even rare alleles, and reducing the need to prepare a different product for each patient based on their HLA type.

[00399] This neoORF may also contain a CD4 epitope although prediction algorithms for CD4 epitopes are not highly accurate. The presence of a CD4 epitope could be assessed in vitro with naive T cells or in patient samples.

Table 1

HLA	peptide 9mers	affinity(nM)	Caucasian	Black	Asian	Hispanic	ENHTAELVIPGNILNVSIKICLTLSPST
A0201	VIPGNILNV	182	28.3%	11.4%	9.7%	19.7%	
B4001	AELVIPGNI	144	4.0%	1.0%	12.0%	1.3%	
A3201	NILNVSIKI	491	3.2%	1.6%	0.3%	2.6%	
A3201	VSIKICLTL	224	3.2%	1.6%	0.3%	2.6%	
A2301	VSIKICLTL	468	2.3%	11.6%	0.2%	3.5%	
B4002	AELVIPGNI	53	1.6%	0.3%	7.6%	5.0%	
B4901	AELVIPGNI	108	1.4%	3.1%	0.0%	2.3%	
B4102	AELVIPGNI	192	1.0%	0.6%	0.0%	0.5%	
A0205	VIPGNILNV	170	0.8%	2.3%	0.1%	1.4%	
B5801	VSIKICLTL	373	0.8%	4.3%	4.5%	1.3%	
A6802	HTAELVIPG	170	0.7%	6.4%	0.0%	2.4%	
B4405	AELVIPGNI	219	0.6%	0.0%	0.0%	0.2%	
B4101	AELVIPGNI	92	0.5%	0.6%	0.0%	1.1%	
B4501	AELVIPGNI	302	0.4%	5.3%	0.0%	1.5%	
B1517	VSIKICLTL	23	0.3%	0.5%	0.1%	0.6%	
A0206	VIPGNILNV	85	0.2%	0.0%	4.7%	4.1%	
A0202	VIPGNILNV	90	0.1%	4.4%	0.0%	0.7%	
A6901	HTAELVIPG	283	0.1%	0.1%	0.0%	0.5%	
A6901	NILNVSIKI	162	0.1%	0.1%	0.0%	0.5%	
B1503	IKICLTLSP	408	0.1%	6.5%	0.1%	1.5%	
B1503	VSIKICLTL	138	0.1%	6.5%	0.1%	1.5%	
A0203	VIPGNILNV	98	0.0%	0.0%	5.2%	0.0%	

Example 2

[00400] Androgen Receptor generates immunogenic epitopes across a variety of HLA alleles. The androgen receptor was identified as another alternate spliced form of a message that results in a neoORF which may be specifically expressed in tumor cells. Alternate splicing results in at least two isoforms that bring in cryptic exons that are.neoORFs.

[00401] Of these alternate transcripts, AR-V1 and AR-V7 were consistently seen in hormone resistant prostate cancer samples.

[00402] The immunogenic potential of these neoORFs was unknown and thus Applicants conducted predicted binding analysis across a number of common HLA alleles. These are shown for HLA A alleles (Table 2).

Table 2

	A0201			A0202			A1101			A3101		
Caucasian		28.30%			13.70%			6.00%			1.60%	
Asian		9.70%			0.90%			22.40%			1.40%	
Hispanic		19.65%			7.59%			4.88%			2.20%	
Black		11.40%			7.10%			1.00%			6.50%	
	RVFGVSEWL	SEQ2	233	RVGNCKHLK	SEQ1	122	RVGNCKHLK	SEQ1	33	RVSNCKHLK	SEQ1	30
	GMTLGAVVV	SEQ2	282				VVVSERILR	SEQ2	359	KFRVGNCKH	SEQ1	103
	MTLGEKFRV	SEQ1	400							KFRVGNCKHL	SEQ1	190

A3301			A3302			A6801			A6802			A	B	
2.40%			3.20%			0.70%			3.40%			30.30%	6.80%	Caucasian
3.40%			0.30%			0.60%			0.30%			28.70%	19.70%	Asian
4.72%			2.62%			1.97%			4.46%			26.46%	7.86%	Hispanic
1.00%			1.60%			1.70%			3.20%			20.40%	2.10%	Black
EAGMTLGEK	SEQ1	70	RVFGVSEWL	SEQ2	41	NCKHLKMSE	SEQ1	385	VVVSERILI	SEQ2	47			
TLGAVVVSE	SEQ2	121	ILRVFGVSE	SEQ2	255	TLGAVVVSE	SEQ2	417	TLGAVVVSE	SEQ2	84			
VVVSERILR	SEQ2	127							EAGMTLGEK	SEQ1	230			
GMTLGEKFR	SEQ1	199							LGAVVVSER	SEQ2	268			
AVVVSERIL	SEQ2	230							AVVVSERIL	SEQ2	339			
AGMTLGEKF	SEQ1	284												
GNCKHLKTS	SEQ1	466												
LGAVVVSER	SEQ2	488												

[00403] Again, as for sPDL1, a number of peptides are predicted to be immunogenic binders and these can be applied across a large subset of patients. These immunogenic peptides can be used across multiple patients.

Example 3

[00404] **Drug Resistant Mutations.** Treatment with various chemotherapeutic agents, particularly with targeted therapies such as tyrosine kinase inhibitors, frequently leads to new mutations in the target molecules that resist the activity of the therapeutic. Multiple strategies to overcome this resistance are being evaluated, including development of second generation therapies that are not affected by these mutations and treatment with multiple agents including those that act downstream of the resistance mutation.

[00405] Applicants have evaluated the immunogenic potential of the mutated peptides created by these resistance mutations and have found that for some, predicted immunogenic peptides are created that can bind to a range of HLA alleles. Two specific examples are provided below as well as data for a range of resistance variants.

BTK/C481S

[00406] A very common mutation to ibrutinib, a molecule targeting Bruton's Tyrosine Kinase (BTK) and used for CLL and certain lymphomas, is a Cysteine to Serine change at position 481. This change produces a number of binding peptides which bind to a range of HLA molecules.

[00407] Shown are results of binding predictions for 9mer peptides. Similar binding peptides can be found for 10mer peptides (Table 3). Only peptides with mutant predicted affinity below

150 nM are included. Expanding the range of peptides up to 500 nM would also significantly increase the number of HLA range.

Table 3

HLA	peptide	affinity(nM) MUT	affinity (nM) NAT	Caucasian	Black	Asian	Hispanic
A0201	SLLNYLREM	97	278	28.3%	11.4%	9.7%	19.7%
A2402	EYMANGSLL	95	120	9.3%	2.0%	23.1%	12.4%
B1801	TEYMANGSL	80	252	6.1%	3.5%	0.4%	4.1%
B1501	MANGSLLNY	91	158	5.8%	0.8%	12.1%	2.6%
B3501	MANGSLLNY	17	17	5.6%	6.1%	2.4%	6.0%
B4001	TEYMANGSL	10	24	4.0%	1.0%	12.0%	1.3%
A3101	LLNYLREMR	43	206	2.4%	1.0%	3.4%	4.7%
A2301	EYMANGSLL	122	133	2.3%	11.6%	0.2%	3.5%
A2902	MANGSLLNY	17	10	2.0%	4.4%	0.0%	4.1%
B4002	TEYMANGSL	45	110	1.6%	0.3%	7.6%	5.0%
B4102	TEYMANGSL	133	341	1.0%	0.6%	0.0%	0.5%
B5801	MANGSLLNY	40	35	0.8%	4.3%	4.5%	1.3%
A3301	LLNYLREMR	91	188	0.7%	1.7%	0.6%	2.0%
A3002	MANGSLLNY	16	15	0.5%	6.6%	0.0%	2.8%
A6804	EYMANGSLL	47	448	0.0%	0.0%	0.0%	0.0%
B1801	TEYMANGSL	44	252	6.1%	3.5%	0.4%	4.1%
B1501	MANGSLLNY	42	158	5.8%	0.8%	12.1%	2.6%
B3501	MANGSLLNY	40	17	5.6%	6.1%	2.4%	6.0%
B4001	TEYMANGSL	38	24	4.0%	1.0%	12.0%	1.3%
A3101	LLNYLREMR	36	206	2.4%	1.0%	3.4%	4.7%
A2301	EYMANGSLL	34	133	2.3%	11.6%	0.2%	3.5%
A2902	MANGSLLNY	32	10	2.0%	4.4%	0.0%	4.1%
B4002	TEYMANGSL	30	110	1.6%	0.3%	7.6%	5.0%

[00408] Such peptide immunogens are preferably utilized prophylactically (prior to detection of resistant disease) to induce an immunogenic response capable of killing any pre-existing or newly mutated cells or could also be used at the time of detection of disease recurrence following or during therapy. These peptides could be utilized across multiple patients (either HLA-restricted or more broadly if the patient is expected with some probability to contain a relevant HLA allele).

EGFR/T790M

[00409] Erlotinib, which targets the tyrosine kinase domain of the Epidermal Growth Factor Receptor (EGFR), is commonly used in the treatment of lung cancer and resistant tumors invariably develop following therapy. A common mutation found in resistant clones is a Threonine to methionine mutation at position 790. This change produces a number of binding peptides which bind to a range of HLA molecules (Table 4).

Table 4

																							SUM
Caucasian	2.3%			3.9%			4.0%			3.2%			3.2%										17%
Black	11.6%			0.3%			1.5%			1.6%			1.6%										17%
Asian	0.2%			0.0%			3.9%			0.3%			0.3%										5%
Hispanic	3.5%			0.9%			2.8%			2.6%			2.6%										12%
	A2301			A2501			A2601			A3201			A3201										
	VQLIMQLMPF		366	STVQLIMQLM		125	STVQLIMQLM		67	QLIMQLMPF		155	QLIMQLMPF		155								
										VQLIMQLMPF		426	VQLIMQLMPF		426								
Caucasian	4.2%			5.8%			2.9%			1.4%			0.4%			1.6%							16%
Black	1.2%			0.8%			0.1%			0.3%			0.1%			0.3%							3%
Asian	1.2%			12.1%			0.2%			2.4%			0.0%			7.6%							24%
Hispanic	1.2%			2.6%			1.8%			1.0%			2.2%			5.0%							14%
	B1302			B1501			B3801			B3901			B3905			B4002							
	MQLMPFGCLL		125	MQLMPFGCLL		488	MQLMPFGCLL		400	MQLMPFGCLL		213	MQLMPFGCLL		400	MQLMPFGCL		221					
				QLIMQLMPF		23										MQLMPFGCLL		103					
				VQLIMQLMPF		73										VQLIMQLMPF		365					

[00410] As stated herein, such peptide immunogens are ideally utilized prophylactically (prior to detection of resistant disease) to induce an immunogenic response capable of killing any pre-existing or newly mutated cells or are also used at the time of detection of disease recurrence following or during therapy. These peptides could be utilized across multiple patients (either HLA-restricted or more broadly if the patient is expected with some probability to contain a relevant HLA allele).

[00411] Note that as an immunogen, only a single long peptide containing the mutated amino acid and at least 10 amino acids on either side of the mutated amino acid would be sufficient to contain all the epitopes listed. Thus, all the HLA alleles shown, as well as any additional alleles that have not been shown in this analysis would be covered. For the Caucasian population, the HLA A alleles shown represent 17% of the population distribution of alleles and the HLA B alleles represent 16% of the population distribution of alleles. As each individual has two HLA A alleles and two HLA B alleles, approximately 50% of Caucasian patients will be expected to have at least one of the alleles shown and thus benefit from immune therapy with a vaccine targeting this molecule. This rationale also applies to any other single amino acid mutation discussed herein.

Other Resistance Variants

[00412] In addition to the specific resistance cases discussed herein, there are many other observed resistance mutations to targeted therapy. Each of these are also used to define immunogenic epitopes that could be utilized as vaccine for immunotherapy targeting those cells containing the resistance mutations (Table 5).

Table 5

Drug	Gene	Resistance m	Sensitive	Refs
Imatinib	BCR-Abl	T315I		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	BCR-Abl	Y253H		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	BCR-Abl	E255K		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	BCR-Abl	E255V		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	c-kit	T670I		http://www.mycancergenome.org/content/disease/gist/kit/50/
Erlotinib/gefitinib	PIK3CA	E545K		PMC1570180; PMC3132801
Erlotinib/gefitinib	HER2	G776(YVMA)		PMID 16843263; 15753357
Erlotinib/gefitinib	EML4-ALK	G1269A		http://www.ncbi.nlm.nih.gov/pubmed/22235099?dopt=Abstract
Crizotinib	KRAS	G12V/D		http://www.ncbi.nlm.nih.gov/pubmed/22235099?dopt=Abstract
Crizotinib	ALK	L1196M		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	G1202R		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	S1206Y		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	1151T(ins)		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	F1174C		http://cancerdiscovery.aacrjournals.org/content/4/6/662
Crizotinib	ROS1	G2032R		http://www.nejm.org/doi/full/10.1056/NEJMoa1215530
Crizotinib	PIK3CA	E542K		http://www.mycancergenome.org/content/disease/breast-cancer/
Trastuzumab	Her2	E545K		http://www.mycancergenome.org/content/disease/breast-cancer/
Trastuzumab	Hwe2	H1047R		http://www.mycancergenome.org/content/disease/breast-cancer/
Trastuzumab	AKT1	E17K		http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2834432/
Trastuzumab	BRAF		V600E	
Vemurafenib	MEK1	Q56P		http://www.ncbi.nlm.nih.gov/pubmed/23569304
Vemurafenib	MEK1	E203K		http://www.ncbi.nlm.nih.gov/pubmed/23569304
Vemurafenib	MEK1	C121S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	NRAS	Q61K/L		http://www.ncbi.nlm.nih.gov/pubmed/23569304
Vemurafenib	NRAS	Q61R		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	NRAS	T58I		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	MEK2	C125S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	MEK1	V60E		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	G128V		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	V154I		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	P124S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	P124L		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	RAC1	P29S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	ESR1	S463P		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	V534E		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	P535H		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	L536Q		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	L536R		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	Y537C		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	Y537S		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	Y537N		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	D538G		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	F876L		http://cancerdiscovery.aacrjournals.org/content/early/2013/06/18/2159-8290.CD-13-0226

[00413] A number of these examples have been used to predict immunogenic epitopes. These results are summarized in Table 6, in which for each resistance mutation, the number of potential binding peptides (with predicted affinity < 500 nM) for each mutation are shown for multiple Human HLA alleles.

Table 6

RES 500	Caucasian	Black	Asian	ABL1:p.T315I	ALK:p.F1174C	ALK:p.F1174L	ALK:p.G1202R	ALK:p.G1269A	ALK:p.L1196M	ALK:p.S1206Y	AR:p.F876L
				80	80	80	80	80	80	80	80
hla_a_01_01	0.143	0.047	0.012							1	
hla_a_02_01	0.283	0.114	0.097			1			2		
hla_a_02_03	0	0	0.052		1	2			2		
hla_a_02_07	0	0	0.08						1		
hla_a_03_01	0.137	0.071	0.009			1		1			
hla_a_11_01	0.06	0.01	0.224				1	1			2
hla_a_23_01	0.023	0.116	0.002	2							
hla_a_24_02	0.093	0.02	0.231	1							
hla_a_30_01	0.016	0.065	0.014		1	1	2		1	1	1
hla_a_30_02	0.005	0.066	0	2						2	
hla_a_33_03	0.004	0.041	0.072				3	1		3	
hla_a_68_02	0.007	0.064	0								
hla_a_74_01	0	0.051	0.001			1	1	1			
hla_b_07_02	0.118	0.062	0.015						2		1
hla_b_08_01	0.098	0.039	0.002						1		
hla_b_15_01	0.058	0.008	0.121	1			1			3	1
hla_b_15_02	0	0	0.066	1			2			3	1
hla_b_15_03	0.001	0.065	0.001	5		3	3	2	4	4	4
hla_b_18_01	0.061	0.035	0.004	2		1	1		1		
hla_b_35_01	0.056	0.061	0.024	3			1		1	2	2
hla_b_40_01	0.04	0.01	0.12	3		1	1		1		1
hla_b_40_02	0.016	0.003	0.076	3	1	1	1	1	1		2
hla_b_42_01	0	0.057	0						2		
hla_b_44_02	0.071	0.014	0.002			1					1
hla_b_45_01	0.004	0.053	0			1					1
hla_b_46_01	0	0	0.082								1
hla_b_51_01	0.051	0.021	0.04						2		
hla_b_53_01	0.003	0.11	0	1						1	

RES 500	Caucasian	Black	Asian	BTK:p.C481S	EGFR:p.T790M	KRAS p.G12D	MAP2K1:p.C121S	MAP2K1:p.E203K	MAP2K1:p.G128V	MAP2K1:p.P124L	MAP2K1:p.P124S
				80	80	80	80	80	80	80	80
hla_a_01_01	0.143	0.047	0.012	2	1					1	2
hla_a_02_01	0.283	0.114	0.097	1	2	1	1	3		2	1
hla_a_02_03	0	0	0.052	2	1	2	1	3		2	1
hla_a_02_07	0	0	0.08								
hla_a_03_01	0.137	0.071	0.009	1						1	
hla_a_11_01	0.06	0.01	0.224	2		2			1		
hla_a_23_01	0.023	0.116	0.002	1	2				1	1	2
hla_a_24_02	0.093	0.02	0.231	1					1	1	1
hla_a_30_01	0.016	0.065	0.014					1			1
hla_a_30_02	0.005	0.066	0	2			3	2	3	4	5
hla_a_33_03	0.004	0.041	0.072	2				1			
hla_a_68_02	0.007	0.064	0	1	2	1		1			1
hla_a_74_01	0	0.051	0.001	1							
hla_b_07_02	0.118	0.062	0.015					2			
hla_b_08_01	0.098	0.039	0.002								
hla_b_15_01	0.058	0.008	0.121	3	2		2	1	3	1	2
hla_b_15_02	0	0	0.066	3	2		2	1	3	3	3
hla_b_15_03	0.001	0.065	0.001	8	7		7	2	6	8	8
hla_b_18_01	0.061	0.035	0.004	2					1	1	1
hla_b_35_01	0.056	0.061	0.024	3	1		2	1	3		3
hla_b_40_01	0.04	0.01	0.12	2	1		2		1	1	1
hla_b_40_02	0.016	0.003	0.076	2	3		3		1	1	1
hla_b_42_01	0	0.057	0								
hla_b_44_02	0.071	0.014	0.002								
hla_b_45_01	0.004	0.053	0				2		1	1	1
hla_b_46_01	0	0	0.082	3	1		1	1	1		
hla_b_51_01	0.051	0.021	0.04					1	1		
hla_b_53_01	0.003	0.11	0	2				2			

RES 500	Caucasian	Black	Asian	MAP2K1:p.Q56P	MAP2K1:p.V154I	MAP2K1:p.V60E	MAP2K2:p.C125S	MAP2K2:p.L46F	MAP2K2:p.N126D	MAP2K2:p.V35M	NRAS:p.Q61R
				80	80	80	80	80	80	80	80
hla_a_01_01	0.143	0.047	0.012								1
hla_a_02_01	0.283	0.114	0.097		1		1		1	1	
hla_a_02_03	0	0	0.052		1		1		1	1	
hla_a_02_07	0	0	0.08								
hla_a_03_01	0.137	0.071	0.009	1							
hla_a_11_01	0.06	0.01	0.224	1	1						
hla_a_23_01	0.023	0.116	0.002								
hla_a_24_02	0.093	0.02	0.231								
hla_a_30_01	0.016	0.065	0.014	2		1					1
hla_a_30_02	0.005	0.066	0				3		4		1
hla_a_33_03	0.004	0.041	0.072		1						
hla_a_68_02	0.007	0.064	0	1							1
hla_a_74_01	0	0.051	0.001								
hla_b_07_02	0.118	0.062	0.015	1							
hla_b_08_01	0.098	0.039	0.002	1							
hla_b_15_01	0.058	0.008	0.121				2	1	1		
hla_b_15_02	0	0	0.066				2		2		
hla_b_15_03	0.001	0.065	0.001		1		7	2	5	1	3
hla_b_18_01	0.061	0.035	0.004						1		
hla_b_35_01	0.056	0.061	0.024				2		2		
hla_b_40_01	0.04	0.01	0.12				2		1	1	
hla_b_40_02	0.016	0.003	0.076				3		1	1	
hla_b_42_01	0	0.057	0								
hla_b_44_02	0.071	0.014	0.002								
hla_b_45_01	0.004	0.053	0				2		1		
hla_b_46_01	0	0	0.082				1				
hla_b_51_01	0.051	0.021	0.04								
hla_b_53_01	0.003	0.11	0								

RES 500	Caucasian	Black	Asian	NRAS:p.T58I	PIK3CA:p.E545K	PLCG2:p.R665W	ROS1:p.G2032A
				80	80	80	80
hla_a_01_01	0.143	0.047	0.012	1			1
hla_a_02_01	0.283	0.114	0.097	1		2	3
hla_a_02_03	0	0	0.052	1		3	3
hla_a_02_07	0	0	0.08				
hla_a_03_01	0.137	0.071	0.009				
hla_a_11_01	0.06	0.01	0.224				2
hla_a_23_01	0.023	0.116	0.002				
hla_a_24_02	0.093	0.02	0.231				
hla_a_30_01	0.016	0.065	0.014			1	
hla_a_30_02	0.005	0.066	0	1		1	2
hla_a_33_03	0.004	0.041	0.072				1
hla_a_68_02	0.007	0.064	0			1	2
hla_a_74_01	0	0.051	0.001				
hla_b_07_02	0.118	0.062	0.015				
hla_b_08_01	0.098	0.039	0.002				
hla_b_15_01	0.058	0.008	0.121			1	2
hla_b_15_02	0	0	0.066			1	2
hla_b_15_03	0.001	0.065	0.001	3	2	4	5
hla_b_18_01	0.061	0.035	0.004			1	2
hla_b_35_01	0.056	0.061	0.024			1	1
hla_b_40_01	0.04	0.01	0.12				3
hla_b_40_02	0.016	0.003	0.076			1	3
hla_b_42_01	0	0.057	0				
hla_b_44_02	0.071	0.014	0.002		1	2	2
hla_b_45_01	0.004	0.053	0				
hla_b_46_01	0	0	0.082			1	
hla_b_51_01	0.051	0.021	0.04			1	
hla_b_53_01	0.003	0.11	0			1	

[00414] In all of the above examples, predictions are only shown for a subset of HLA alleles. These are often but not exclusively the most abundant alleles in each ethnic population. Additional alleles are readily predicted.

[00415] Moreover, for a given immunization designed to attack resistant variants for a given resistance mutation, multiple peptides, each targeting a separate possible resistance variant that may arise, are utilized to benefit the broadest set of patients.

Example 4

[00416] **Cancer Subtype Specific Immunogenic compositions**. Table 7 shows a data summary for the number of mutations found within a population of samples specific to a cancer subtype. Each mutation found within the data set for each disease leads to at least one predicted binder to any one of 33 HLA alleles selected based on being found in at least 5% of any one of the three ethnic populations (Caucasian, Black, Asian). A combination of neoantigenic peptides

derived from polypeptides resulting from these mutations can be used in an immunogenic composition. Based on the number of peptides from the mutations selected, a larger percentage of patients may receive a benefit from the vaccine. Table 7 shows the number of mutations that are recurrent in each cancer specific data set. Also shown are the percentage of subjects in each data set that will have at least a single mutation when selecting recurrent mutations. For example, an immunogenic composition for SKCM that includes neoantigenic peptides derived from 64 recurrent mutations described herein covers 90.91% of patients in this population, whereby each subject will contain at least one of the neoantigenic mutations.

Table 7

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
SKCM	5	64	230	253	90.91
SKCM	4	200	241	253	95.26
SKCM	3	707	247	253	97.63
SKCM	2	4437	250	253	98.81
SKCM	1	103732	253	253	100
ACC	5	161	90	90	100
ACC	4	219	90	90	100
ACC	3	299	90	90	100
ACC	2	546	90	90	100
ACC	1	10310	90	90	100
BLCA	5	6	35	130	26.92
BLCA	4	9	47	130	36.15
BLCA	3	26	77	130	59.23
BLCA	2	181	121	130	93.08
BLCA	1	25605	130	130	100
BRCA	5	18	320	888	36.04
BRCA	4	25	337	888	37.95
BRCA	3	35	357	888	40.2
BRCA	2	148	475	888	53.49
BRCA	1	31457	886	888	99.77
CESC	5	4	46	194	23.71

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
CESC	4	7	55	194	28.35
CESC	3	12	65	194	33.51
CESC	2	145	133	194	68.56
CESC	1	25585	194	194	100
CRC	5	15	132	233	56.65
CRC	4	22	142	233	60.94
CRC	3	53	160	233	68.67
CRC	2	711	209	233	89.7
CRC	1	55287	233	233	100
DLBCL	5	0	0	58	0
DLBCL	4	2	8	58	13.79
DLBCL	3	4	13	58	22.41
DLBCL	2	30	38	58	65.52
DLBCL	1	7435	57	58	98.28
HNSC	5	10	83	384	21.61
HNSC	4	15	97	384	25.26
HNSC	3	27	123	384	32.03
HNSC	2	154	227	384	59.11
HNSC	1	43143	384	384	100
KICH	5	0	0	66	0
KICH	4	0	0	66	0
KICH	3	0	0	66	0
KICH	2	24	33	66	50
KICH	1	2576	66	66	100
KIRP	5	9	68	161	42.24
KIRP	4	18	86	161	53.42
KIRP	3	35	104	161	64.6
KIRP	2	117	139	161	86.34
KIRP	1	10482	161	161	100
LIHC	5	2	13	198	6.57
LIHC	4	5	25	198	12.63

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
LIHC	3	10	38	198	19.19
LIHC	2	33	73	198	36.87
LIHC	1	18574	198	198	100
LUAD	5	11	134	401	33.42
LUAD	4	17	152	401	37.91
LUAD	3	35	185	401	46.13
LUAD	2	611	330	401	82.29
LUAD	1	101222	399	401	99.5
MM	5	6	49	205	23.9
MM	4	8	55	205	26.83
MM	3	16	71	205	34.63
MM	2	51	101	205	49.27
MM	1	7116	204	205	99.51
PRAD	5	24	104	261	39.85
PRAD	4	38	133	261	50.96
PRAD	3	83	174	261	66.67
PRAD	2	205	213	261	81.61
PRAD	1	10174	261	261	100
STAD	5	150	141	289	48.79
STAD	4	245	156	289	53.98
STAD	3	613	201	289	69.55
STAD	2	2729	269	289	93.08
STAD	1	97578	289	289	100
TGCT	5	14	80	155	51.61
TGCT	4	25	99	155	63.87
TGCT	3	64	124	155	80
TGCT	2	338	149	155	96.13
TGCT	1	7632	155	155	100
THCA	5	5	283	405	69.88
THCA	4	5	283	405	69.88
THCA	3	7	287	405	70.86

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
THCA	2	31	300	405	74.07
THCA	1	4439	405	405	100
UCS	5	2	9	56	16.07
UCS	4	10	31	56	55.36
UCS	3	19	41	56	73.21
UCS	2	55	53	56	94.64
UCS	1	3805	56	56	100
CLL	5	6	46	263	17.49
CLL	4	19	74	263	28.14
CLL	3	38	100	263	38.02
CLL	2	157	167	263	63.5
CLL	1	7870	263	263	100
GBM	5	14	100	291	34.36
GBM	4	24	125	291	42.96
GBM	3	45	153	291	52.58
GBM	2	221	252	291	86.6
GBM	1	14142	291	291	100
KIRC	5	4	25	417	6
KIRC	4	8	41	417	9.83
KIRC	3	23	78	417	18.71
KIRC	2	291	292	417	70.02
KIRC	1	17725	417	417	100
LAML	5	11	93	196	47.45
LAML	4	12	95	196	48.47
LAML	3	16	101	196	51.53
LAML	2	27	114	196	58.16
LAML	1	1458	195	196	99.49
LUSC	5	2	14	178	7.87
LUSC	4	4	22	178	12.36
LUSC	3	15	50	178	28.09
LUSC	2	130	138	178	77.53

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
LUSC	1	42062	178	178	100
OV	5	10	72	316	22.78
OV	4	12	80	316	25.32
OV	3	14	86	316	27.22
OV	2	56	151	316	47.78
OV	1	12840	316	316	100
PAAD	5	53	146	146	100
PAAD	4	69	146	146	100
PAAD	3	123	146	146	100
PAAD	2	398	146	146	100
PAAD	1	23715	146	146	100
UCEC	5	30	168	248	67.74
UCEC	4	81	196	248	79.03
UCEC	3	302	217	248	87.5
UCEC	2	2797	237	248	95.56
UCEC	1	112636	248	248	100
COAD	5	3	19	70	27.14%
COAD	4	7	20	70	28.57%
COAD	3	11	25	70	35.71%
COAD	2	84	44	70	62.86%
COAD	1	16670	70	70	100.00%
READ	5	0	0	39	0.00%
READ	4	2	8	39	20.51%
READ	3	5	16	39	41.03%
READ	2	33	29	39	74.36%
READ	1	12132	39	39	100.00%

[00417] Table 8 shows the specific recurrent mutations for each cancer subtype, as well as the peptides that each mutation generates and the flanking peptide that includes the peptides ("ACC", "BLCA", "BRCA", "CESC", "COAD", "CLL", "CRC", "DLBCL", "GBM", "HNSC", "KICH", "KIRC", "KIRP", "LAML", "LIHC", "LUAD", "LUSC", "MM", "OV", "PAAD",

"PRAD", "READ", "SKCM", "STAD", "TGCT", "THCA", "UCEC", and "UCS"). Frameshift muations are denoted with a "fs". "Del" and "Ins" indicate deletions and inserts. The number of peptides that are generated from each mutation that binds to a specific HLA allele are shown. The recurrent mutations include frameshift mutations and create HLA binders across many alleles.

Table 8

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
A2M	c.2195G>A	p.R732Q	FYESDVMGRGHARLVHVEEPHTETV[p.R732Q]QKYFPETWIWDLVVVNSAGVAEVGVT	VQKYFPETW,QKYFPETWI,ETVQKYFPET,VQKYFPETWI,QKYFPETWIW,EPHTETVQKY	CRC
A2ML1	c.1960_1961insC	p.S654fs	YDQCPVSGPWDFPQPLIDPMPQGHS[p.S654fs]EPAFHYLEALVL*	HSEPAFHYL,MPQGHSEPA,PQGHSEPAF,GHSEPAFHY,FHYLEALVL,EPAFHYLEA,QGHSEPAFHY,EPAFHYLEAL,MPQGHSEPAF,SEPAFHYLEA	LUAD
AADACL4	c.796G>A	p.A266T	VPLLSRKFMVTSLCNYLAIDLSWRD[p.A266T]TILNGTCVPPDVWRKYEKWLSPDNIP	IDLSWRDTI,SWRDTILNG,DTILNGTCV,IDLSWRDTIL	CRC
AASS	c.2634_2635insC	p.T878fs	KTIDLVAYGDINGFSAMAKTVGLPT[p.T878fs]RHGSQNVA*	MAKTVGLPTR,LPTRHGSQNV	GBM
ABCA11P	c.1154G>T	p.R385I	TGEKPYTCGECGKTFRQSANLYVHR[p.R385I]IIHTGEKPYKCEDCGKAFGRYTALNQ	VHRIIHTGEK,QSANLYVHRI	UCEC
ABCA3	c.285G>C	p.E95D	TFPPPGDTWELAYIPSHSDAAKTVT[p.E95D]DTVRRALVINMRVRGFPSEKDFEDYI	KTVTDTVRR,VTDTVRRALV,AAKTVTDTVR,DAAKTVTDTV,TVTDTVRRAL	KIRC
ABCA5	c.4427G>A	p.R1476Q	PQITLLDEPSTGMDPKAKQHMWRAI[p.R1476Q]QTAFKNRKRAAILTTHYMEEAEAVCD	HMWRAIQTA,IQTAFKNRK,MWRAIQTAF,AIQTAFKNR,QTAFKNRKR,MWRAIQTAFK,AIQTAFKNRK,HMWRAIQTAF,KQHMWRAIQT,RAIQTAFKNR,QHMWRAIQTA	UCEC
ABCA6	c.917delT	p.L306fs	FVTIIITFTQIIVMTGFMVIFILFF[p.L306fs]YMAYLW*	MVIFILFFY,VIFILFFYM,ILFFYMAYL,LFFYMAYLW,FILFFYMAY,MVIFILFFYM,VIFILFFYMA,FILFFYMAYL,ILFFYMAYLW,FMVIFILFFY,IFILFFYMAY	STAD
ABCA8	c.2086G>A	p.A696T	STQFMDEADILADRKVFLSQGKLKC[p.A696T]TGSSLFLKKKWGIGYHLSLQLNEICV	KLKCTGSSL,CTGSSLFLK,TGSSLFLKK,LKCTGSSLF,FLSQGKLKCT,CTGSSLFLKK,KCTGSSLFLK,KLKCTGSSLF,GKLKCTGSSL,LKCTGSSLFL	CRC
ABCA8	c.2525G>A	p.R842Q	RLVEMEQVLSSLNKMRKTIGGVALW[p.R842Q]QQQICAIARVRLLKLKHERKALLALL	ALWQQQICA,WQQQICAIA,ALWQQQICAI	CRC
ABCA8	c.3472G>A	p.E1158K	NSGIWSFCFYVVTVFSVAGFAFSIF[p.E1158K]KSDIPFIFTFLIPPATMIGCLFLSSH	AGFAFSIFK,IFKSDIPFI,SIFKSDIPF,FKSDIPFIF,SIFKSDIPFI,VAGFAFSIFK,IFKSDIPFIF,KSDIPFIFTF,FAFSIFKSDI,FSIFKSDIPF	CRC
ABCB1	c.1400G>T	p.R467L	RLYDPTEGMVSVDGQDIRTINVRFL[p.R467L]LEIIGVVSQEPVLFATTIAENIRYGR	RTINVRFLL,FLLEIIGVV,RFLLEIIGV,INVRFLLEI,FLLEIIGVVS,TINVRFLLEI,RFLLEIIGVV,RTINVRFLLE	LUAD
ABCB1	c.1581_1582delAG	p.R527fs	VKEANAYDFIMKLPHKFDTLVGERG[p.R527fs]PVEWWAEAEDRHCTCPGSQPQDPPAG*	TLVGERGPV,GERGPVEWW,AEAEDRHCT,DTLVGERGPV,GERGPVEWWA	STAD
ABCB6	c.953delG	p.G318fs	LTEKAPWNSLAWTVTSYVFLKFLQG[p.G318fs]VALAVQAS*	FLQGVALAV,FLKFLQGVA,LKFLQGVAL,YVFLKFLQGV,FLKFLQGVAL,KFLQGVALAV,LKFLQGVALA	STAD
ABCB8	c.1034G>A	p.R345H	SRQCQEQIARAMGVADEALGNVRTV[p.R345H]HAFAMEQREEERYGAELEACRCRAEE	NVRTVHAFA,GNVRTVHAF,VRTVHAFAM,ALGNVRTVHA,TVHAFAMEQR,NVRTVHAFAM,LGNVRTVHAF	CRC
ABCC10	c.1708C>T	p.R570W	RMLILPLNNFPWVINGLLEAKVSLD[p.R570W]WIQLFLDLPNHNPQAYYSPDPPAEPS	SLDWIQLFL,VSLDWIQLF,DWIQLFLDL,LEAKVSLDW,KVSLDWIQLF,AKVSLDWIQL,LEAKVSLDWI,LDWIQLFLDL	GBM
ABCC4	c.2648delT	p.L883fs	VAVIPWIAIPLVPLGIIFIFLRRYF[p.L883fs]WKRQEM*	IFLRRYFWK,FIFLRRYFW,RYFWKRQEM,FLRRYFWKR,FIFLRRYFWK,IFIFLRRYFW,IFLRRYFWKR,RRYFWKRQEM	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ABCC5	c.3269delT	p.L1090fs	HAYNKGQEFLHRYQELLDDNQAPFF[p.L1090fs]CLRVRCGGWLCGWTSSASPSSPPRG*	WLCGWTSSA,SASPSSPPR,RVRCGGWLC,NQAPFFCLR,QAPFFCLRV,NQAPFFCLRV,SSASPSSPPR,RVRCGGWLCG,DNQAPFFCLR,CLRVRCGGWL	KIRC
ABCC8	c.1535A>G	p.Y512C	STLEYSNERLKQTNEMLRGIKLLKL[p.Y512C]CAWENIFRTRVETTRRKEMTSLRAFA	IKLLKLCAW,LKLCAWENI,KLCAWENIF,LLKLCAWENI,KLCAWENIFR,CAWENIFRTR,LKLCAWENIF	TGCT
ABCC9	c.1397T>C	p.L466P	IIMGVILLYNLLGSSALVGAAVIVL[p.L466P]PAPIQYFIATKLAEAQKSTLDYSTER	AVIVLPAPI,IVLPAPIQY,VLPAPIQYF,LPAPIQYFI,VLPAPIQYFI,IVLPAPIQYF,AAVIVLPAPI,VIVLPAPIQY,LPAPIQYFIA	TGCT
ABCD1	c.1816T>C	p.S606P	DVVHLHHILQREGGWEAMCDWKDVL[p.S606P]PGGEKQRIGMARMFYHRPKYALLDEC	LPGGEKQRI,DVLPGGEKQR	CESC
ABCD1	c.507C>A	p.H169Q	ATFVNSAIRYLEGQLALSFRSRLVA[p.H169Q]QAYRLYFSQQTYYRVSNMDGRLRNPD	RLVAQAYRL,VAQAYRLYF,RSRLVAQAY,LVAQAYRLY,RLVAQAYRLY,RSRLVAQAYR,LVAQAYRLYF,SFRSRLVAQA,FRSRLVAQAY,SRLVAQAYRL	TGCT
ABI1	c.1335G>T	p.K445N	DYEDEEAAVVQYNDPYADGDPAWAP[p.K445N]NNYIEKVVAIYDYTKDKDDELSFMEG	DPAWAPNNY,AWAPNNYIEK,WAPNNYIEKV,DPAWAPNNYI	UCEC
ABL2	c.55C>A	p.P19T	MGQQVGRVGEAPGLQQPQ[p.P19T]TRGIRGSSAARPSGRRRDPAGRTTET	LQQPQTRGI,QTRGIRGSSA	TGCT
ABTB1	c.747_748insC	p.L249fs	TIEPPPADPRLREDMALLADCALPP[p.L249fs]RAPR*	CALPPRAPR,LLADCALPPR,DCALPPRAPR	LAML
ACACA	c.5191C>T	p.R1731C	ARAEGIPRIYVSANSGARIGLAEEI[p.R1731C]CHMFHVAWVDPEDPYKGYRYLYLTPQ	GLAEEICHM,EICHMFHVA,LAEEICHMF,ICHMFHVAW,EEICHMFHV,GLAEEICHMF,IGLAEEICHM,EEICHMFHVA,AEEICHMFHV	CRC
ACACB	c.6952G>C	p.E2318Q	VAVQFADFHDTPGRMLEKGVISDIL[p.E2318Q]QWKTARTFLYWRLRRLLLEDQVKQEI	ILQWKTART,VISDILQWK,QWKTARTFL,DILQWKTAR,LQWKTARTF,GVISDILQWK,ILQWKTARTF,QWKTARTFLY,LQWKTARTFL	BLCA
ACACB	c.763delG	p.G255fs	EHKKLDLHRDFTVASPAEFVTRFGG[p.G255fs]IGSSRRCLLPTTGLPP*	SSRRCLLPT,RFGGIGSSR,RCLLPTTGL,SSRRCLLPTT,AEFVTRFGGI,RRCLLPTTGL	STAD
ACADM	c.143T>G	p.F48C	QHTKANRQREPGLGFSFEFTEQQKE[p.F48C]CQATARKFAREEIIPVAAEYDKTGEY	QQKECQATA,QQKECQATAR,CQATARKFAR,KECQATARKF,TEQQKECQAT	CRC
ACADS	c.989G>A	p.R330H	TKLQVIQFKLADMALALESARLLTW[p.R330H]HAAMLKDNKKPFIKEAAMAKLAASEA	RLLTWHAAM,LLTWHAAML,LTWHAAMLK,HAAMLKDNK,SARLLTWHA,ARLLTWHAA,RLLTWHAAML,LLTWHAAMLK,SARLLTWHAA,HAAMLKDNKK,ESARLLTWHA,LESARLLTWH,ARLLTWHAAM	KIRC,PRAD
ACBD3	c.671G>T	p.R224L	REEEERERLQKEEEKRRREEEERLR[p.R224L]LEEEERRRIEEERLRLEQQKQQIMAA	REEEERLRL	LUAD
ACOT9	c.149G>A	p.R50Q	GPQNPKKQGIFHIIHEACSSIHVNHV[p.R50Q]QDKLREIVGASTNWRDHVKAMEERKL	VQDKLREIV,SIHVNHVQDK,HVNHVQDKLR	CRC
ACP1	c.368delA	p.Q123fs	DLNRKSNQVKTCKAKIELLGSYDPQ[p.Q123fs]NNLLLKIPIMGMTLTLRRCTSSVSGAAERSWRRPTEAGSCPAAASLTRPHPEVLHFSVGV*	SLTRPHPEV,LLKIPIMGM,TLRRCTSSV,IMGMTLTLR,MGMTLTLRR,SSVSGAAER,RSWRRPTEA,LTRPHPEVL,GAAERSWRR,CTSSVSGAA,EVLHFSVGV,RPHPEVLHF,HPEVLHFSV,NLLLKIPIM,GSYDPQNNL,TEAGSCPAA,GSCPAAASL,AAASLTRPH,AERSWRRPT,LLLKIPIMGM,LTLRRCTSSV,SLTRPHPEVL,IMGMTLTLRR,SYDPQNNLLL,ASLTRPHPEV,LTRPHPEVLH,PIMGMTLTLR,SGAAERSWRR,IPIMGMTLTL,RPTEAGSCPA,GSYDPQNNLL,LKIPIMGMTL,TEAGSCPAAA,PEVLHFSVGV,DPQNNLLLKI	STAD
ACP6	c.86T>G	p.V29G	GVFSMRLWTPVGVLTSLAYCLHQRR[p.V29G]GALAELQEADGQCPVDRSLLKLMVQ	CLHQRRGAL,HQRRGALAE,QRRGALAEL,CLHQRRGALA,HQRRGALAEL,YCLHQRRGAL	KIRP
ACPP	c.127C>T	p.R43W	FLFLLFFWLDRSVLAKELKFVTLVF[p.R43W]WHGDRSPIDTFPTDPIKESSWPQGFG	TLVFWHGDR,LKFVTLVFW,FWHGDRSPI,VTLVFWHGDR,VFWHGDRSPI	BRCA
ACPP	c.314G>A	p.R105Q	ELGEYIRKRYRKFLNESYKHEQVYI[p.R105Q]QSTDVDRTLMSAMTNLAALFPPEGVS	HEQVYIQST,IQSTDVDRTL	CRC

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ACPP	c.961G>A	p.E321K	LQMALDVYNGLLPPYASCHLTELYF[p.E321K]KKGEYFVEMYYRNETQHEPYPLMLPG	HLTELYFKK,LYFKKGEYF,ELYFKKGEY,KKGEYFVEM,LYFKKGEYFV,SCHLTELYFK,ELYFKKGEYF,TELYFKKGEY,FKKGEYFVEM,KKGEYFVEMY	BLCA
ACR	c.837G>T	p.W279C	YVVVGITSWGVGCARAKRPGIYTAT[p.W279C]CPYLNWIASKIGSNALRMIQSATPPP	GIYTATCPY,IYTATCPYL,CPYLNWIAS,TATCPYLNW,GIYTATCPYL,YTATCPYLNW,TATCPYLNWI	KICH
ACSBG2	c.750T>G	p.I250M	AVLIYTSGTTGIPKGVMLSHDNITW[p.I250M]MAGAVTKDFKLTDKHETVVSYLPLSH	NITWMAGAV,TWMAGAVTK,MAGAVTKDF,LSHDNITWM,MLSHDNITWM,ITWMAGAVTK,MAGAVTKDFK,DNITWMAGAV,WMAGAVTKDF	KIRP
ACSL3	c.562A>T	p.T188S	AIFCETRAEWMIAAQACFMYNFQLV[p.T188S]SLYATLGGPAIVHALNETEVTNIITS	FMYNFQLVS,FQLVSLYAT,QLVSLYATL,MYNFQLVSL,YNFQLVSLY,FMYNFQLVSL,FQLVSLYATL,SLYATLGGPA,MYNFQLVSLY,YNFQLVSLYA	CLL
ACSM2A	c.1206_1207insC	p.L402fs	PGYMGTAASCYDVQIIDDKGNVLPP[p.L402fs]RHRRRHWHQGQTHQAYRHLLWLCGQSRQDSSQHSRRLLAPWRPGNQR*	HQAYRHLLW,AYRHLLWLC,SSQHSRRLL,SQHSRRLLA,HSRRLLAPW,RLLAPWRPG,HQGQTHQAY,NVLPPRHRR,VLPPRHRRR,QGQTHQAYR,RHWHQGQTH,QAYRHLLWL,HQAYRHLLWL,THQAYRHLLW,QTHQAYRHLL,SSQHSRRLLA,HSRRLLAPWR,WHQGQTHQAY,NVLPPRHRRR,HQGQTHQAYR,HLLWLCGQSR,LAPWRPGNQR,GQTHQAYRHL,GQSRQDSSQH,SQHSRRLLAP,QHSRRLLAPW	KIRC
ACSM2B	c.585G>T	p.K195N	VASECPSLRIKLLVSEKSCDGWLNF[p.K195N]NKLLNEASTTHHCVETGSQEASAIYF	GWLNFNKLL	UCEC
ACTA1	c.823G>T	p.G275C	ITIGNERFRCPETLFQPSFIGMESA[p.G275C]CIHETTYNSIMKCDIDIRKDLYANNV	FIGMESACI,SACIHETTY,ESACIHETT,MESACIHET,ESACIHETTY,CIHETTYNSI,SFIGMESACI,MESACIHETT	LUAD
ACTG1	c.64G>C	p.A22P	MEEEIAALVIDNGSGMCKAGF[p.A22P]PGDDAPRAVFPSIVGRPRHQGVMVGM	FPGDDAPRA,FPGDDAPRAV	MM
ACTL6A	c.264delA	p.L88fs	GPTYYIDTNALRVPRENMEAISPLK[p.L88fs]MGWLKTGIVSKLFWIIPTKCMSNQKPVSILFSCQRHRGILEQRERN*	KMGWLKTGI,GIVSKLFWI,WLKTGIVSK,KLFWIIPTK,ILFSCQRHR,VSILFSCQR,IVSKLFWII,NQKPVSILF,PTKCMSNQK,MEAISPLKM,LKTGIVSKL,SKLFWIIPT,MSNQKPVSI,KMGWLKTGIV,WLKTGIVSKL,GIVSKLFWII,KLFWIIPTKC,AISPLKMGWL,CMSNQKPVSI,ISPLKMGWLK,GWLKTGIVSK,SILFSCQRHR,NMEAISPLKM,LKMGWLKTGI,LKTGIVSKLF,MSNQKPVSIL,SNQKPVSILF,FSCQRHRGIL,EAISPLKMGW	STAD
ACTL7B	c.1061G>A	p.R354H	TGFKEEMAANVLLCGGCTMLDGFPE[p.R354H]HFQRELSLLCPGDSPAVAAAPERKTS	HFQRELSLL,DGFPEHFQR,FPEHFQREL,TMLDGFPEH,MLDGFPEHF,EHFQRELSL,TMLDGFPEHF	CRC
ACTL7B	c.631G>A	p.E211K	IYSYGKTSGLVVESGHGVSHVVPIS[p.E211K]KGDVLPGLTSRADYAGGDLTNYLMQL	VSHVVPISK,VPISKGDVL,GVSHVVPISK,HVVPISKGDV	CESC
ACTL9	c.992G>A	p.R331H	EVPGLSPVGLSTMAKQSLRKLSLEM[p.R331H]HADLAQNVLLCGGSSLFTGFEGRFRA	LEMHADLAQ,HADLAQNVL,KLSLEMHADL,EMHADLAQNV,MHADLAQNVL	CRC
ACTN2	c.2677G>T	p.D893Y	AYSGPGSVPGALDYAAFSSALYGES[p.D893Y]YL*	SSALYGESY,SALYGESYL,FSSALYGESY,SSALYGESYL	LUAD
ACVR1	c.617G>A	p.R206H	ADLLDHSCTSGSGSGLPFLVQRTVA[p.R206H]HQITLLECVGKGRYGEVWRGSWQGEN	HQITLLECV,TVAHQITLL,RTVAHQITL,FLVQRTVAH,VQRTVAHQI,RTVAHQITLL,VQRTVAHQIT,QRTVAHQITL,HQITLLECVG	UCEC
ACVR1	c.869C>T	p.S290L	FIASDMTSRHSSTQLWLITHYHEMG[p.S290L]LLYDYLQLTTLDTVSCLRIVLSIASG	GLLYDYLQL,LLYDYLQLT,ITHYHEMGL,HYHEMGLLY,HEMGLLYDY,GLLYDYLQLT,LLYDYLQLTT,ITHYHEMGLL,THYHEMGLLY,YHEMGLLYDY,HEMGLLYDYL,MGLLYDYLQL	CRC
ADAD1	c.32C>T	p.S11L	MASNNHWFQS[p.S11L]LQVPSFAQMLKKNLPVQPATKTITTP	SNNHWFQSL,FQSLQVPSF,LQVPSFAQM,FQSLQVPSFA,SLQVPSFAQM,LQVPSFAQML,WFQSLQVPSF,ASNNHWFQSL	UCEC
ADAD2	c.131G>A	p.G44E	LAASLQISPQPRPWRPLPAQAQSAW[p.G44E]EPAPAPATYRAEGGWPQVSVLRDSGP	QSAWEPAPA,EPAPAPATY,AQAQSAWEP,AQSAWEPAP,WEPAPAPAT,AQSAWEPAPA,AQAQSAWEPA,SAWEPAPAPA,WEPAPAPATY	ACC
ADAM23	c.1139A>T	p.K380M	EKDQIDITTNPVQMLHEFSKYRQRI[p.K380M]MQHADAVHLISRVTFHYKRSSLSYFG	RIMQHADAV,MQHADAVHL,KYRQRIMQH,FSKYRQRIM,IMQHADAVH,IMQHADAVHL,MQHADAVHLI,KYRQRIMQHA,RQRIMQHADA,SKYRQRIMQH,RIMQHADAVH	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ADAM28	c.217_218insA	p.K73fs	QEQFETELKYKMTINGKIAVLYLKK[p.K73fs]KQEPPCTRLHGNIL*	CTRLHGNIL,KQEPPCTRL,KIAVLYLKKK,YLKKKQEPPC,KKQEPPCTRL,KQEPPCTRLH	STAD
ADAM29	c.613G>A	p.V205I	IDNSTQKQSSYVGWWIHFRIVEIVV[p.V205I]IIDNYLYIRYERNDSKLLEDLYVIVN	RIVEIVVII,VIIDNYLYI,VVIIDNYLY,IVVIIDNYL,FRIVEIVVI,IIDNYLYIRY,VVIIDNYLYI,VIIDNYLYIR,HFRIVEIVVI,IVVIIDNYLY,EIVVIIDNYL,VEIVVIIDNY	GBM
ADAM30	c.2223G>T	p.Q741H	LKPKQEKMPLSKAKTEQEESKTKTV[p.Q741H]HEESKTKTGQEESEAKTGQEESKAKT	KTKTVHEES,KTKTVHEESK,KTVHEESKTK	LUAD
ADAM30	c.289_290GG>TT	p.G97L	KHVLHLWPKRLLLPRHLRVFSFTEH[p.G97L]LELLEDHPYIPKDCNYMGSVKESLDSK	RVFSFTEHL,SFTEHLELL,FSFTEHLEL,LELLEDHPY,HLELLEDHPY,VFSFTEHLEL,LRVFSFTEHL,FSFTEHLELL,LELLEDHPYI	SKCM
ADAM30	c.941C>A	p.S314Y	SSDWAHLYLQRKYNDALAWSFGKVC[p.S314Y]YLEYAGSVSTLLDTNILAPATWSAHE	WSFGKVCYL,CYLEYAGSV,AWSFGKVCY,FGKVCYLEY,SFGKVCYLEY,LAWSFGKVCY	CRC
ADAM32	c.1676G>A	p.R559Q	DRNNKYVFCGWRNLICGRLVCTYPT[p.R559Q]QKPFHQENGDVIYAFVRDSVCITVDY	LVCTYPTQK,CTYPTQKPF,RLVCTYPTQK,CTYPTQKPFH,VCTYPTQKPF	CRC
ADAM9	c.767G>A	p.R256Q	NQTAVREEMILLANYLDSMYIMLNI[p.R256Q]QIVLVGLEIWTNGNLINIVGGAGDVL	YIMLNIQIV,IMLNIQIVL,MLNIQIVLV,MYIMLNIQI,SMYIMLNIQI,YIMLNIQIVL,IMLNIQIVLV,MYIMLNIQIV,IQIVLVGLEI	UCEC
ADAMTS12	c.1075G>A	p.E359K	LNPVHHDVAVLLTRKDICAGFNRPC[p.E359K]KTLGLSHLSGMCQPHRSCNINEDSGL	CAGFNRPCK,CKTLGLSHL,KTLGLSHLSG,FNRPCKTLGL,AGFNRPCKTL	UCS
ADAMTS12	c.3157C>G	p.P1053A	RPRMLTTPTGPESMSTSTPAISSPS[p.P1053A]ATTASKEGDLGGKQWQDSSTQPELSS	TPAISSPSA,ISSPSATTA,AISSPSATTA,SSPSATTASK,STPAISSPSA,TPAISSPSAT	CESC
ADAMTS14	c.712G>T	p.G238C	QQEWAEPDGDLHNEAFGLGDLPNLL[p.G238C]CLVGDQLGDTERKRRHAKPGSYSIEV	DLPNLLCLV,NLLCLVGDQL	LUAD
ADAMTS16	c.2449G>A	p.D817N	LRRYYLNGHWTVDWPGRYKFSGTTF[p.D817N]NYRRSYNEPENLIATGPTNETLIVEL	FSGTTFNYR,KFSGTTFNY,TTFNYRRSY,SGTTFNYRR,FSGTTFNYRR,KFSGTTFNYR,YKFSGTTFNY,GTTFNYRRSY	CRC
ADAMTS17	c.1715A>C	p.N572T	SPWGAWSMCSRTCGTGARFRQRKCD[p.N572T]TPPPGPGGTHCPGASVEHAVCENLPC	RQRKCDTPP,RQRKCDTPPP	TGCT
ADAMTS2	c.2842G>A	p.D948N	WEPCSQTCGRTGMQVRSVRCIQPLH[p.D948N]NNTTRSVHAKHCNDARPESRRACSRE	LHNNTTRSV,SVRCIQPLHN,LHNNTTRSVH	CLL
ADAMTS20	c.1622G>T	p.R541L	KLHKGCFTQHVPPADGTDCGPGMHC[p.R541L]LHGLCVNKETETRPVNGEWGPWEPYS	CLHGLCVNK,GMHCLHGLCV,GPGMHCLHGL	LUAD
ADAMTS20	c.3751C>A	p.R1251S	GKTTRQVLCMNYHQPIDENYCDPEV[p.R1251S]SPLMEQECSLAACPPAHSHFPSSPVQ	SPLMEQECSL	LUAD
ADAMTS4	c.466C>T	p.R156W	TINGDPESVASLHWDGGALLGVLQY[p.R156W]WGAELHLQPLEGGTPNSAGGPGAHIL	VLQYWGAEL,ALLGVLQYW,QYWGAELHL,LQYWGAELH,LLGVLQYWGA,LQYWGAELHL,GALLGVLQYW,WGAELHLQPL	CRC
ADAMTS5	c.1645C>A	p.L549M	QGQMVCLTKKLPAVEGTPCGKGRIC[p.L549M]MQGKCVDKTKKKYYSTSSHGNWGSWG	KGRICMQGK,TPCGKGRICM	LUAD
ADAMTS8	c.1570G>A	p.V524M	TPCGPGHLCSEGSCLPEEEVERPKP[p.V524M]MADGGWAPWGPWGECSRTCGGGVQFS	KPMADGGWA,EEVERPKPM,MADGGWAPW,PMADGGWAPW,EEEVERPKPM	GBM
ADAMTS9	c.1975G>T	p.G659W	FKSCNTEPCLKQKRDFRDEQCAHFD[p.G659W]WKHFNINGLLPNVRWVPKYSGILMKD	HFDWKHFNI,CAHFDWKHF,WKHFNINGL,DEQCAHFDW,AHFDWKHFNI,WKHFNINGLL	LUAD

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ADAMTSL4	c.2332_2333insG	p.G778fs	TSCSRSCGPGTQHRQLQCRQEFGGG[p.G778fs]WLLGAPGALWTSPPAQHHPVLPAAPLWPLGSWLSLEPVLRAVRPGPEKPAGSLCWEQW*	WLLGAPGAL,GSWLSLEPV,SLEPVLRAV,RAVRPGPEK,SWLSLEPVL,HPVLPAAPL,LPAAPLWPL,SPPAQHHPV,PPAQHHPVL,WPLGSWLSL,GPEKPAGSL,RQEFGGGWL,QEFGGGWLL,LLGAPGALW,AQHHPVLPA,QHHPVLPAA,APLWPLGSW,VLPAAPLWPL,AQHHPVLPAA,WLSLEPVLRA,LWPLGSWLSL,AVRPGPEKPA,SWLSLEPVLR,SLEPVLRAVR,TSPPAQHHPV,SPPAQHHPVL,APLWPLGSWL,RQEFGGGWLL,WLLGAPGALW,GSWLSLEPVL,QEFGGGWLLG,HPVLPAAPLW	STAD
ADCY2	c.260C>T	p.A87V	LAVFFALGLEVEDHVAFLITVPTAL[p.A87V]VIFFAIFILVCIESVFKKLLRLFSLV	LVIFFAIFI,VIFFAIFIL,LITVPTALV,TVPTALVIF,TALVIFFAI,PTALVIFFA,ALVIFFAIF,ITVPTALVI,VPTALVIFF,FLITVPTALV,ALVIFFAIFI,VIFFAIFILV,ITVPTALVIF,TVPTALVIFF,TALVIFFAIF,PTALVIFFAI,LVIFFAIFIL,VPTALVIFFA	DLBCL
ADCY2	c.2662G>A	p.V888I	HVAEHFLARSLKNEELYHQSYDCVC[p.V888I]IMFASIPDFKEFYTESDVNKEGLECL	SYDCVCIMF,IMFASIPDF,QSYDCVCIM,HQSYDCVCI,IMFASIPDFK,CIMFASIPDF,HQSYDCVCIM,QSYDCVCIMF	OV
ADCY2	c.3046C>A	p.P1016T	SFNDFKLRVGINHGPVIAGVIGAQK[p.P1016T]TQYDIWGNTVNVASRMDSTGVLDKIQ	AQKTQYDIW,TQYDIWGNTV,GVIGAQKTQY	LUAD
ADCY5	c.1982G>A	p.R661H	SIETFLILRCTQKRKEEKAMIAKMN[p.R661H]HQRTNSIGHNPPHWGAERPFYNHLGG	MIAKMNHQR,KAMIAKMNH,KMNHQRTNS,HQRTNSIGH,MNHQRTNSI,KMNHQRTNSI,AMIAKMNHQR	CRC
ADD3	c.1708G>A	p.E570K	HGPPAPPNPFSHLTEGELEEYKRTI[p.E570K]KRKQQGLEDAEQELLSDDASSVSQIQ	TIKRKQQGL,RTIKRKQQGL	UCEC
ADGB	c.3371C>T	p.S1124L	PCNSFAIKEIRDYYIPNDKKILFRY[p.S1124L]LVKVLTPQPATIQVRTSKPDAFIKLQ	ILFRYLVKV,KILFRYLVK,LFRYLVKVL,KKILFRYLV,KILFRYLVKV,ILFRYLVKVL,KKILFRYLVK,LVKVLTPQPA	UCEC
ADH1A	c.461A>T	p.D154V	SRFTCRRKPIHHFLGISTFSQYTVV[p.D154V]VENAVAKIDAASPLEKVCLIGCGFST	YTVVVENAV,VVVENAVAK,TFSQYTVVV,SQYTVVVEN,STFSQYTVVV,SQYTVVVENA,VVVENAVAKI,TVVVENAVAK,YTVVVENAVA,VENAVAKIDA	KIRC
ADNP2	c.965delC	p.S322fs	NSPSPAAGQPVTVAQGAPGSLTHSP[p.S322fs]LLLANPT*	SLTHSPLLL,GSLTHSPLL,LTHSPLLLA,SLTHSPLLLA,APGSLTHSPL	STAD
AFF2	c.1790G>A	p.R597H	VKTNASQVPAEPKERPLLSLIREKA[p.R597H]HPRPTQKIPETKALKHKLSTTSETVS	KAHPRPTQK,LIREKAHPR,REKAHPRPT,KAHPRPTQKI,SLIREKAHPR	PRAD
AFF3	c.2755G>A	p.E919K	INKNEKMLRSPISPLSDASKHKYTS[p.E919K]KDLTSSSRPNGNSLFTSASSSKKPKA	ASKHKYTSK,TSKDLTSSSR,SKHKYTSKDL	BLCA
AFP	c.545C>G	p.A182G	TFMNKFIYEIARRHPFLYAPTILLW[p.A182G]GARYDKIIPSCCKAENAVECFQTKAA	LLWGARYDK,LWGARYDKI,TILLWGARY,PTILLWGAR,PTILLWGARY,YAPTILLWGA,LLWGARYDKI,ILLWGARYDK,LYAPTILLWG	LUAD
AGAP1	c.381delC	p.G127fs	GGRFKKEIVVDGQSYLLLIRDEGGP[p.G127fs]RRRSLPCGWTLLYLSSAWRMK*	LPCGWTLLY,SLPCGWTLL,LLYLSSAWR,YLSSAWRMK,RSLPCGWTL,LYLSSAWRM,WTLLYLSSA,GPRRRSLPC,TLLYLSSAW,LLYLSSAWRM,RSLPCGWTLL,LIRDEGGPRR,LYLSSAWRMK,SLPCGWTLLY,TLLYLSSAWR,RRSLPCGWTL,WTLLYLSSAW,LPCGWTLLYL	STAD
AGAP3	c.2296C>T	p.R766W	VWEGALGGYSKPGPDACREEKERWI[p.R766W]WAKYEQKLFLAPLPSSDVPLGQQLLR	WIWAKYEQK,IWAKYEQKL,KERWIWAKY,WAKYEQKLF,EEKERWIWA,WIWAKYEQKL,IWAKYEQKLF,RWIWAKYEQK,REEKERWIWA	GBM
AGAP6	c.207delC	p.D69fs	MAAAVQPAEVTVEVGEDLHMHHVRD[p.D69fs]GRCLKLWSLTFLPIQSQAQYSRGTLKQKLWSLTLLPIQRQAQYSRGTLKQML*	TLKQKLWSL,HVRDGRCLK,CLKLWSLTF,LWSLTFLPI,YSRGTLKQK,KQKLWSLTL,HMHHVRDGR,LPIQSQAQY,LKLWSLTFL,SQAQYSRGT,QKLWSLTLL,KLWSLTFLPI,KLWSLTLLPI,CLKLWSLTFL,KQKLWSLTLL,RCLKLWSLTF,HVRDGRCLKL,FLPIQSQAQY,LTFLPIQSQA,DGRCLKLWSL,SQAQYSRGTL,LKQKLWSLTL,YSRGTLKQML	KIRC
AGAP6	c.380G>T	p.S127I	NPSANPEASTIFQRNSQTDVVEIRR[p.S127I]INCTNHVSAVRFSQQYSLCSTIFLDD	RRINCTNHV,RINCTNHVSA	CLL,PRAD
AGAP7	c.211delG	p.E71fs	AAAVQPAEVTVEVGEDLHMHHVRDR[p.E71fs]RCLKLWSLTLLPIQRQAQYSRGTLKQML*	HMHHVRDRR,HVRDRRCLK,CLKLWSLTL,RRCLKLWSL,LKLWSLTLL,KLWSLTLLPI,CLKLWSLTLL,HVRDRRCLKL,DRRCLKLWSL,RCLKLWSLTL,YSRGTLKQML	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
AGAP9	c.742A>G	p.M248V	STSQEDPQFSVPPTANTPTPVCKLS[p.M248V]VRWSNLFTSEKGSDPDKERKAPENHA	KLSVRWSNL,LSVRWSNLF,SVRWSNLFT,KLSVRWSNLF,SVRWSNLFTS,TPTPVCKLSV,CKLSVRWSNL,TPVCKLSVRW	SKCM
AGBL5	c.1260_1261insC	p.I420fs	KLNSVWIMPQQSAGLEESAPDTIPP[p.I420fs]QREWRCLLCGPAWTCFQKGLLHVRKQL*	CFQKGLLHV,TIPPQREWR,FQKGLLHVR,RCLLCGPAW,LCGPAWTCF,REWRCLLCG,CGPAWTCFQK,DTIPPQREWR,CFQKGLLHVR,LLCGPAWTCF,WRCLLCGPAW,REWRCLLCGP	STAD
AGMAT	c.937G>A	p.V313M	TGTPEIAGLTPSQALEIIRGCQGLN[p.V313M]MMGCDLVEVSPPYDLSGNTALLAANL	MMGCDLVEV,IRGCQGLNM,RGCQGLNMM,GLNMMGCDLV,NMMGCDLVEV,IIRGCQGLNM,IRGCQGLNMM	CRC
AGPAT4	c.634G>A	p.A212T	ISMQVARAKGLPRLKHHLLPRTKGF[p.A212T]TITVRSLRNVVSAVYDCTLNFRNNEN	RTKGFTITV,FTITVRSLR,LPRTKGFTI,LLPRTKGFTI,RTKGFTITVR,KGFTITVRSL,GFTITVRSLR,LPRTKGFTIT	CRC
AGRN	c.3851_3853delTGA	p.1284_1285VT>A	GATSGAIAAGATARATTASRLPSSA[p.1284_1285VT>A]APRAPHPSHTSQPVAKTTAAPTTRRPPT	ASRLPSSAA,RLPSSAAPR,SSAAPRAPH,APRAPHPSH,LPSSAAPRA,RLPSSAAPRA,APRAPHPSHT	KICH
AGXT2	c.1504C>T	p.R502C	FSQTFRIAPSMCITKPEVDFAVEVF[p.R502C]CSALTQHMERRAK*	FAVEVFCSA,FCSALTQHM,VEVFCSALT,FAVEVFCSAL,CSALTQHMER,VFCSALTQHM	UCEC
AHI1	c.909_910insA	p.K303fs	DDEISSMEQSTEDSMQDDTKPKPKK[p.K303fs]NKKED*	KPKPKKNKK	STAD
AHNAK	c.12449C>T	p.S4150F	KAPKISMPEVDLNLKGPKMKGDVDV[p.S4150F]FLPKVEGDLKGPEVDIKGPKVDIDVP	KMKGDVDVF,KMKGDVDVFL,KGDVDVFLPK,PKMKGDVDVF	BLCA
AHNAK	c.15_16insGAG	p.5_6insE	MEKEE[p.5_6insE]ETTRELLLPNWQGSGSHGLTIAQRDDGV	KEEETTREL,EEETTRELL,KEEETTRELL,EEETTRELLL	KIRC
AHNAK	c.3658G>A	p.V1220I	ISMPDVDLHLKGPKVKGDVDVSVPK[p.V1220I]IEGEMKVPDVEIKGPKMDIDAPDVEV	IEGEMKVPDV,VPKIEGEMKV	CLL
AHNAK	c.6341C>G	p.A2114G	PDVSLEGPEGKLKGPKLKMPEMHFK[p.A2114G]GPKISMPDVDLHLKGPKVKGDVDVSL	HFKGPKISM,MHFKGPKISM,PEMHFKGPKI	CLL
AHNAK	c.8665G>C	p.D2889H	LKGPEVDLKGPKVDIDVPDVNVQGP[p.D2889H]HWHLKMPKMKMPKFSMPGFKAEGPEV	VQGPHWHLK,NVQGPHWHL,NVQGPHWHLK,HWHLKMPKMK,VQGPHWHLKM	BLCA
AHNAK2	c.3643C>T	p.P1215S	APKVEADVSLPSMQGDLKTTDLSIQ[p.P1215S]SPSADLEVHAGQVDVKLLEGHVPEGA	SPSADLEVH	KIRP
AHNAK2	c.4918C>A	p.L1640M	PDVKMSLSSMEVDVQAPRAKLDGAQ[p.L1640M]MEGDLSLADKAVTAKDSKFKMPKFKM	AQMEGDLSL,QMEGDLSLA,RAKLDGAQM,AQMEGDLSLA	TGCT
AHNAK2	c.6497C>T	p.S2166F	LANKDLTTKDSKFKMPKFKMPSFGV[p.S2166F]FAPGKSIEASVDVSPPKVEADMSLPS	KMPSFGVFA,SFGVFAPGK,FKMPSFGVF,GVFAPGKSI,MPSFGVFAP,PSFGVFAPGK,KFKMPSFGVF,MPSFGVFAPG,FKMPSFGVFA	KIRP
AICDA	c.391C>G	p.R131G	LRIFTARLYFCEDRKAEPEGLRRLH[p.R131G]GAGVQIAIMTFKDYFYCWNTFVENHE	RLHGAGVQI,GLRRLHGAGV,RLHGAGVQIA,RRLHGAGVQI,LHGAGVQIAI,HGAGVQIAIM	LUSC
AICDA	c.431A>T	p.Y144F	RKAEPEGLRRLHRAGVQIAIMTFKD[p.Y144F]FFYCWNTFVENHERTFKAWEGLHENS	IMTFKDFFY,MTFKDFFYC,FFYCWNTFV,TFKDFFYCW,DFFYCWNTF,IAIMTFKDF,AIMTFKDFF,KDFFYCWNT,AIMTFKDFFY,IAIMTFKDFF,MTFKDFFYCW,KDFFYCWNTF,DFFYCWNTFV	GBM
AIDA	c.740A>T	p.K247M	VDIELQKHVEKLTKGAAIFFEFKHY[p.K247M]MPKKRFTSTKCFAFMEMDEIKPGPIV	IFFEFKHYM,EFKHYMPKK,MPKKRFTST,FEFKHYMPK,KHYMPKKRF,YMPKKRFTST,MPKKRFTSTK,FFEFKHYMPK,EFKHYMPKKR,AIFFEFKHYM,FKHYMPKKRF	KIRC
AK302879	c.572A>G	p.Q191R	AVSTQQQEEDRSSSCREAVLQWRLQ[p.Q191R]RTIKEQALLNAHVTQVTESLKQVQLE	AVLQWRLQR,QWRLQRTIK,RTIKEQALL,LQWRLQRTI,VLQWRLQRTI,EAVLQWRLQR,LQRTIKEQAL	PRAD
AK7	c.476C>T	p.A159V	SALSEEVSHFEKRKLFILLSTVMTW[p.A159V]VRSKALDPEDSEVPFTEEDYRRRKSH	LLSTVMTWV,VMTWVRSKA,TVMTWVRSK,MTWVRSKAL,LSTVMTWVR,ILLSTVMTWV,TVMTWVRSKA,VMTWVRSKAL,STVMTWVRSK,LLSTVMTWVR	GBM
AK8	c.728A>C	p.D243A	KLLEYHRNIVRVIPSYPKILKVISA[p.D243A]AQPCVDVFYQALTYVQSNHRTNAPFT	KILKVISAA,VISAAQPCV,AQPCVDVFY,AAQPCVDVF,KVISAAQPCV,AAQPCVDVFY,SAAQPCVDVF	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
AKAP12	c.3844G>A	p.E1282K	ILSKTEGTQEADQYADEKTKDVPFF[p.E1282K]KGLEGSIDTGITVSREKVTEVALKGE	KTKDVPFFK,KDVPFFKGL,KTKDVPFFKG	CRC
AKAP13	c.8353delA	p.K2785fs	QAPASTSASTRLFGLTKPKEKKEKK[p.K2785fs]RRTKPAALSPVMVPRQKYQQRVKRSSADPLPLC*	ALSPVMVPR,KRRTKPAAL,RTKPAALSP,RQKYQQRVK,QQRVKRSSA,RVKRSSADP,RSSADPLPL,KPAALSPVM,EKKRRTKPA,YQQRVKRSS,VKRSSADPL,RTKPAALSPV,AALSPVMVPR,RQKYQQRVKR,RVKRSSADPL,MVPRQKYQQR,KPAALSPVMV,VPRQKYQQRV,KKRRTKPAAL,TKPAALSPVM,YQQRVKRSSA,KRSSADPLPL,SPVMVPRQKY	STAD
AKAP9	c.10444C>A	p.L3482I	RRILYQNLNEPTTWSLTSDRTRNWV[p.L3482I]IQQKIEGETKESNYAKLIEMNGGGTG	RTRNWVIQQ,SDRTRNWVI,RNWVIQQKI,RTRNWVIQQK	CRC
AKAP9	c.11229delG	p.M3743fs	YLLLLLGGFQECEDATLALLARMGG[p.M3743fs]SQLSRI*	RMGGSQLSR,LARMGGSQL,RMGGSQLSRI,LLARMGGSQL	STAD
AKD1	c.3625delA	p.R1209fs	DMKAKIRVDTIAKRRAELILERDKK[p.R1209fs]GGRMLLEMMKRLVRKNLKKTMMILKTSLKMSFQKMRKR*	MLLEMMKRL,TMMILKTSL,NLKKTMMIL,RMLLEMMKR,EMMKRLVRK,RLVRKNLKK,MMILKTSLK,TSLKMSFQK,KMSFQKMRK,MSFQKMRKR,KRLVRKNLK,KNLKKTMMI,LKKTMMILK,KTMMILKTS,KTSLKMSFQ,SLKMSFQKM,MKRLVRKNL,MILKTSLKM,KGGRMLLEM,RKNLKKTMM,LKTSLKMSF,MLLEMMKRLV,MMILKTSLKM,NLKKTMMILK,TMMILKTSLK,KTSLKMSFQK,KMSFQKMRKR,GGRMLLEMMK,MMKRLVRKNL,MKRLVRKNLK,KRLVRKNLKK,KTMMILKTSL,SLKMSFQKMR,ILKTSLKMSF,LERDKKGGRM,KKGGRMLLEM,RMLLEMMKRL,RKNLKKTMMI,TSLKMSFQKM	STAD
AKNAD1	c.1859A>G	p.K620R	AEMTAPSPSCAFCRRLLEWKQNVEK[p.K620R]RGHGRINCGRFSIVLHEKAPHSDSTP	NVEKRGHGR,RGHGRINCGR	HNSC
AKT1	c.49G>A	p.E17K	MSDVAIVKEGWLHKRG[p.E17K]KYIKTWRPRYFLLKNDGTFIGYKERP	WLHKRGKYI,LHKRGKYIK,RGKYIKTWR,KYIKTWRPR,GWLHKRGKY,WLHKRGKYIK,KYIKTWRPRY,HKRGKYIKTW	BRCA,CESC,THCA
AKT2	c.867C>G	p.I289M	EYLHSRDVVYRDIKLENLMLDKDGH[p.I289M]MKITDFGLCKEGISDGATMKTFCGTP	LMLDKDGHM,HMKITDFGL,MLDKDGHMK,MLDKDGHMKI,LMLDKDGHMK	BRCA
ALAS1	c.904G>C	p.G302R	PRVCGAVMDTLKQHGAGAGGTRNIS[p.G302R]RTSKFHVDLERELADLHGKDAALLFS	GTRNISRTS,ISRTSKFHV,RTSKFHVDL,RNISRTSKF,NISRTSKFHV,GTRNISRTSK,TRNISRTSKF	KIRC
ALB	c.881C>T	p.S294L	CCHGDLLECADDRADLAKYICENQD[p.S294L]LISSKLKECCEKPLLEKSHCIAEVEN	YICENQDLI,KYICENQDL,NQDLISSKL,CENQDLISS,KYICENQDLI,AKYICENQDL	CRC
ALDH1A2	c.253C>T	p.R85C	PATGEQVCEVQEADKADIDKAVQAA[p.R85C]CLAFSLGSVWRRMDASERGRLLDKLA	CLAFSLGSV,QAACLAFSL,AVQAACLAF,VQAACLAFSL,KAVQAACLAF,CLAFSLGSVW	PRAD
ALDH1L1	c.2608G>A	p.A870T	KALYVSDKLQAGTVFVNTYNKTDVA[p.A870T]TPFGGFKQSGFGKDLGEAALNEYLRV	VATPFGGFK,DVATPFGGF,NKTDVATPF,DVATPFGGFK,YNKTDVATPF,TDVATPFGGF	CRC
ALDH2	c.858delG	p.L286fs	TEIGRVIQVAAGSSNLKRVTLELGG[p.L286fs]RAPTSSCQMPIWIGPWNRPTSPCSSTRASAAVPAPGPSCRRTSMMSLWSGALPGPSLGWSGTPLIARPSRGRRWMKLSLRRSSATSTRGSKRGRSCCVVGALLLTVVTSSSPLCLEMCRMA*	SMMSLWSGA,MMSLWSGAL,SLGWSGTPL,VVGALLLTV,KLSLRRSSA,ATSTRGSKR,QMPIWIGPW,STRASAAVP,RTSMMSLWS,IARPSRGRR,PSRGRRWMK,RGRRWMKLS,RWMKLSLRR,SLRRSSATS,SATSTRGSK,STRGSKRGR,RGRSCCVVG,SSSPLCLEM,PIWIGPWNR,SSTRASAAV,TVVTSSSPL,RPTSPCSST,GPSCRRTSM,RPSRGRRWM,LELGGRAPT,RAPTSSCQM,CRRTSMMSL,RRTSMMSLW,SLWSGALPG,SGALPGPSL,LGWSGTPLI,GRRWMKLSL,RSCCVVGAL,MPIWIGPWN,SMMSLWSGAL,SLGWSGTPLI,CVVGALLLTV,VVGALLLTVV,SSATSTRGSK,CQMPIWIGPW,STRASAAVPA,RASAAVPAPG,SCRRTSMMSL,RTSMMSLWSG,TSMMSLWSGA,RPSRGRRWMK,RGRRWMKLSL,GSKRGRSCCV,RGRSCCVVGA,RSCCVVGALL,MPIWIGPWNR,LIARPSRGRR,SATSTRGSKR,CSSTRASAAV,LTVVTSSSPL,APTSSCQMPI,GPWNRPTSPC,SPCSSTRASA,GPSCRRTSMM,GRAPTSSCQM,CRRTSMMSLW,MSLWSGALPG,WSGALPGPSL,GALPGPSLGW,IARPSRGRRW,MKLSLRRSSA,GRSCCVVGAL,TSSSPLCLEM,LELGGRAPTS,SPLCLEMCRM	STAD

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ALDH3A1	c.1685delC	p.P562fs	ETFSHRRSCLVRPLMNDEGLKVRYP[p.P562fs]RARPR*	GLKVRYPRA,KVRYPRARP,EGLKVRYPR,GLKVRYPRAR,KVRYPRARPR	STAD
ALG2	c.905C>A	p.S302Y	NVEHYQELKKMVQQSDLGQYVTFLR[p.S302Y]YFSDKQKISLLHSCTCVLYTPSNEHF	TFLRYFSDK,QYVTFLRYF,RYFSDKQKI,GQYVTFLRY,YVTFLRYFS,LGQYVTFLRY,VTFLRYFSDK,FLRYFSDKQK,GQYVTFLRYF	CRC
ALKBH1	c.409A>G	p.K137E	WHWVKQCLKLYSQKPNVCNLDKHMS[p.K137E]EEETQDLWEQSKEFLRYKEATKRRPR	SEEETQDLW,HMSEEETQDL,MSEEETQDLW	LUAD
ALPK2	c.1067delT	p.L356fs	ECSDVMTDYSNAVWQRNLLGTEHVF[p.L356fs]Y*	LLGTEHVFY,NLLGTEHVFY	STAD
ALPK2	c.1568delA	p.K523fs	LLSGESENSGMSQCWETAADKRVGG[p.K523fs]RTYGARGVQGNLPG*	RVGGRTYGA,RTYGARGVQ,RVGGRTYGAR,RTYGARGVQG,TAADKRVGGR,ADKRVGGRTY	UCEC
ALPK2	c.157G>A	p.D53N	DAVLRCIISGQPKPEVTWYKNGQAI[p.D53N]NGSGIISNYEFFENQYIHVLHLSCCT	NGSGIISNY,GQAINGSGI,INGSGIISNY,GQAINGSGII	LUSC
ALPPL2	c.92G>C	p.W31S	VLLLLGLRLQLSLGIIPVEEENPDF[p.W31S]SNRQAAEALGAAKKLQPAQTAAKNLI	SNRQAAEAL,FSNRQAAEAL	TGCT
ALX4	c.377G>A	p.R126Q	PPPQPQPQQQQPQPQPPAQPHLYLQ[p.R126Q]QGACKTPPDGSLKLQEGSSGHSAALQ	YLQQGACKT,HLYLQQGACK,LQQGACKTPP	BLCA
AMBN	c.674C>A	p.S225Y	QGPSLPGLDFADPQGSTIFQIARLI[p.S225Y]YHGPMPQNKQSPLYPGMLYVPFGANQ	IFQIARLIY,FQIARLIYH,ARLIYHGPM,TIFQIARLIY,IARLIYHGPM,IYHGPMPQNK,FQIARLIYHG	UCEC
AMDHD1	c.7A>G	p.S3G	MA[p.S3G]GGHSLLLENAQQVVLVCARGERFLAR	MAGGHSLLL	ACC
AMPH	c.874C>T	p.R292W	PSPLPSPTASPNHTLAPASPAPARP[p.R292W]WSPSQTRKGPPVPPLPKVTPTKELQQ	APARPWSPS,RPWSPSQTRK	CRC
ANAPC1	c.1609A>G	p.T537A	PGLPAPSLTMSNTMPRPSTPLDGVS[p.T537A]APKPLSKLLGSLDEVVLLSPVPELRD	VSAPKPLSK,APKPLSKLL,GVSAPKPLSK	PAAD,PRAD
ANK2	c.1358A>G	p.N453S	TESGLTPIHVAAFMGHLNIVLLLLQ[p.N453S]SGASPDVTNIRGETALHMAARAGQVE	VLLLLQSGA,LQSGASPDV,LLQSGASPDV,LQSGASPDVT	KIRC
ANK2	c.9227A>T	p.Q3076L	DDEAFEARVKEEEQKIFGLMVDRQS[p.Q3076L]LGTTPDTTPARTPTEEGTPTSEQNPF	GLMVDRQSL,RQSLGTTPD,LMVDRQSLGT,FGLMVDRQSL,RQSLGTTPDT	LUAD
ANK3	c.3966T>A	p.D1322E	LATQLYRELICVPYMAKFVVFAKMN[p.D1322E]EPVESSLRCFCMTDDKVDKTLEQQEN	KMNEPVESS,VVFAKMNEPV,KMNEPVESSL,EPVESSLRCF	TGCT
ANKDD1A	c.71G>A	p.R24H	MQEELAWETDGLLPLERQLHEAA[p.R24H]HQNNVGRMQELIGRRVNTRARNHVGR	HEAAHQNNV,AHQNNVGRM,EAAHQNNVGR,LERQLHEAAH,RQLHEAAHQN,AAHQNNVGRM	UCEC
ANKFN1	c.840G>T	p.M280I	YRLYRRMKTGFEHARAPEMPTNVCL[p.M280I]IVTSSTSLTVSFQEPLSVNAAVVTRY	EMPTNVCLI,LIVTSSTSL,MPTNVCLIV,CLIVTSSTSL,EMPTNVCLIV,IVTSSTSLTV,MPTNVCLIVT,PEMPTNVCLI	LUSC
ANKLE1	c.1930_1933delTGTT	p.C644fs	TAAPISGFRRGVCVCVCVCVCVCVC[p.C644fs]VCVCVCREHPGRSPPG*	CVCREHPGR,REHPGRSPP,CVCVCVCVCR,REHPGRSPPG	TGCT
ANKLE1	c.1932_1933delTT	p.C644fs	TAAPISGFRRGVCVCVCVCVCVCVC[p.C644fs]VCVCVCVGSTQADLPQAERGLCYRWYCWRGSK*	RWYCWRGSK,CYRWYCWRG,QAERGLCYR,LCYRWYCWR,PQAERGLCY,AERGLCYRW,RGLCYRWYCW,GLCYRWYCWR,LPQAERGLCY,AERGLCYRWY	TGCT
ANKMY1	c.905A>T	p.N302I	KELDARIFLNEIPPFVEDGEPWFII[p.N302I]IETPLLVKIQKQTYKFRNKPAHTSWN	FIIIETPLL,IIIETPLLV,IIETPLLVK,IETPLLVKI,FIIIETPLLV,IIIETPLLVK,WFIIIETPLL,GEPWFIIIET	THCA
ANKRD11	c.1106A>G	p.K369R	KDEYEFDEDDEQDRVPPVDDKHLLK[p.K369R]RDYRKETKSNSFISIPKMEVKSYTKN	HLLKRDYRK,KHLLKRDYR,KHLLKRDYRK	TGCT
ANKRD11	c.6044A>C	p.Y2015S	SPKRFCPADPLHSAAPGPFSASEAP[p.Y2015S]SPAPPASPAPYALPVAEPGLEDVKDG	SASEAPSPA,EAPSPAPPA,SPAPPASPA,FSASEAPSPA,SPAPPASPAP,SEAPSPAPPA	TGCT

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ANKRD12	c.1879G>A	p.E627K	HKEKSKHQKDFHLEFGEKSNAKIKD[p.E627K]KDHSPTFENSDCTLKKMDKEGKTLKK	KSNAKIKDK,KDKDHSPTF,IKDKDHSPTF	BLCA
ANKRD12	c.2161G>C	p.E721Q	WKENFFKSDETEDLFLNMEHESLTL[p.E721Q]QKKSKLEKNIKDDKSTKEKHVSKERN	LQKKSKLEK,TLQKKSKLEK	CESC
ANKRD32	c.2996C>A	p.T999N	SEFILASKGLTHLNELLMACKSHKE[p.T999N]NTSVHTDWLLDLYAGNIKTLQKLPHI	KSHKENTSV,NTSVHTDWL,NTSVHTDWLL,KSHKENTSVH,KENTSVHTDW	BLCA
ANKRD36	c.1010C>G	p.P337R	TSDKDDSVSNTATEIKDEQKSGTVL[p.P337R]RAVEQCLNRSLYRPDAVAQPVTENEF	KSGTVLRAV,EQKSGTVLR,QKSGTVLRAV	CLL
ANKRD36	c.1133A>G	p.K378R	VAQPVTENEFSLESEIISKLYIPKR[p.K378R]RIISPRSIKDVLPPVEEAVDRCLYLL	RIISPRSIK,LYIPKRRII,KLYIPKRRI,KRRIISPRS,IPKRRIISP,RRIISPRSI,ISKLYIPKRR,KLYIPKRRII,KRRIISPRSI,IPKRRIISPR	KIRC
ANKRD36	c.3040G>T	p.D1014Y	SEKPPGLKATSDEKDSVLNIARGKK[p.D1014Y]YGEKTRTVSSQKPPTLKATSDEEDSV	RGKKYGEKTR,KKYGEKTRTV	CLL
ANKRD36	c.3431T>C	p.M1144T	KSRTVSSPKQPALKAICDKEDSVPN[p.M1144T]TATEKKDEQISGTVSCQKQPALKATS	SVPNTATEK,KEDSVPNTA,SVPNTATEKK,KEDSVPNTAT	CESC
ANKRD36C	c.1313A>G	p.H438R	LEKDTIKNQNLEKKYLKDFEIVKRK[p.H438R]REDLQKA	IVKRKREDL	PAAD,PRAD
ANKRD50	c.1909G>A	p.V637M	WTALRSAAWGGHTEVVSALLYAGVK[p.V637M]MDCADADSRTALRAAAWGGHEDIVLN	ALLYAGVKM,SALLYAGVKM	TGCT
ANKRD6	c.1435C>T	p.R479C	TQHQMRVLDKLMVERLSAERTECLN[p.R479C]CLQQHSDTEKHEGEKRQISLVDELKT	CLQQHSDTEK,AERTECLNCL	CRC
ANO2	c.1000C>T	p.R334C	PLHDGEYDSPEDDMNDRKLLYQEWA[p.R334C]CYGVFYKFQPIDLIRKYFGEKIGLYF	YQEWACYGV,WACYGVFYK,ACYGVFYKF,LLYQEWACY,EWACYGVFY,QEWACYGVF,LYQEWACYGV,YQEWACYGVF,WACYGVFYKF,KLLYQEWACY,EWACYGVFYK,QEWACYGVFY	GBM
ANO3	c.121G>T	p.A41S	GMNISKSEITKETSLKPSRRSLPCL[p.A41S]SQSYAYSKSLSQSTSLFQSTESESQA	LSQSYAYSK,SLPCLSQSY,SLPCLSQSYA,CLSQSYAYSK,RSLPCLSQSY,SQSYAYSKSL,LPCLSQSYAY	LUAD
ANO3	c.2868G>T	p.M956I	IAYLIPDVPKGLHDRIRREKYLVQE[p.M956I]IMYEAELEHLQQQRRKSGQPVHHEWP	LVQEIMYEA,KYLVQEIMY,IMYEAELEH,REKYLVQEI,EKYLVQEIM,QEIMYEAEL,YLVQEIMYEA,IMYEAELEHL,RREKYLVQEI,REKYLVQEIM,EKYLVQEIMY,VQEIMYEAEL	CESC
ANXA6	c.692G>A	p.R231Q	RSKQHLRLVFDEYLKTTGKPIEASI[p.R231Q]QGELSGDFEKLMLAVVKCIRSTPEYF	IQGELSGDF,IEASIQGEL	HNSC
AOC3	c.237_238insG	p.L79fs	QSQLFADLSREELTAVMRFLTQRLG[p.L79fs]ARAGGCSPGPALGQLCLLSGVAAASQGCSPGSLGQGEPPTCPGGTGHRLLWQATPAQRE*	GQLCLLSGV,CLLSGVAAA,RLLWQATPA,RFLTQRLGA,FLTQRLGAR,LWQATPAQR,SPGPALGQL,GPALGQLCL,CPGGTGHRL,TQRLGARAG,SQGCSPGSL,FLTQRLGARA,RFLTQRLGAR,LLWQATPAQR,GPALGQLCLL,CPGGTGHRLL,MRFLTQRLGA,GQLCLLSGVA,HRLLWQATPA	STAD
AOX1	c.1520C>T	p.A507V	GRHWNEQMLDIACRLILNEVSLLGS[p.A507V]VPGGKVEFKRTLIISFLFKFYLEVSQ	LLGSVPGGK,NEVSLLGSV,LLGSVPGGKV,SLLGSVPGGK,SVPGGKVEFK,GSVPGGKVEF	GBM
AP1G1	c.2168G>T	p.R723L	NDIAAGIPSITAYSKNGLKIEFTFE[p.R723L]LSNTNPSVTVITIQASNSTELDMTDF	ELSNTNPSV,LKIEFTFEL,FELSNTNPS,IEFTFELSN,GLKIEFTFEL,IEFTFELSNT,FELSNTNPSV	LUAD
AP1G2	c.727G>A	p.D243N	PQLVHILRTLVTMGYSTEHSISGVS[p.D243N]NPFLQVQILRLLRILGRNHEESSETM	GVSNPFLQV,NPFLQVQIL,SISGVSNPF,SISGVSNPFL,HSISGVSNPF,NPFLQVQILR,VSNPFLQVQI	HNSC
AP3S1	c.121_124delAAGA	p.K41fs	LSKFYQPYSEDTQQQIIRETFHLVS[p.K41fs]EMKMFVIS*	LVSEMKMFV,TFHLVSEMK,ETFHLVSEM,FHLVSEMKM,HLVSEMKMF,SEMKMFVIS,RETFHLVSE,HLVSEMKMFV,LVSEMKMFVI,ETFHLVSEMK,RETFHLVSEM,FHLVSEMKMF	PAAD
AP4B1	c.826C>T	p.R276W	VVMGATKLFLILAKMFPHVQTDVLV[p.R276W]WVKGPLLAACSSESRELCFVALCHVR	VQTDVLVWV,VLVWVKGPL,QTDVLVWVK,HVQTDVLVW,VLVWVKGPLL,HVQTDVLVWV,VQTDVLVWVK,DVLVWVKGPL	PRAD

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APBA1	c.1870G>A	p.E624K	LIAQSIGQAFSVAYQEFLRANGINP[p.E624K]KDLSQKEYSDLLNTQDMYNDDLIHFS	FLRANGINPK,GINPKDLSQK,NPKDLSQKEY	CRC
APBA1	c.2190G>T	p.K730N	QIMSINGTSLVGLPLSTCQSIIKGL[p.K730N]NNQSRVKLNIVRCPPVTTVLIRRPDL	GLNNQSRVK,KGLNNQSRVK,IIKGLNNQSR	CRC
APBB2	c.729_730insC	p.T243fs	EDGQVATVSSSPETKKDHPKTGAKT[p.T243fs]RLCTAPDPEPGTER*	GAKTRLCTA,KTRLCTAPD,KTRLCTAPDP,HPKTGAKTRL	LUAD
APC	c.2540delA	p.E847fs	PYLNTTVLPSSSSSRGSLDSSRSEK[p.E847fs]IEVWRENAELV*	SSRSEKIEV,EVWRENAEL,EVWRENAELV,SSRSEKIEVW,IEVWRENAEL	CRC
APC	c.4060delT	p.F1354fs	PRTKSSRLQGSSLSSESARHKAVEF[p.F1354fs]LQERNLPPKVVLRHPKVHLNTMFRRPHSCLADVLLSVHLIVLRVVRLPAPFRVNHAVEW*	CLADVLLSV,VLLSVHLIV,LLSVHLIVL,TMFRRPHSC,SVHLIVLRV,KVHLNTMFR,LSVHLIVLR,VVRLPAPFR,RVVRLPAPF,KVVLRHPKV,VLRHPKVHL,MFRRPHSCL,VLRVVRLPA,KAVEFLQER,NLPPKVVLR,HLIVLRVVR,DVLLSVHLI,HPKVHLNTM,RPHSCLADV,APFRVNHAV,ARHKAVEFL,RNLPPKVVL,FRVNHAVEW,LPAPFRVNH,VEFLQERNL,QERNLPPKV,ADVLLSVHL,TMFRRPHSCL,VLLSVHLIVL,SVHLIVLRVV,HLIVLRVVRL,FLQERNLPPK,KVHLNTMFRR,RVVRLPAPFR,SARHKAVEFL,RNLPPKVVLR,MFRRPHSCLA,VVRLPAPFRV,LLSVHLIVLR,DVLLSVHLIV,LSVHLIVLRV,HPKVHLNTMF,RPHSCLADVL,LPAPFRVNHA,NTMFRRPHSC,LQERNLPPKV,RHPKVHLNTM,HLNTMFRRPH,CLADVLLSVH,LRVVRLPAPF,ADVLLSVHLI	CRC
APOB	c.128C>T	p.A43V	LLLLLAGARAEEEMLENVSLVCPKD[p.A43V]VTRFKHLRKYTYNYEAESSSGVPGTA	VTRFKHLRK,LVCPKDVTR,DVTRFKHLR,VTRFKHLRKY,SLVCPKDVTR,DVTRFKHLRK,LVCPKDVTRF	CRC
APOB	c.2917C>A	p.L973M	TKTEVIPPLIENRQSWSVCKQVFPG[p.L973M]MNYCTSGAYSNASSTDSASYYPLTGD	GMNYCTSGA,KQVFPGMNY,MNYCTSGAY,GMNYCTSGAY,SVCKQVFPGM,CKQVFPGMNY,KQVFPGMNYC	LUAD
APOB	c.9306C>A	p.F3102L	FLSPSAQQASWQVSARFNQYKYNQN[p.F3102L]LSAGNNENIMEAHVGINGEANLDFLN	NQYKYNQNL,YKYNQNLSA,NLSAGNNENI,QYKYNQNLSA,FNQYKYNQNL,NQYKYNQNLS,YKYNQNLSAG,LSAGNNENIM	UCEC
APOB	c.9406C>T	p.R3136C	MEAHVGINGEANLDFLNIPLTIPEM[p.R3136C]CLPYTIITTPPLKDFSLWEKTGLKEF	TIPEMCLPY,PEMCLPYTI,LTIPEMCLPY,PEMCLPYTII,IPLTIPEMCL,IPEMCLPYTI	CRC
APOBR	c.2519G>T	p.R840L	SQVEAFESREGGPWGGRVEAEESAG[p.R840L]VEDSCGLDPAGSQTARAEGMGAMVEA	VEAEESAGV,VEDSCGLDPA	LUAD
APOD	c.344C>T	p.S115L	IEGEATPVNLTEPAKLEVKFSWFMP[p.S115L]LAPYWILATDYENYALVYSCTCIIQL	FMPLAPYWI,WFMPLAPYW,KFSWFMPLA,SWFMPLAPY,MPLAPYWIL,VKFSWFMPL,FSWFMPLAPY,FMPLAPYWIL,SWFMPLAPYW,WFMPLAPYWI,EVKFSWFMPL,VKFSWFMPLA,MPLAPYWILA	CESC
APOE	c.388T>C	p.C130R	EETRARLSKELQAAQARLGADMEDV[p.C130R]RGRLVQYRGEVQAMLGQSTEELRVRL	RGRLVQYRG,MEDVRGRLV,DVRGRLVQYR	ACC
APOOL	c.412A>C	p.I138L	PKMGVITVSGLAGLVSARKGSKFKK[p.I138L]LTYPLGLATLGATVCYPVQSVIIAKV	KLTYPLGLA,KFKKLTYPL,GSKFKKLTY,KKLTYPLGL,LTYPLGLATL,KFKKLTYPLG,KGSKFKKLTY,SKFKKLTYPL,FKKLTYPLGL	CLL
APPL1	c.2002C>T	p.R668W	ERVKEKQQKELNKQKQIEKDLEEQS[p.R668W]WLIAASSRPNQASSEGQFVVLSSSQS	SWLIAASSR,LEEQSWLIA,EEQSWLIAA,QSWLIAASSR,IEKDLEEQSW,LEEQSWLIAA,EEQSWLIAAS,KDLEEQSWLI	CRC
AQP10	c.782A>T	p.Q261L	SAGNGWWWVPVVAPLVGATVGTATY[p.Q261L]LLLVALHHPEGPEPAQDLVSAQHKAS	GTATYLLLV,ATYLLLVAL,ATVGTATYL,TVGTATYLL,GTATYLLLVA,ATYLLLVALH,ATVGTATYLL	LUAD
AQP2	c.203A>C	p.N68T	QIAMAFGLGIGTLVQALGHISGAHI[p.N68T]TPAVTVACLVGCHVSVLRAAFYVAAQ	HITPAVTVA,SGAHITPAV,TPAVTVACL,AHITPAVTV,HISGAHITPA,ITPAVTVACL,TPAVTVACLV,AHITPAVTVA	KIRP
AQPEP	c.925G>A	p.A309T	KEDVNGSKWTVTTFSTTPHMPTYLV[p.A309T]TFVICDYDHVNRTERGKEIRIWARKD	HMPTYLVTF,PTYLVTFVI,TYLVTFVIC,LVTFVICDY,MPTYLVTFV,HMPTYLVTFV,PHMPTYLVTF,YLVTFVICDY,MPTYLVTFVI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ARAP3	c.3677G>T	p.R1226L	ASLLLKKVPLAQAGCLFTGIRRESP[p.R1226L]LVGLLRCREEPPRLLGSRFQERFFLL	GIRRESPLV,TGIRRESPL,RRESPLVGL,RESPLVGLL,FTGIRRESPL,IRRESPLVGL	LUAD
ARF4	c.446G>A	p.R149H	FANKQDLPNAMAISEMTDKLGLQSL[p.R149H]HNRTWYVQATCATQGTGLYEGLDWLS	SLHNRTWYV,HNRTWYVQA,QSLHNRTWY,LQSLHNRTW,QSLHNRTWYV,LQSLHNRTWY,KLGLQSLHNR,GLQSLHNRTW	CRC
ARFGAP2	c.113G>A	p.S38N	LFKRLRAVPTNKACFDCGAKNPSWA[p.S38N]NITYGVFLCIDCSGVHRSLGVHLSFI	SWANITYGV,NPSWANITY,WANITYGVF,AKNPSWANI,ANITYGVFL,SWANITYGVF,GAKNPSWANI,KNPSWANITY,NITYGVFLCI,WANITYGVFL	PRAD
ARFGAP3	c.896delA	p.N299fs	SLRLAYKDLEIQMKKDEKMNISGKK[p.N299fs]MLTQTDSAWDLEIAEVLFHIQ*	KMLTQTDSA,EIAEVLFHI,KMNISGKKM,DSAWDLEIA,MLTQTDSAW,TQTDSAWDL,LEIAEVLFH,WDLEIAEVL,QTDSAWDLEI,SAWDLEIAEV,KMNISGKKML,EKMNISGKKM,KKMLTQTDSA,KMLTQTDSAW,LEIAEVLFHI,WDLEIAEVLF	PRAD
ARFGEF1	c.4654_4655insC	p.P1552fs	LDIFKTTIPHALLTWRPNSGETAPP[p.P1552fs]TSISCK*	ETAPPTSIS,GETAPPTSI,ETAPPTSISC	STAD
ARFGEF1	c.4894G>A	p.D1632N	KFPEQKLFAALLIKCVVQLELIQTI[p.D1632N]NNIVFFPATSKKEDAENLAAAQRDAV	ELIQTINNI,LIQTINNIV,QTINNIVFF,IQTINNIVF,TINNIVFFPA,ELIQTINNIV,IQTINNIVFF,LIQTINNIVF,LELIQTINNI	CRC
ARFIP2	c.257G>T	p.R86L	GLIPTGSGRHPSHSTTPSGPGDEVA[p.R86L]LGIAGEKFDIVKKWGINTYKCTKQLL	VALGIAGEK,ALGIAGEKF,DEVALGIAG,VALGIAGEKF,DEVALGIAGE	LUAD
ARHGAP24	c.103A>G	p.T35A	NPQQGQGRQNAIKCGWLRKQGGFVK[p.T35A]AWHTRWFVLKGDQLYYFKDEDETKPL	KAWHTRWFV,AWHTRWFVL,GFVKAWHTR,RKQGGFVKA,KQGGFVKAW,FVKAWHTRW,VKAWHTRWF,AWHTRWFVLK,GFVKAWHTRW,KAWHTRWFVL,FVKAWHTRWF,RKQGGFVKAW	TGCT
ARHGAP32	c.3757G>A	p.E1253K	LEFADKSPTPPNLPSDKIYPPSGSP[p.E1253K]KENTSTATMTYMTTTPATAQMSTKEA	SPKENTSTA,KENTSTATM,KIYPPSGSPK,SPKENTSTAT,KENTSTATMT	CRC
ARHGAP36	c.382C>T	p.R128C	GQQRAVSHKTFGISLEEVLVNEFTR[p.R128C]CKHLELTATMQVEEATGQAAGRRRGN	LVNEFTRCK,FTRCKHLEL,CKHLELTAT,NEFTRCKHL,VLVNEFTRCK,CKHLELTATM	CRC
ARHGAP36	c.440C>T	p.A147V	VNEFTRRKHLELTATMQVEEATGQA[p.A147V]VGRRRGNVVRRVFGRIRRFFSRRRNE	VGRRRGNVV,VEEATGQAV,VGRRRGNVVR	CRC
ARHGAP36	c.47C>A	p.P16H	MGGCIPFLKAARALC[p.P16H]HRIMPPLLLLSAFIFLVSVLGGAPGH	KAARALCHR,AARALCHRI,RALCHRIMP,LKAARALCH,ARALCHRIM,HRIMPPLLL,ALCHRIMPPL,KAARALCHRI,AARALCHRIM,RALCHRIMPP,HRIMPPLLLL	LUAD
ARHGAP5	c.2071A>T	p.M691L	ESLSFIGEFIGKIRTEASQIRKDKY[p.M691L]LANLPFTLILANQRDSISKNLPILRH	YLANLPFTL,KYLANLPFT,QIRKDKYLA,LANLPFTLI,DKYLANLPF,SQIRKDKYL,RKDKYLANL,YLANLPFTLI,KYLANLPFTL,KDKYLANLPF,LANLPFTLIL	GBM
ARHGAP5	c.2670delT	p.D890fs	RAFLSEVQDTIPVQLVAVTDSQADF[p.D890fs]LKMRLSKS*	VTDSQADFL,FLKMRLSKS,DFLKMRLSK,VTDSQADFLK,SQADFLKMRL,DSQADFLKMR	CRC,STAD
ARHGAP9	c.409C>T	p.R137C	QQVSLAEGDRFLLLRKTNSDWWLAR[p.R137C]CLEAPSTSRPIFVPAAYMIEESIPSQ	SDWWLARCL,WLARCLEAPS	BRCA
ARHGEF17	c.1844delC	p.A615fs	VQEARQVFEKIQRMGAQQDDGSDAP[p.A615fs]LEALTGQGM*	LEALTGQGM,QQDDGSDAPL	STAD
ARHGEF5	c.1460A>G	p.E487G	PISLLGSFLTEESPDKEIDQNSQQE[p.E487G]GSRLRKGTVSSQGTEVVFASASVTPP	GSRLRKGTV,SQQEGSRLRK	KIRC
ARHGEF5	c.4535delC	p.S1512fs	EKLRWISALAMPREELDLLECYNSP[p.S1512fs]RYSAFEPTSPERMMNWHWRKPTW*	RMMNWHWRK,NWHWRKPTW,CYNSPRYSA,LLECYNSPR,YNSPRYSAF,LECYNSPRY,LLECYNSPRY,MMNWHWRKPT,SAFEPTSPER,CYNSPRYSAF,RMMNWHWRKP,DLLECYNSPR,SPRYSAFEPT,MNWHWRKPTW,FEPTSPERMM,SPERMMNWHW	STAD
ARID1A	c.1841C>T	p.S614L	QTAYSQQRFPPPQELSQDSFGSQAS[p.S614L]LAPSMTSSKGGQEDMNLSLQSRPSSL	SLAPSMTSS,LAPSMTSSK,DSFGSQASL,SQASLAPSM,SLAPSMTSSK,DSFGSQASLA,GSQASLAPSM,SQASLAPSMT	BLCA
ARID1A	c.3211delA	p.K1071fs	KPLDLYRLYVSVKEIGGLTQVNKNK[p.K1071fs]NGGNLQPTSMWAHQAVLPAP*	SMWAHQAVL,NLQPTSMWA,TSMWAHQAV,WAHQAVLPA,LQPTSMWAH,TSMWAHQAVL,SMWAHQAVLP,MWAHQAVLPA	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ARID1A	c.3972delC	p.Y1324fs	STGAPQPNLMPSNPDSGMYSPSRYP[p.Y1324fs]RSSSSSSSNDMIPMAISSPPKAPLLAAPSPASRLQCINSNSRITSGQWMAHMALLPSGTKGRCTACHTALGRGSLSSSSCPQPSPLPASNKLPSLPLSKMYTTSMAMPILPLPQLLLSADQQAAPRTNFHSSLAETVSLHPLAPMPSKTCHHK*	GQWMAHMAL,KMYTTSMAM,YTTSMAMPI,SMAMPILPL,HMALLPSGT,LLSADQQAA,MALLPSGTK,KLPSLPLSK,PMAISSPPK,QWMAHMALL,MYSPSRYPR,KGRCTACHT,LSKMYTTSM,RTNFHSSLA,HPLAPMPSK,LAAPSPASR,TACHTALGR,HTALGRGSL,TTSMAMPIL,ETVSLHPLA,YPRSSSSSS,IPMAISSPP,SPASRLQCI,LPASNKLPS,LPSLPLSKM,MPILPLPQL,APRTNFHSS,QQAAPRTNF,SSSNDMIPM,VSLHPLAPM,SSSSSSNDM,ISSPPKAPL,SRITSGQWM,MAHMALLPS,AHMALLPSG,RCTACHTAL,SNKLPSLPL,SKMYTTSMA,FHSSLAETV,SSLAETVSL,AETVSLHPL,LPLPQLLLS,GQWMAHMALL,AMPILPLPQL,LLLSADQQAA,WMAHMALLPS,KLPSLPLSKM,GMYSPSRYPR,HMALLPSGTK,CTACHTALGR,MYTTSMAMPI,IPMAISSPPK,RLQCINSNSR,KGRCTACHTA,ASNKLPSLPL,LSKMYTTSMA,TSMAMPILPL,RTNFHSSLAE,ITSGQWMAHM,LLAAPSPASR,LSADQQAAPR,SSNDMIPMAI,YTTSMAMPIL,TVSLHPLAPM,YPRSSSSSSS,SPPKAPLLAA,APLLAAPSPA,CPQPSPSLPA,SPSLPASNKL,LPASNKLPSL,MPILPLPQLL,APRTNFHSSL,SKMYTTSMAM,LPSLPLSKMY,SSSSSSSNDM,SSSSNDMIPM,ISSPPKAPLL,LAAPSPASRL,LQCINSNSRI,SGQWMAHMAL,GRCTACHTAL,SSCPQPSPSL,KMYTTSMAMP,DQQAAPRTNF,QQAAPRTNFH,HSSLAETVSL,LAETVSLHPL,LPLPQLLLSA,AETVSLHPLA	STAD
ARID1A	c.5542delG	p.G1848fs	VDCSDKLGRVQEFDSGLLHWRIGGG[p.G1848fs]TPLSISRPTSRARQSCCLPGLTHPAHQPLGSM*	RQSCCLPGL,CLPGLTHPA,LSISRPTSR,ISRPTSRAR,RARQSCCLP,LTHPAHQPL,RPTSRARQS,WRIGGGTPL,LPGLTHPAH,GLTHPAHQPL,LLHWRIGGGT,SISRPTSRAR,HWRIGGGTPL,TSRARQSCCL,RARQSCCLPG,RPTSRARQSC,HPAHQPLGSM,RIGGGTPLSI,ARQSCCLPGL,RQSCCLPGLT	STAD
ARID1A	c.6415delC	p.P2139fs	RLVLETLSKLSIQDNNVDLILATPP[p.P2139fs]SAAWRSCIALWCASSVTERTRCAGRWLWYCWPTWLRGTAWQLVPLQCRRAVSATSWAS*	IALWCASSV,ALWCASSVT,WLRGTAWQL,GTAWQLVPL,ILATPPSAA,AWRSCIALW,RWLWYCWPT,WLWYCWPTW,LWYCWPTWL,RTRCAGRWL,RAVSATSWA,RCAGRWLWY,WYCWPTWLR,QLVPLQCRR,WPTWLRGTA,VPLQCRRAV,SAAWRSCIA,LATPPSAAW,AAWRSCIAL,LQCRRAVSA,RRAVSATSW,CIALWCASSV,WLWYCWPTWL,WLRGTAWQLV,CAGRWLWYCW,RWLWYCWPTW,TWLRGTAWQL,RTRCAGRWLW,LATPPSAAWR,LWCASSVTER,VTERTRCAGR,LWYCWPTWLR,SAAWRSCIAL,WPTWLRGTAW,ILATPPSAAW,AAWRSCIALW,TERTRCAGRW,RGTAWQLVPL,LQCRRAVSAT,CRRAVSATSW,RAVSATSWAS	STAD
ARID3A	c.1649_1650delGA	p.G550fs	NGIMYTGVLFAQPPAPTPTSAPNKG[p.G550fs]RRRRRQQQQRRRPGRKHRNQRRPGWASGAVHTLHIYLK*	QQRRRPGRK,AVHTLHIYL,GAVHTLHIY,WASGAVHTL,RPGWASGAV,NQRRPGWAS,AVHTLHIYLK,GWASGAVHTL,QQQRRRPGRK,SGAVHTLHIY,RQQQQRRRPG	CLL
ARID4A	c.3462T>A	p.D1154E	LNVSKPQKLARSPARISPHIKDGEK[p.D1154E]EKHREKHPNSSPRTYKWSFQLNELDN	HIKDGEKEK	CLL
ARL13B	c.1073G>T	p.R358L	ETDRPSLESANGKKKTKKLRMKRNH[p.R358L]LVEPLNIDDCAPESPTPPPPPPPVGW	KLRMKRNHL,RMKRNHLVE,LRMKRNHLV,KRNHLVEPL,KLRMKRNHLV,RMKRNHLVEP,MKRNHLVEPL,KKLRMKRNHL	LUAD
ARL16	c.16G>A	p.G6R	MRVAG[p.G6R]RRALSRGAELRVPGGAKHGMCLLLGA	RVAGRRALS,MRVAGRRAL,RVAGRRALSR,AGRRALSRGA,RRALSRGAEL	SKCM
ARL6IP1	c.223A>T	p.M75L	GVVSLVFLIIYYLDPSVLSGVSCFV[p.M75L]LFLCLADYLVPILAPRIFGSNKWTTE	GVSCFVLFL,SGVSCFVLF,VLFLCLADY,LSGVSCFVL,VLSGVSCFVL,VLFLCLADYL,LSGVSCFVLF,FVLFLCLADY	MM
ARMC3	c.1540G>A	p.A514T	LRSKNDEVRKHASWAVMVCAGDELT[p.A514T]TNELCRLGALDILEEVNVSGTRKNKF	TTNELCRLGA	TGCT
ARMC4	c.64G>A	p.E22K	MGVALRKLTQWTAAGHGTGIL[p.E22K]KITPLNEAILKEIIVFVESFIYKHPQ	KITPLNEAI,AGHGTGILK,TGILKITPL,LKITPLNEA,ILKITPLNEA,AAGHGTGILK,LKITPLNEAI	SKCM
ARNTL	c.1184C>T	p.T395M	GTSCYEYFHQDDIGHLAECHRQVLQ[p.T395M]MREKITTNCYKFKIKDGSFITLRSRW	RQVLQMREK,LQMREKITT,AECHRQVLQM,RQVLQMREKI,LQMREKITTN,MREKITTNCY	CRC
ARPC1A	c.636C>A	p.F212L	SKMPFGQLMSEFGGSGTGGWVHGVS[p.F212L]LSASGSRLAWVSHDSTVSVADASKSV	WVHGVSLSA,SLSASGSRL,GGWVHGVSL,SLSASGSRLA,GVSLSASGSR,VSLSASGSRL,LSASGSRLAW	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ARPP21	c.1013G>A	p.R338H	SSSENELKWSDHQRAWSSTDSDSSN[p.R338H]HNLKPAMTKTASFGGITVLTRGDSTS	HNLKPAMTK,SNHNLKPAM,SSNHNLKPAM	CRC
ARPP21	c.388delA	p.I130fs	HNVEKQDIATYYCALWEVHSKLGKK[p.I130fs]SRYLVPEQSLSLQINNLMQMFPPSPLFFFLQLLKQSSRRLEHTFVFLRNFSLMLLRYIGKKRRATRFWDPRRGTP*	SLSLQINNL,MQMFPPSPL,RLEHTFVFL,FVFLRNFSL,FLRNFSLML,LQINNLMQM,LFFFLQLLK,LMLLRYIGK,MLLRYIGKK,RNFSLMLLR,RATRFWDPR,RYLVPEQSL,QMFPPSPLF,MFPPSPLFF,RRLEHTFVF,VFLRNFSLM,HSKLGKKSR,KLGKKSRYL,LGKKSRYLV,KSRYLVPEQ,KQSSRRLEH,SSRRLEHTF,RYIGKKRRA,IGKKRRATR,ATRFWDPRR,NFSLMLLRY,LLRYIGKKR,SPLFFFLQL,LLKQSSRRL,YIGKKRRAT,QINNLMQMF,HTFVFLRNF,SKLGKKSRY,LSLQINNLM,LRNFSLMLL,GKKRRATRF,KKRRATRFW,FPPSPLFFF,PPSPLFFFL,KLGKKSRYLV,YLVPEQSLSL,LMQMFPPSPL,FVFLRNFSLM,FLRNFSLMLL,SLSLQINNLM,PLFFFLQLLK,RLEHTFVFLR,SLMLLRYIGK,LMLLRYIGKK,LQINNLMQMF,MQMFPPSPLF,QMFPPSPLFF,MFPPSPLFFF,RRLEHTFVFL,TFVFLRNFSL,VFLRNFSLML,KSRYLVPEQS,SSRRLEHTFV,HTFVFLRNFS,RATRFWDPRR,ATRFWDPRRG,HSKLGKKSRY,RNFSLMLLRY,FLQLLKQSSR,MLLRYIGKKR,LLRYIGKKRR,YIGKKRRATR,FPPSPLFFFL,SPLFFFLQLL,SRYLVPEQSL,SLQINNLMQM,LKQSSRRLEH,KQSSRRLEHT,QSSRRLEHTF,SRRLEHTFVF,VPEQSLSLQI	STAD
ARRB2	c.295A>C	p.T99P	LSFRKDLFIATYQAFPPVPNPPRPP[p.T99P]PRLQDRLLRKLGQHAHPFFFTVRMPL	RPPPRLQDRL	TGCT
ARRDC4	c.235A>G	p.T79A	ALRLEAQGRATAAWGPSTCPRASAS[p.T79A]AAALAVFSEVEYLNVRLSLREPPAGE	RASASAAAL,ASASAAALA,SASAAALAV,CPRASASAA,ASAAALAVF,AAALAVFSEV,STCPRASASA,RASASAAALA,ASASAAALAV,CPRASASAAA,SASAAALAVF	ACC
ARSD	c.701C>G	p.A234G	LGILTLAAGQTCGFFSVSARAVTGM[p.A234G]GGVGCLFFISWYSSFGFVRRWNCILM	MGGVGCLFF,SARAVTGMG,GMGGVGCLF,GMGGVGCLFF,SARAVTGMGG,TGMGGVGCLF	KIRC
ARSD	c.701_709delCCGGCGTGG	p.AGV234del	LGILTLAAGQTCGFFSVSARAVTGM[p.AGV234del]GCLFFISWYSSFGFVRRWNCILMRNHDVTEQPMV	TGMGCLFFI,VTGMGCLFF,SARAVTGMG,AVTGMGCLF,GMGCLFFISW,MGCLFFISWY,RAVTGMGCLF,AVTGMGCLFF	KIRC
ARSG	c.391G>A	p.V131I	FAVTSVGGLPLNETTLAEVLQQAGY[p.V131I]ITGIIGKWHLGHHGSYHPNFRGFDYY	QQAGYITGI,EVLQQAGYI,LQQAGYITG,LQQAGYITGI,QQAGYITGII,AGYITGIIGK,GYITGIIGKW,AEVLQQAGYI	CRC
ART1	c.729delC	p.I243fs	IWTCLGAPIKGYSFFPGEEEVLIPP[p.I243fs]LRPSK*	LIPPLRPSK,EEEVLIPPL,VLIPPLRPSK,GEEEVLIPPL	STAD
ASB16	c.745A>G	p.T249A	QHVALYLEHGADVGLRTSQGETALN[p.T249A]AACAGAEGPGSCRRHQAAARRLLEAG	ALNAACAGA,ETALNAACA,SQGETALNA,GETALNAAC,SQGETALNAA,GETALNAACA	ACC
ASCC1	c.619C>T	p.H207Y	QEEVLAKCSMDHGVDSSIFQNPKKL[p.H207Y]YLTIGMLVLLSEEEIQQTCEMLQQCK	YLTIGMLVL,FQNPKKLYL,KLYLTIGML,LYLTIGMLV,IFQNPKKLY,NPKKLYLTI,KKLYLTIGM,KLYLTIGMLV,YLTIGMLVLL,IFQNPKKLYL,LYLTIGMLVL,SIFQNPKKLY,KKLYLTIGML	CESC
ASCC2	c.1094G>T	p.R365L	CDNIQGFIEEFLQIFSSLLQEKRFL[p.R365L]LDYDALFPVAEDISLLQQASSVLDET	LLQEKRFLL,FLLDYDALF,RFLLDYDAL,QEKRFLLDY,LDYDALFPV,SLLQEKRFLL,FLLDYDALFP,LLDYDALFPV,RFLLDYDALF,LQEKRFLLDY,KRFLLDYDAL,LDYDALFPVA	LUAD
ASCC3	c.3590G>A	p.R1197Q	VKQCVHQIPSVMMEASIQPITRTVL[p.R1197Q]QVTLSIYADFTWNDQVHGTVGEPWWI	TVLQVTLSI,VLQVTLSIY,LQVTLSIYA,VLQVTLSIYA,ITRTVLQVTL,RTVLQVTLSI,TVLQVTLSIY,QPITRTVLQV	CRC
ASCC3	c.407G>A	p.R136Q	ETKAIKQMFGPFPSSSATAACNATN[p.R136Q]QIISHFSQDDLTALVQMTEKEHGDRV	ATNQIISHF,TAACNATNQI,NATNQIISHF	UCEC
ASCL4	c.105delC	p.D35fs	ALPYSLRTAPLGVPGTLPGLPRRDP[p.D35fs]SGSPCVWTPRAGSGRAAAAHGDGSTCPCRWTAPSSPPSSASATSASGSGCAA*	RAGSGRAAA,STCPCRWTA,WTAPSSPPS,TPRAGSGRA,APSSPPSSA,DPSGSPCVW,RAGSGRAAAA,RWTAPSSPPS,SGSPCVWTPR,TPRAGSGRAA	STAD
ASIC2	c.137G>T	p.R46L	RMAREEPAPAALAAAGQPGGGRGGE[p.R46L]LALQGPGVARRGRPSLSRAKLHGLRH	ELALQGPGV,GELALQGPG,QPGGGRGGEL,GELALQGPGV	KIRP

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ASPDH	c.797A>G	p.Q266R	AVHTRRENPAEPGAVTGSATVTAFW[p.Q266R]RSLLACCQLPSRPGIHLC*	SATVTAFWR,TAFWRSLLA,RSLLACCQL,TVTAFWRSL,VTAFWRSLL,GSATVTAFWR,ATVTAFWRSL,TVTAFWRSLL,VTAFWRSLLA,WRSLLACCQL	ACC
ASPM	c.719C>T	p.S240F	EENKIPISPISPAFNECHGATCLPL[p.S240F]FVRRSTTYSSLHASENRELLNVHSAN	ATCLPLFVR,HGATCLPLF,FVRRSTTYS,LFVRRSTTY,TCLPLFVRR,LPLFVRRST,ATCLPLFVRR,LPLFVRRSTT,PLFVRRSTTY,CHGATCLPLF	LUAD
ASPN	c.201delT	p.F67fs	DDDDDDDDDEDNSLFPTREPRSHFF[p.F67fs]HLICFQCVHLDVSAIHELYIAQI*	DVSAIHELY,SHFFHLICF,CFQCVHLDV,RSHFFHLIC,EPRSHFFHL,HLICFQCVH,LDVSAIHEL,HLICFQCVHL,HLDVSAIHEL,AIHELYIAQI,RSHFFHLICF,DVSAIHELYI,EPRSHFFHLI,REPRSHFFHL,FQCVHLDVSA,LDVSAIHELY	STAD
ASTN2	c.661_663delCTG	p.L221del	EIVEEQMHILHISVMGGLIALLLLL[p.L221del]VFTVALYAQRRWQKRRRIPQKSASTEAT	LIALLLLV,ALLLLLVFT,IALLLLLVF,GLIALLLLV,ALLLLLVFTV,LIALLLLVF	PRAD
ASXL2	c.3242C>T	p.S1081L	EGLSKATQDQILQTLIQRVRRQNLL[p.S1081L]LVVPPSQFNFAHSGFQLEDISTSQRF	RVRRQNLLL,LLVVPPSQF,RRQNLLLVV,RQNLLLVVP,RVRRQNLLLV,LLLVVPPSQF,LVVPPSQFNF,RQNLLLVVPP	LUSC
ASXL3	c.2618delA	p.E873fs	SIPELASTEMIKVKNHSVLQRTEKK[p.E873fs]CYLHHWNYLSFLKGQIIREMSFHLLNYRTSNISHQWIRLHFQKALEIKHISKGVHRVG*	EMSFHLLNY,YLHHWNYLS,IIREMSFHL,YLSFLKGQI,LLNYRTSNI,HISKGVHRV,MSFHLLNYR,ALEIKHISK,HWNYLSFLK,QWIRLHFQK,CYLHHWNYL,LHHWNYLSF,SHQWIRLHF,WIRLHFQKA,KCYLHHWNY,RTSNISHQW,SFLKGQIIR,SNISHQWIR,EIKHISKGV,GQIIREMSF,LQRTEKKCY,HHWNYLSFL,LSFLKGQII,LKGQIIREM,REMSFHLLN,IRLHFQKAL,LHFQKALEI,FQKALEIKH,YLHHWNYLSF,HLLNYRTSN,YLSFLKGQI,FLKGQIIREM,QIIREMSFHL,IIREMSFHLL,RLHFQKALEI,HQWIRLHFQK,KALEIKHISK,HHWNYLSFLK,LSFLKGQIIR,CYLHHWNYLS,NYLSFLKGQI,ISHQWIRLHF,KCYLHHWNYL,RTSNISHQWI,KKCYLHHWNY,REMSFHLLNY,EMSFHLLNYR,TSNISHQWIR,MSFHLLNYRT,WIRLHFQKAL,LQRTEKKCYL,LHHWNYLSFL,KGQIIREMSF,LNYRTSNISH,YRTSNISHQW,FQKALEIKHI,LEIKHISKGV,KHISKGVHRV,TEKKCYLHHW	STAD
ASXL3	c.4409C>A	p.P1470Q	NRADNSGKPQQPPGGFAPAAINRSI[p.P1470Q]QCKVIVDHSTTLTSSLSLTVSVESSE	AINRSIQCK,RSIQCKVIV,AINRSIQCKV,AAINRSIQCK	LUAD
ATAD5	c.913A>G	p.I305V	EIPDSTMSICVPSETVDEIVKSGYI[p.I305V]GESENSEISQQVRFKTVTVLAQVHPI	YIGESENSEI	TGCT
ATM	c.2399C>T	p.S800F	SLRNMMQLCTRCLSNCTKKSPNKIA[p.S800F]FGFFLRLLTSKLMNDIADICKSLASF	KIAFGFFLR,AFGFFLRLL,SPNKIAFGF,KKSPNKIAF,NKIAFGFFL,IAFGFFLRL,KIAFGFFLRL,KSPNKIAFGF,NKIAFGFFLR,SPNKIAFGFF,TKKSPNKIAF,IAFGFFLRLL	CESC
ATP10B	c.3910C>A	p.L1304I	CNSPTNPYWVMEGQLSNPTFYLVCF[p.L1304I]ITPVVALLPRYFFLSLQGTCGKSLIS	YLVCFITPV,LVCFITPVV,FITPVVALL,CFITPVVAL,YLVCFITPVV,FYLVCFITPV,CFITPVVALL,ITPVVALLPR,NPTFYLVCFI	UCEC
ATP10D	c.932G>A	p.R311H	AVVGIVVYAGHETKAMLNNSGPRYK[p.R311H]HSKLERRANTDVLWCVMLLVIMCLTG	SGPRYKHSK,RYKHSKLER,GPRYKHSKL,NSGPRYKHSK	CRC
ATP12A	c.2572C>T	p.R858C	LGTDIIPSIALAYEKAESDIMNRKP[p.R858C]CHKNKDRLVNQPLAVYSYLHIGLMQA	IMNRKPCHK,MNRKPCHKNK,DIMNRKPCHK	BLCA
ATP2A1	c.2110G>T	p.G704C	VEPSHKSKIVEYLQSYDEITAMTGD[p.G704C]CVNDAPALKKAEIGIAMGSGTAVAKT	CVNDAPALK,ITAMTGDCV,AMTGDCVNDA,CVNDAPALKK,EITAMTGDCV	KIRC
ATP2A1	c.2457_2458insC	p.R819fs	LVTDGLPATALGFNPPDLDIMDRPP[p.R819fs]PEPQGAPHQWLALLPLHGNRGLCGCSHRGSSCLVVPVR*	HQWLALLPL,GSSCLVVPV,RGLCGCSHR,ALLPLHGNR,SSCLVVPVR,APHQWLALL,LPLHGNRGL,CSHRGSSCL,EPQGAPHQW,LLPLHGNRGL,GSSCLVVPVR,CSHRGSSCLV,LALLPLHGNR,HQWLALLPLH,SHRGSSCLVV,RGSSCLVVPV	STAD
ATP2B4	c.548G>A	p.R183H	SVIIVVLVTAFNDWSKEKQFRGLQC[p.R183H]HIEQEQKFSIRNGQLIQLPVAEIVV	KQFRGLQCH,CHIEQEQKF,KQFRGLQCHI	CLL
ATP2C1	c.2170G>A	p.E724K	GTDVCKEAADMILVDDDFQTIMSAI[p.E724K]KEGKGIYNNIKNFVRFQLSTSIAALT	IMSAIKEGK,AIKEGKGIY,TIMSAIKEGK,SAIKEGKGIY,DFQTIMSAIK,KEGKGIYNNI	UCEC

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ATP6AP2	c.355G>C	p.E119Q	ISYPLENAVPFSLDSVANSIHSLFS[p.E119Q]QETPVVLQLAPSEERVYMVGKANSVF	SLFSQETPV,FSQETPVVL,QETPVVLQL,SLFSQETPVV,HSLFSQETPV,LFSQETPVVL,SQETPVVLQL,QETPVVLQLA	HNSC
ATP6V0A4	c.572G>A	p.R191Q	MTGKLGFIAGVINRERMASFERLLW[p.R191Q]QICRGNVYLKFSEMDAPLEDPVTKEE	SFERLLWQI,WQICRGNVY,FERLLWQIC,LLWQICRGNV,WQICRGNVYL,QICRGNVYLK,LWQICRGNVY,ASFERLLWQI	CRC
ATP6V1A	c.710T>C	p.L237P	RQVRPVTEKLPANHPLLTGQRVLDA[p.L237P]PFPCVQGGTTAIPGAFGCGKTVISQS	VLDAPFPCV,GQRVLDAPF,RVLDAPFPCV,TGQRVLDAPF	THCA
ATP6V1B1	c.1149delC	p.Y383fs	DLTGFITEGQIYVDRQLHNRQIYPP[p.Y383fs]STCSLPCRG*	IYPPSTCSL,RQIYPPSTC,QIYPPSTCSL,RQIYPPSTCS	STAD
ATP6V1C2	c.934_935insAG	p.R312fs	STFPDHKVKVTPLGNPDRPAAGQTD[p.R312fs]KERERVRARVRAPCCAGSR*	KERERVRAR,RERVRARVR,RVRARVRAP,RARVRAPCC,RVRAPCCAG,RAPCCAGSR,RVRARVRAPC,RARVRAPCCA,RVRAPCCAGS,KERERVRARV,RERVRARVRA	STAD
ATP7A	c.2968_2969insA	p.Q990fs	IVETYFPGYNRSISRTETIIRFAFQ[p.Q990fs]SLYHSSVYCMSLFTGTGHSNCCDGGYRSRCSKWHTNKRWRAIGDGS*	HSNCCDGGY,FQSLYHSSV,SLYHSSVYC,LYHSSVYCM,IIRFAFQSL,RFAFQSLYH,GGYRSRCSK,RSRCSKWHT,RCSKWHTNK,CSKWHTNKR,KWHTNKRWR,HTNKRWRAI,RWRAIGDGS,IRFAFQSLY,QSLYHSSVY,SSVYCMSLF,FAFQSLYHS,HSSVYCMSL,MSLFTGTGH,SKWHTNKRW,SLYHSSVYCM,TIIRFAFQSL,HSNCCDGGYR,IIRFAFQSLY,RSRCSKWHTN,KWHTNKRWRA,HTNKRWRAIG,FQSLYHSSVY,HSSVYCMSLF,GHSNCCDGGY,ETIIRFAFQS,FAFQSLYHSS,YHSSVYCMSL,GGYRSRCSKW	KIRC
ATP9A	c.1556G>A	p.R519Q	VYQASSPDEVALVQWTESVGLTLVG[p.R519Q]QDQSSMQLRTPGDQILNFTILQIFPF	LVGQDQSSM,GQDQSSMQL,TLVGQDQSSM	BLCA
ATP9A	c.869G>A	p.R290Q	ASGTVVGVVLYTGRELRSVMNTSNP[p.R290Q]QSKIGLFDLEVNCLTKILFGALVVVS	NTSNPQSKI,NPQSKIGLF,VMNTSNPQSK	UCEC
ATP9B	c.115A>G	p.S39G	AAAAANRKRAAYYSAAGPRPGADRH[p.S39G]GRYQLEDESAHLDEMPLMMSEEGFEN	RPGADRHGRY	ACC
ATR	c.5440delA	p.R1814fs	NYLAADGKSTTWSVRLGQLLLSAKK[p.R1814fs]EISQLFMTH*	AKKEISQLF,KKEISQLFM,KEISQLFMT,SAKKEISQLF,AKKEISQLFM,KEISQLFMTH	UCEC
ATRN	c.590C>A	p.P197Q	LRFNHFATECSWDHLYVYDGDSIYA[p.P197Q]QLVAAFSGLIVPERDGNETVPEVVAT	SIYAQLVAA,QLVAAFSGL,IYAQLVAAF,AQLVAAFSG,AQLVAAFSGL,QLVAAFSGLI,SIYAQLVAAF,DSIYAQLVAA	LUAD
ATRNL1	c.3732A>T	p.L1244F	IAFSQHNTIMDLVQFFVTFFSCFLS[p.L1244F]FLLVAAVVWKIKQTCWASRRREQLLR	FSCFLSFLL,FLSFLLVAA,FFSCFLSFL,LSFLLVAAV,TFFSCFLSF,FLLVAAVVW,FSCFLSFLLV,FFSCFLSFLL,FLSFLLVAAV,VTFFSCFLSF,TFFSCFLSFL,SFLLVAAVVW,LSFLLVAAVV	CLL
ATRX	c.5807A>G	p.K1936R	IASDSDETSMSLSSDDYTKKKKKGK[p.K1936R]RGKKDSSSSGSGSDNDVEVIKVWNSR	YTKKKKKGKR	TGCT
ATXN1	c.651G>T	p.Q217H	GHKAEQQQQQQQQQQQQQHQHQQQQQ[p.Q217H]HQQQQQQQQHLSRAPGLITPGSPPPA	HQHQQQQQH,HQQQQQQQQH	LIHC
AURKA	c.1160C>T	p.S387L	RLLKHNPSQRPMLREVLEHPWITAN[p.S387L]LSKPSNCQNKESASKQS*	HPWITANLS,LSKPSNCQNK,LEHPWITANL	CESC
AVIL	c.190G>T	p.G64W	EGDCYVILSTRRVASLLSQDIHFWI[p.G64W]WKDSSQDEQSCAAIYTTQLDDYLGGS	SQDIHFWIW,SQDIHFWIWK,LSQDIHFWIW	LUAD
AVIL	c.896_897insG	p.G299fs	DLLNHDDCYILDQSGTKIYVWKGKG[p.G299fs]SHKG*	VWKGKGSHK,YVWKGKGSHK	KIRC
AVL9	c.102C>A	p.F34L	DGVPRGPVLHIVVVGFHHKKGCQVE[p.F34L]LSYPPLIPGDGHDSHTLPEEWKYLPF	KGCQVELSY,HKKGCQVEL,CQVELSYPP,VELSYPPLI,CQVELSYPPL,KKGCQVELSY	UCEC
AVL9	c.21_22insG	p.G7fs	MEKARRGG[p.G7fs]GWRPPGARTAHRGGRISPQEGLPG*	KARRGGGWR,RTAHRGGRI,RPPGARTAH,GRISPQEGL,KARRGGGWRP,GWRPPGARTA,GARTAHRGGR,MEKARRGGGW	ACC

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AVPR1A	c.1053delT	p.F351fs	ENPTITITALLGSLNSCCNPWIYMF[p.F351fs]LVAISFKTVFKASHAAKT*	WIYMFLVAI,YMFLVAISF,FLVAISFKT,LVAISFKTV,TVFKASHAA,MFLVAISFK,AISFKTVFK,IYMFLVAIS,KTVFKASHA,VFKASHAAK,VAISFKTVF,ISFKTVFKA,FKTVFKASH,NPWIYMFLV,FLVAISFKTV,AISFKTVFKA,YMFLVAISFK,VAISFKTVFK,TVFKASHAAK,PWIYMFLVAI,IYMFLVAISF,SFKTVFKASH,KTVFKASHAA,LVAISFKTVF,NPWIYMFLVA	STAD
AVPR1B	c.115G>A	p.G39R	RGTLSAPNATTPWLGRDEELAKVEI[p.G39R]RVLATVLVLATGGNLAVLLTLGQLGR	RVLATVLVL,ELAKVEIRV,EIRVLATVL,VEIRVLATV,RVLATVLVLA,KVEIRVLATV,EIRVLATVLV,AKVEIRVLAT,VEIRVLATVL,IRVLATVLVL,EELAKVEIRV	TGCT
AXDND1	c.2790G>T	p.E930D	WRESAKQGTLAQKYLEAMAVIEHMQ[p.E930D]DKLLEVENRARQAEEKFEDAYEKLHH	HMQDKLLEV,AVIEHMQDK,IEHMQDKLL,AVIEHMQDKL	CRC
AXDND1	c.301T>C	p.W101R	CPENLLPPKKIKTPKGTLPRLVDHV[p.W101R]RHHPVRRNKFKYLIDHPVSLTGAGRD	HVRHHPVRR,RHHPVRRNK,RLVDHVRHH,LVDHVRHHPV,HVRHHPVRRN,RHHPVRRNKF	LUAD
AXIN2	c.1988_1994delGGGGGGG	p.W663fs	QSTKKAYPLESARSSPGERASRHHL[p.W663fs]STAGTPAPPPVPTCSPRTLRCLP*	HLSTAGTPA,RASRHHLST,ASRHHLSTA,PTCSPRTLR,TPAPPPVPT,VPTCSPRTL,RASRHHLSTA,ASRHHLSTAG,HHLSTAGTPA	CRC
AXIN2	c.1993_1994insG	p.G665fs	KKAYPLESARSSPGERASRHHLWGG[p.G665fs]QQRAPPHHPPCPPVHPGPCDASPDPTQHAGSAGGGLSQAS*	HLWGGQQRA,GQQRAPPHH	CRC
AXIN2	c.1994delG	p.G665fs	TKKAYPLESARSSPGERASRHHLWG[p.G665fs]ATAGTPAPPPVPTCSPRTLRCLP*	HLWGATAGT,ASRHHLWGA,PTCSPRTLR,TPAPPPVPT,VPTCSPRTL,RHHLWGATA,WGATAGTPA,RASRHHLWGA,ASRHHLWGAT,RHHLWGATAG	STAD
B2M	c.1A>G	p.M1V	[p.M1V]VSRSVALAVLALLSLSGLEAIQRTPK	VSRSVALAV,VSRSVALAVL	OV
B2M	c.37_38delCT	p.L13fs	MSRSVALAVLALLS[p.L13fs]FWPGGYPAYSKDSGLLTSSSREWKVKFPELLCVWVSSIRH*	LLSFWPGGY,LLCVWVSSI,LTSSSREWK,SSSREWKVK,KFPELLCVW,KVKFPELLC,FWPGGYPAY,TSSSREWKV,EWKVKFPEL,LAVLALLSF,SFWPGGYPA,LLTSSSREW,SSREWKVKF,WKVKFPELL,VKFPELLCV,REWKVKFPE,FPELLCVWV,ELLCVWVSSI,ALLSFWPGGY,LLTSSSREWK,TSSSREWKVK,SFWPGGYPAY,KFPELLCVWV,KVKFPELLCV,DSGLLTSSSR,LLCVWVSSIR,LSFWPGGYPA,LTSSSREWKV,YPAYSKDSGL,ALAVLALLSF,LAVLALLSFW,GLLTSSSREW,SSSREWKVKF,REWKVKFPEL,VKFPELLCVW	CRC,STAD
B2M	c.3G>A	p.M1I	[p.M1I]ISRSVALAVLALLSLSGLEAIQRTPK	ISRSVALAV,ISRSVALAVL	HNSC
B3GALNT1	c.434G>A	p.R145Q	QEAEKEDKMLALSLEDEHLLYGDII[p.R145Q]QQDFLDTYNNLTLKTIMAFRWVTEFC	IQQDFLDTY,LYGDIIQQDF,IIQQDFLDTY	CRC
B3GAT1	c.374G>T	p.R125L	AELTRMANTLLHVPNLHWLVVEDAP[p.R125L]LRTPLTARLLRDTGLNYTHLHVETPR	WLVVEDAPL,VEDAPLRTPL	LUAD
B3GNT5	c.88delT	p.F30fs	GRRVKKWQLIIQLFATCFLASLMFF[p.F30fs]GNQSIITL*	FLASLMFFG,LMFFGNQSI,MFFGNQSII,FGNQSIITL,FLASLMFFGN,SLMFFGNQSI,LMFFGNQSII,FFGNQSIITL	STAD
B4GALNT1	c.263_264insG	p.G88fs	PVRIKEQVVGLLAWNNCSCESSGGG[p.G88fs]PPPPLPETSPSY*	PLPETSPSY,PPLPETSPSY	PRAD
BACH1	c.1613G>A	p.R538Q	ESCSAREQECEVKLPFNAQRIISLS[p.R538Q]QNDFQSLLKMHKLTPEQLDCIHDIRR	SQNDFQSLL,AQRIISLSQ,IISLSQNDF,LSQNDFQSL,SLSQNDFQSL,SQNDFQSLLK,RIISLSQNDF,LSQNDFQSLL	CRC
BAG1	c.133G>C	p.G45R	RLRALRPGREPRQSEPPAQRGPPPS[p.G45R]RRPPARSTASGHDRPTRGAAAGARRP	AQRGPPPSR,AQRGPPPSRR,GPPPSRRPPA	ACC
BAI2	c.692C>G	p.A231G	EECGRAAGRACGFAQPGCSCPGEAG[p.A231G]GGSTTTTSPGPPAAHTLSNALVPGGP	GEAGGGSTT,GEAGGGSTTT	TGCT
BAIAP2L2	c.1186G>A	p.V396M	SSASGWFPEAYVKALEEGPVNPMTP[p.V396M]MTPMTSMTSMSPMTPMNPGNELPSRS	NPMTPMTPM,GPVNPMTPM,TPMTPMTSM,MTPMTPMTSM,MTPMTSMTSM,TPMTPMTSMT	KIRP

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BAP1	c.233A>G	p.N78S	IEERRSRRKVSTLVDDTSVIDDDIV[p.N78S]SNMFFAHQLIPNSCATHALLSVLLNC	IVSNMFFAH,DIVSNMFFA,SNMFFAHQL,SNMFFAHQLI,VSNMFFAHQL	KIRC
BAP1	c.679C>T	p.R227C	WTDKARRVIMERIGLATAGEPYHDI[p.R227C]CFNLMAVVPDRRIKYEARLHVLKVNR	PYHDICFNL,DICFNLMAV,YHDICFNLM,GEPYHDICF,HDICFNLMA,PYHDICFNLM,DICFNLMAVV,EPYHDICFNL,HDICFNLMAV	OV
BARX2	c.203G>C	p.R68P	SLYSVCPSLVVRPKPLHSCTGSPSL[p.R68P]PAYPLLSVITRQPTVISHLVPATPGI	TGSPSLPAY,LPAYPLLSV,SPSLPAYPL,CTGSPSLPAY,SLPAYPLLSV,SPSLPAYPLL,LPAYPLLSVI	LUAD
BAX	c.114_115insG	p.M38fs	SEQIMKTGALLLQGFIQDRAGRMGG[p.M38fs]GGTRAGPGPGASGCVHQEAERVSQAHRGRTGQ*	RMGGGGTRA,GTRAGPGPG,RVSQAHRGR,QEAERVSQA,AGRMGGGGTR,GTRAGPGPGA,RMGGGGTRAG,HQEAERVSQA,QEAERVSQAH	STAD
BBOX1	c.526T>G	p.F176V	RLTGASDKPGEVSKLGKRMGFLYLT[p.F176V]VYGHTWQVQDKIDANNVAYTTGKLSF	RMGFLYLTV,TVYGHTWQV,YLTVYGHTW,MGFLYLTVY,FLYLTVYGHT,LTVYGHTWQV,RMGFLYLTVY,LYLTVYGHTW,KRMGFLYLTV	CRC
BBS9	c.802delT	p.F268fs	ALDICIVSFNQSASSVFVLGERNFF[p.F268fs]ALRIMDKFDS*	VLGERNFFA,FALRIMDKF,RNFFALRIM,FVLGERNFFA,VLGERNFFAL,NFFALRIMDK,FFALRIMDKF,GERNFFALRI,ERNFFALRIM	PRAD
BC139719	c.398T>G	p.L133R	SSKSRNAPRSSCGNCGARAPEHPPV[p.L133R]RRVESLNLPLLNGLREEGPGVFSRSV	PPVRRVESL,HPPVRRVESL,RRVESLNLPL	PRAD
BCAS3	c.641C>T	p.T214M	DLHCNKRILVVVLQEKIAAFDSCTF[p.T214M]MKKFFVTSCYPCPGPNMNPIALGSRW	CTFMKKFFV,AFDSCTFMK,TFMKKFFVT,AAFDSCTFM,FMKKFFVTS,MKKFFVTSC,FMKKFFVTSC,AAFDSCTFMK,AFDSCTFMKK,MKKFFVTSCY,IAAFDSCTFM,FDSCTFMKKF	BLCA
BCKDHA	c.111delC	p.H37fs	RGLSQAALLLLRQPGARGLARSHPP[p.H37fs]GSSSSFHLWMTSPSSQGPRRSL*	SSSSFHLWM,RSHPPGSSS,HPPGSSSSF,SSQGPRRSL,GSSSSFHLW,FHLWMTSPS,WMTSPSSQG,MTSPSSQGPR,RGLARSHPPG,RSHPPGSSSS,SHPPGSSSSF,GSSSSFHLWM,FHLWMTSPSS	STAD
BCKDHA	c.385_395delGGGGACTGGGC	p.G129fs	LCCFWPVGIAAFCLAQKVSLCVGLG[p.G129fs]IKEKNAPQKQRAIYLRREGGR*	SLCVGLGIK,CVGLGIKEK,KQRAIYLRR,IYLRREGGR,APQKQRAIY,KVSLCVGLGI,VSLCVGLGIK,GIKEKNAPQK,KQRAIYLRRE,AIYLRREGGR,APQKQRAIYL	PAAD
BCL11A	c.1735G>A	p.E579K	SMQHFSEAFHQVLGEKHKRGHLAEA[p.E579K]KGHRDTCDEDSVAGESDRIDDGTVNG	HLAEAKGHR,AEAKGHRDT	HNSC
BCL2	c.515A>G	p.N172S	IVAFFEFGGVMCVESVNREMSPLVD[p.N172S]SIALWMTEYLNRHLHTWIQDNGGWDA	LVDSIALWM,SIALWMTEY,EMSPLVDSI,MSPLVDSIA,SPLVDSIAL,REMSPLVDS,DSIALWMTEY,SIALWMTEYL,MSPLVDSIAL,REMSPLVDSI,SPLVDSIALW	DLBCL
BCL2	c.60T>G	p.H20Q	MAHAGRTGYDNREIVMKYI[p.H20Q]QYKLSQRGYEWDAGDVGAAPPGAAPA	VMKYIQYKL,IVMKYIQYK,YIQYKLSQR,IQYKLSQRG,REIVMKYIQ,IVMKYIQYKL,EIVMKYIQYK,IQYKLSQRGY,KYIQYKLSQR,REIVMKYIQY	DLBCL
BCL2	c.97G>A	p.G33R	GYDNREIVMKYIHYKLSQRGYEWDA[p.G33R]RDVGAAPPGAAPAPGIFSSQPGHTPH	YEWDARDVG,SQRGYEWDAR,YEWDARDVGA	DLBCL
BCL2L11	c.272G>A	p.R91Q	PPASPGPFATRSPLFIFMRRSSLLS[p.R91Q]QSSSGYFSFDTDRSPAPMSCDKSTQT	QSSSGYFSF,LLSQSSSGY,LSQSSSGYF,SQSSSGYFS,SQSSSGYFSF,SLLSQSSSGY,LLSQSSSGYF,FMRRSSLLSQ	CRC
BCL2L11	c.560_561insA	p.L187fs	YARRVFLNNYQAAEDHPRMVILRLL[p.L187fs]TLHCPPGVENALTGSLRSRDTMQTFCLFKPTRPSTAVSWCHYYAASGSLVEGAGDVSEDTELDGTTFLFITTQQNF*	STAVSWCHY,TAVSWCHYY,ELDGTTFLF,LTLHCPPGV,AVSWCHYYA,SLVEGAGDV,MVILRLLTL,TMQTFCLFK,DTMQTFCLF,HYYAASGSL,YYAASGSLV,LFITTQQNF,RSRDTMQTF,LFKPTRPST,VSWCHYYAA,TFCLFKPTR,CPPGVENAL,KPTRPSTAV,RMVILRLLT,VENALTGSL,GSLRSRDTM,TELDGTTFL,STAVSWCHYY,ELDGTTFLFI,RMVILRLLTL,LLTLHCPPGV,AVSWCHYYAA,FLFITTQQNF,DTMQTFCLFK,QTFCLFKPTR,HYYAASGSLV,TELDGTTFLF,RSRDTMQTFC,LFKPTRPSTA,PSTAVSWCHY,NALTGSLRSR,TAVSWCHYYA,LRSRDTMQTF,RDTMQTFCLF,MQTFCLFKPT,CHYYAASGSL	UCS
BCL7A	c.155C>T	p.T52M	KVRKWEKKWVTVGDTSLRIYKWVPV[p.T52M]MEPKVDDKNKNKKKGKDEKCGSEVTT	RIYKWVPVM,KWVPVMEPK,LRIYKWVPVM	CRC
BCL9L	c.2938G>T	p.G980C	PQTPSQMVPLPSANPPGPLKSPQVL[p.G980C]CSSLSVRSPTGSPSRLKSPSMAVPSP	QVLCSSLSV,SPQVLCSSL,QVLCSSLSVR	LUAD

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BCL9L	c.3379_3380insC	p.P1127fs	YHNAIKTIATSDDELLPDRPLLPPP[p.P1127fs]TTTAGLRARDQQQPAQPDAPELSRCPEPYGHEPARPAAPVP*	LLPPPTTTA,RARDQQQPA,LSRCPEPYG,ELSRCPEPY,TTTAGLRAR,EPARPAAPV,RPLLPPPTTT,LPPPTTTAGL,QPAQPDAPEL,YGHEPARPAA,HEPARPAAPV	STAD
BCLAF1	c.109_110insCA	p.R37fs	RSKSRSQSSSRSRSRSHSRKKRYSS[p.R37fs]TGLVPEHIQGLVVEIVCILEIIVAITEIIEE*	LVVEIVCIL,CILEIIVAI,IIVAITEII,LVPEHIQGL,HIQGLVVEI,GLVVEIVCI,EIVCILEII,EIIVAITEI,SRKKRYSST,KKRYSSTGL,KRYSSTGLV,VEIVCILEI,VPEHIQGLV,GLVPEHIQGL,LVPEHIQGLV,HIQGLVVEIV,GLVVEIVCIL,HSRKKRYSST,KKRYSSTGLV,EIVCILEIIV,EIIVAITEII,VPEHIQGLVV,RKKRYSSTGL,LEIIVAITEI,VEIVCILEII	CRC
BCOR	c.4376A>G	p.N1459S	LPCSSSPQETTQSRPMPPEARRLIV[p.N1459S]SKNAGETLLQRAARLGYEEVVLYCLE	EARRLIVSK,VSKNAGETL,SKNAGETLL	LUAD
BEND2	c.1607C>A	p.P536Q	RILFSKEILISSSVDIHLKDSQSLD[p.P536Q]QNKMAALREYLATTFPTCDLHEHGKD	DQNKMAALR,SQSLDQNKM,SLDQNKMAAL	LUAD
BEND2	c.1888G>A	p.E630K	NDQRGRDGGEGCSWMFQPMNNSKMR[p.E630K]KKRNLQPNSNAIPEGMREPSTDNPEE	PMNNSKMRK,MNNSKMRKK,KMRKKRNLQ,SKMRKKRNL,KMRKKRNLQP,MNNSKMRKKR,NSKMRKKRNL	MM
BEND3	c.793delG	p.D265fs	FQPPPEYQLTAAELKQIVDQSLSGG[p.D265fs]TWPAACWCSSSPSSSATWTSPGAAVPVALRPSASWSRCTCSSSATMWRSTTPR*	SLSGGTWPA,TMWRSTTPR,GAAVPVALR,CSSSATMWR,TSPGAAVPV,VPVALRPSA,RPSASWSRC,CTCSSSATM,DQSLSGGTW,VALRPSASW,WPAACWCSS,SLSGGTWPAA,ATWTSPGAAV,WTSPGAAVPV,ALRPSASWSR,ATMWRSTTPR,WSRCTCSSSA,SSATWTSPGA,SPGAAVPVAL,RPSASWSRCT,SSSPSSSATW,RCTCSSSATM,WPAACWCSSS	STAD
BEND5	c.592C>T	p.R198C	LEDAVVPRALYEELLRNYQQQQEEM[p.R198C]CHLQQELERTRRQLVQQAKKLKEYGA	QQQEEMCHL,YQQQQEEMCH,QQQQEEMCHL,EEMCHLQQEL	CRC
BEST3	c.1148C>T	p.P383L	SFLGSTVQMGKQMPKNEWKMEDIKI[p.P383L]LLPQPQFQCAKSDPGG*	KMEDIKILL,WKMEDIKIL,KILLPQPQF,LLPQPQFQCA,WKMEDIKILL,IKILLPQPQF	TGCT
BEST3	c.1331_1332insC	p.P444fs	SSMFLPRDDLSPARDLLDVPSRNPP[p.P444fs]QGLTHLEEILLPRRKPHAALQHGRAVHHQGDQPDKHFTEPDPTVQCENFPHQNATGT*	HLEEILLPR,LPRRKPHAA,AALQHGRAV,FPHQNATGT,LQHGRAVHH,CENFPHQNA,LLPRRKPHAA,HLEEILLPRR,HAALQHGRAV,VPSRNPPQGL,LPRRKPHAAL,AALQHGRAVH,LQHGRAVHHQ,HQGDQPDKHF,KHFTEPDPTV,CENFPHQNAT	STAD
BHLHE22	c.185T>A	p.L62Q	STPPGMDLSLAPPPRERPASSSSSP[p.L62Q]QGCFEPADPEGAGLLLPPPGGGGGGS	SPQGCFEPA,SSSSPQGCF,RPASSSSSPQ,SSSSSPQGCF	ACC
BICD2	c.485G>A	p.R162H	SENERLASVAQELKEINQNVEIQRG[p.R162H]HLRDDIKEYKFREARLLQDYSELEEE	RGHLRDDIK,HLRDDIKEY,HLRDDIKEYK,NVEIQRGHLR,IQRGHLRDDI,GHLRDDIKEY	CRC
BIRC6	c.1240G>C	p.V414L	SCFGSGSCPHFLAAATKRGKICIWD[p.V414L]LSKLMKVHLKFEINAYDPAIVQQLIL	KICIWDLSK,CIWDLSKLMK,LSKLMKVHLK,ICIWDLSKLM	TGCT
BIRC8	c.673_674GC>AT	p.A225M	VFIPCGHLVTCKQCAEAVDRCPMCS[p.A225M]MVIDFKQRVFMS*	MVIDFKQRV,MCSMVIDFK,VDRCPMCSM,PMCSMVIDF,SMVIDFKQRV,PMCSMVIDFK,CSMVIDFKQR,CPMCSMVIDF,MVIDFKQRVF	TGCT
BLM	c.1980T>A	p.H660Q	ASRNLKHERFQSLSFPHTKEMMKIF[p.H660Q]QKKFGLHNFRTNQLEAINAALLGEDC	KIFQKKFGL,EMMKIFQKK,KEMMKIFQK,MMKIFQKKF,FQKKFGLHN,QKKFGLHNF,KIFQKKFGLH,EMMKIFQKKF,FQKKFGLHNF,KEMMKIFQKK,MMKIFQKKFG,MKIFQKKFGL	KIRC
BLVRA	c.131C>T	p.S44L	AGSVRMRDLRNPHPSSAFLNLIGFV[p.S44L]LRRELGSIDGVQQISLEDALSSQEVE	FLNLIGFVL,VLRRELGSI,NLIGFVLRR,IGFVLRREL,FVLRRELGSI,AFLNLIGFVL,FLNLIGFVLR	CRC
BMP2K	c.1461C>G	p.H487Q	QQQQQQQQQQQQQQQQQQQQQQQQQQQ[p.H487Q]QHHHHHHHLLQDAYMQQYQHATQQQQ	QQHHHHHHHL,QHHHHHHHLL	TGCT
BMP3	c.1030C>T	p.R344W	KPYKTLQAQAPEKSKNKKKQRKGPH[p.R344W]WKSQTLQFDEQTLKKARRKQWIEPRN	HWKSQTLQF,KQRKGPHWK,GPHWKSQTL,KKQRKGPHW,KKQRKGPHWK,KQRKGPHWKS,KKKQRKGPHW,PHWKSQTLQF	CRC
BMP6	c.353A>T	p.Q118L	PRPLHGLQQPQPPALRQQEEQQQQQ[p.Q118L]LLPRGEPPPGRLKSAPLFMLDLYNAL	QEEQQQQQL,QQEEQQQQQL,QEEQQQQQLL	KIRP

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BMPER	c.1329_1340delGCGCATCGCGCT	p.RIAL444del	KSVELVLGESRVSLQQHLTVRWNGS[p.RIAL444del]PCRAPHFHIDLDGYLLKVTTKAGLEISWDGDSFVEVM	RWNGSPCRA,TVRWNGSPCR,NGSPCRAPHF,SPCRAPHFHI	KIRC
BMPER	c.722G>A	p.R241Q	PPGQCCPKCLGQRKVFDLPFGSCLF[p.R241Q]QSDVYDNGSSFLYDNCTACTCRDSTV	SCLFQSDVY,GSCLFQSDVY,LPFGSCLFQS	UCEC
BMS1	c.1364G>T	p.G455V	KAIFGDEDESGDSDDEEDDEMSEDD[p.G455V]VLENGSSDEEAEEEENAEMTDQYMAV	DEMSEDDVL	LUAD
BMS1	c.2634G>T	p.E878D	GEMQKQAQLNRAEFEDQDDEARVQY[p.E878D]DGFRPGMYVRIEIENVPCEFVQNFDP	YDGFRPGMY,DGFRPGMYV,VQYDGFRPG,QYDGFRPGMY,EARVQYDGFR,DGFRPGMYVR,VQYDGFRPGM,DEARVQYDGF	KIRP
BNC1	c.2809T>A	p.Y937N	MEKADQSLASLPSGLPITCHLCQKT[p.Y937N]NSNKGTFRAHYKTVHLRQLHKCKVPG	KTNSNKGTF,TNSNKGTFR,HLCQKTNSNK,KTNSNKGTFR,QKTNSNKGTF	CLL
BNC2	c.1534C>T	p.R512W	NRHSANPNPRLHMPMLRNNRDKDLI[p.R512W]WATSGAATPVIASTKSNLALTSPGRP	LIWATSGAA,DLIWATSGA,DLIWATSGAA,WATSGAATPV	CRC
BNC2	c.1723A>C	p.S575R	LQNPLPSQLVFSGLKTVQPVPPFYR[p.S575R]RLLTPGEMVSPPTSLPTSPIIPTSGT	RLLTPGEMV,QPVPPFYRR,VPPFYRRLL,RRLLTPGEM,QPVPPFYRRL,YRRLLTPGEM	STAD
BPI	c.765G>T	p.M255I	IDSVAGINYGLVAPPATTAETLDVQ[p.M255I]IKGEFYSENHHNPPPFAPPVMEFPAA	LDVQIKGEF,TTAETLDVQI,LDVQIKGEFY	BLCA
BRAF	c.1208delC	p.P403fs	NIDDLIRDQGFRGDGGSTTGLSATP[p.P403fs]LPHYLAH*	LSATPLPHY,SATPLPHYL,GLSATPLPH,TPLPHYLAH,GLSATPLPHY,STTGLSATPL,LSATPLPHYL	STAD
BRAF	c.1397G>T	p.G466V	LGRRDSSDDWEIPDGQITVGQRIGS[p.G466V]VSFGTVYKGKWHGDVAVKMLNVTAPT	SVSFGTVYK,GSVSFGTVY,GQRIGSVSF,RIGSVSFGTV,GSVSFGTVYK,VSFGTVYKGK,IGSVSFGTVY,ITVGQRIGSV,VGQRIGSVSF	LUAD
BRAF	c.1406G>C	p.G469A	RDSSDDWEIPDGQITVGQRIGSGSF[p.G469A]ATVYKGKWHGDVAVKMLNVTAPTPQQ	GSGSFATVY,SGSFATVYK,SFATVYKGK,FATVYKGKW,RIGSGSFATV,GSGSFATVYK,GSFATVYKGK,SFATVYKGKW,GQRIGSGSFA,IGSGSFATVY	MM,PRAD
BRAF	c.1406G>T	p.G469V	RDSSDDWEIPDGQITVGQRIGSGSF[p.G469V]VTVYKGKWHGDVAVKMLNVTAPTPQQ	SGSFVTVYK,SFVTVYKGK,GSGSFVTVY,RIGSGSFVTV,GSGSFVTVYK,GSFVTVYKGK,SFVTVYKGKW,GQRIGSGSFV,IGSGSFVTVY	LUAD
BRAF	c.1798_1799GT>AA	p.V600K	RDLKSNNIFLHEDLTVKIGDFGLAT[p.V600K]KKSRWSGSHQFEQLSGSILWMAPEVIR	ATKKSRWSG,KKSRWSGSH,ATKKSRWSGS,DFGLATKKSR,FGLATKKSRW	SKCM
BRAF	c.1799T>A	p.V600E	RDLKSNNIFLHEDLTVKIGDFGLAT[p.V600E]EKSRWSGSHQFEQLSGSILWMAPEVI	DFGLATEKSR,FGLATEKSRW	CRC,GBM,LUAD,MM,SKCM,THCA
BRAF	c.1801A>G	p.K601E	DLKSNNIFLHEDLTVKIGDFGLATV[p.K601E]ESRWSGSHQFEQLSGSILWMAPEVIR	VESRWSGSH,DFGLATVESR,ESRWSGSHQF,FGLATVESRW	DLBCL,SKCM
BRAF	c.1803A>T	p.K601N	DLKSNNIFLHEDLTVKIGDFGLATV[p.K601N]NSRWSGSHQFEQLSGSILWMAPEVIR	GLATVNSRW,DFGLATVNSR,NSRWSGSHQF,FGLATVNSRW	CLL
BRD3	c.70_71insC	p.P24fs	MSTATTVAPAGIPATPGPVNPPPP[p.P24fs]GGLQPQQARPQDQPAAVHAECGGEDALETPVRLALLPARGRNQIEPAGLS*	RGRNQIEPA,ETPVRLALL,RPQDQPAAV,LPARGRNQI,AECGGEDAL,LETPVRLAL,GEDALETPV,LLPARGRNQI,PVRLALLPAR,RLALLPARGR,TPVRLALLPA,QQARPQDQPA,ALETPVRLAL,LETPVRLALL	STAD
BRD9	c.988G>T	p.G330W	HAADEARDRINRFLPGGKMGYLKRN[p.G330W]WDGSLLYSVVNTAEPDADEEETHPVD	RNWDGSLLY,KMGYLKRNW,LKRNWDGSL,KRNWDGSLL,WDGSLLYSV,YLKRNWDGSL,KRNWDGSLLY,GKMGYLKRNW,LKRNWDGSLL,WDGSLLYSVV	LUAD
BRF1	c.1405G>T	p.V469L	DGELDLSGIDDLEIDRYILNESEAR[p.V469L]LKAELWMRENAEYLREQREKEARIAK	ILNESEARL,RLKAELWMR,SEARLKAEL,ARLKAELWM,NESEARLKA,YILNESEARL,ILNESEARLK,SEARLKAELW	LUAD
BRK1	c.208A>C	p.K70Q	SRLATLNEKLTALERRIEYIEARVT[p.K70Q]QGETLT*	ARVTQGETL,IEARVTQGET	KIRC

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BRMS1	c.321delG	p.G107fs	LSQLRLRLEEVGAERAPEYTEPLGG[p.G107fs]CSGASRFAFRWQGSTRASVWM*	WQGSTRASV,SGASRFAFR,ASRFAFRWQ,AFRWQGSTR,GGCSGASRF,CSGASRFAF,FAFRWQGST,FRWQGSTRA,GASRFAFRW,CSGASRFAFR,FAFRWQGSTR,ASRFAFRWQG,RFAFRWQGST,AFRWQGSTRA,RWQGSTRASV,LGGCSGASRF,GCSGASRFAF,SGASRFAFRW,FRWQGSTRAS,WQGSTRASVW	STAD
BRPF1	c.196C>T	p.R66C	HLYHYDHDNPPPPQQTPLRKHKKKG[p.R66C]CQSRPANKQSPSPSEVSQSPGREVMS	GCQSRPANK,KHKKKGCQSR,KGCQSRPANK	CRC
BRWD1	c.3956A>G	p.K1319R	TSSGRRRVHDGKKSIRATNYVESNW[p.K1319R]RKQCKELVNLIFQCEDSEPFRQPVDL	NYVESNWRK,ATNYVESNWR,RKQCKELVNL	TGCT
BRWD3	c.2359C>T	p.R787C	TVEKKKKPSYTTQRNDYEPSCGRSL[p.R787C]CRTQRKRQHTYQTRSNIEHNSQASCQ	RSLCRTQRK,CGRSLCRTQR,RSLCRTQRKR	CRC
BRWD3	c.478C>A	p.H160N	VNYVKPPNVVNITSARQLTGCSRFG[p.H160N]NIFPSSAYQHIKMHKRILGHLSSVYC	CSRFGNIFP,RFGNIFPSS,GNIFPSSAY,GCSRFGNIF,SRFGNIFPS,CSRFGNIFPS,RFGNIFPSSA,FGNIFPSSAY,TGCSRFGNIF	LUAD
BST1	c.107G>C	p.G36A	LLQLLLQLLLLLLLLAAGGARARWR[p.G36A]AEGTSAHLRDIFLGRCAEYRALLSPE	RARWRAEGT,RWRAEGTSA,WRAEGTSAH,RAEGTSAHL,GARARWRAEG,RARWRAEGTS,RWRAEGTSAH,ARWRAEGTSA,WRAEGTSAHL	KIRP
BTBD11	c.1352delC	p.T451fs	LSDLVSRAMHHLQPLNAKHHGNGTP[p.T451fs]CTTSRGHCTGSPRPCTPFAISCTAHKWNGKTPTWSLPKSTSRWKGPSSCCRR*	CTAHKWNGK,KTPTWSLPK,FAISCTAHK,KWNGKTPTW,RGHCTGSPR,TSRWKGPSS,WSLPKSTSR,SPRPCTPFA,NGKTPTWSL,KHHGNGTPC,GSPRPCTPF,HKWNGKTPT,TPFAISCTA,SLPKSTSRWK,RWKGPSSCCR,TWSLPKSTSR,CTPFAISCTA,SPRPCTPFAI,AKHHGNGTPC,TGSPRPCTPF,FAISCTAHKW,HKWNGKTPTW,WSLPKSTSRW,TPFAISCTAH	STAD
BTBD11	c.1682C>T	p.A561V	LLPGVDCEPRQLRADDCFCASRKLD[p.A561V]VVAIEAKFKQDLGFRMLNCGRTDLVK	KLDVVAIEA,VVAIEAKFK,ASRKLDVVA,KLDVVAIEAK,ASRKLDVVAI,DVVAIEAKFK,RKLDVVAIEA,LDVVAIEAKF	STAD
BTBD11	c.794G>C	p.G265A	CMESLFRDIYSRVVASGVPRSCSGP[p.G265A]ASGSGSGPGPSSGPGAAPAADKEREA	VPRSCSGPA,VPRSCSGPAS	ACC
BTBD7	c.1307C>T	p.S436L	HPYGSKWVHRQALHFLCEEFSQVMT[p.S436L]LDVFYELSKDHLLTAIQSDYLQASEQ	MTLDVFYEL,QVMTLDVFY,SQVMTLDVF,EEFSQVMTL,VMTLDVFYEL,TLDVFYELSK,FSQVMTLDVF,SQVMTLDVFY,MTLDVFYELS,CEEFSQVMTL	CRC
BTG1	c.91C>T	p.L31F	TRAATMIGEIAAAVSFISKFLRTKG[p.L31F]FTSERQLQTFSQSLQELLAEHYKHHW	RTKGFTSER,FLRTKGFTS,SKFLRTKGF,KGFTSERQL,FLRTKGFTSE,FTSERQLQTF,ISKFLRTKGF	DLBCL
BTLA	c.256C>A	p.Q86K	KYCANRPHVTWCKLNGTTCVKLEDR[p.Q86K]KTSWKEEKNISFFILHFEPVLPNDNG	KLEDRKTSW,KLEDRKTSWK,TTCVKLEDRK,VKLEDRKTSW	CLL
BTN2A2	c.43C>T	p.L15F	MEPAAALHFSLPAS[p.L15F]FLLLLLLLLSLCALVSAQFTVVGPA	FSLPASFLL,SLPASFLLL,SFLLLLLLL,LPASFLLLL,LHFSLPASF,ASFLLLLLL,FSLPASFLLL,SLPASFLLLL,HFSLPASFLL,SFLLLLLLL,ALHFSLPASF,LPASFLLLLL,LHFSLPASFL,ASFLLLLLLL	TGCT
BTN3A2	c.457G>A	p.E153K	FQDGDFYEKALVELKVAALGSNLHV[p.E153K]KVKGYEDGGIHLECRSTGWYPQPQIQ	ALGSNLHVK,GSNLHVKVK,NLHVKVKGY,ALGSNLHVKV,AALGSNLHVK	UCEC
BTRC	c.1248T>G	p.I416M	FNNGMMVTCSKDRSIAVWDMASPTD[p.I416M]MTLRRVLVGHRAAVNVVDFDDKYIVS	MASPTDMTL,WDMASPTDM,MASPTDMTLR,MTLRRVLVGH,DMASPTDMTL,SPTDMTLRRV	KIRC
BTRC	c.778G>T	p.G260W	TDSLWRGLAERRGWGQYLFKNKPPD[p.G260W]WNAPPNSFYRALYPKIIQDIETIESN	KNKPPDWNA,WNAPPNSFY,YLFKNKPPDW,DWNAPPNSFY,WNAPPNSFYR	LUAD
BUB1B	c.2988C>A	p.F996L	VFWDGSFWKLSQNISELKDGELWNK[p.F996L]LFVRILNANDEATVSVLGELAAEMNG	KLFVRILNA,LWNKLFVRI,ELWNKLFVR,GELWNKLFV	CRC
BZRAP1	c.4248_4249insA	p.P1416fs	CLEDMPGLVGGSSRRRGGGSPEKPP[p.P1416fs]KPQAASRSPRTLQPTSQQQWAPGLWTTGPHTGEGWPPRN*	SQQQWAPGL,HTGEGWPPR,QQQWAPGLW,QWAPGLWTT,ASRSPRTLQ,AASRSPRTL,LQPTSQQQW,QQWAPGLWT,SQQQWAPGLW,ASRSPRTLQP,TLQPTSQQQW,QQWAPGLWTT	STAD

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BZRAP1	c.4879G>A	p.V1627I	VLRPSTAELVPARSPSETLAYQHLP[p.V1627I]IRIFVALFDYDPVSMSPNPDAGEEEL	TLAYQHLPI,HLPIRIFVA,AYQHLPIRI,LAYQHLPIR,LPIRIFVAL,YQHLPIRIF,YQHLPIRIFV,HLPIRIFVAL,AYQHLPIRIF,IRIFVALFDY,TLAYQHLPIR,ETLAYQHLPI,LPIRIFVALF,LAYQHLPIRI	CRC
C10orf95	c.253G>T	p.A85S	GRRRRSCSPAPTWPPLCCYPQSRPT[p.A85S]SSAAGPGACMRASGRPHGNTTASTAP	QSRPTSSAA,YPQSRPTSS,YPQSRPTSSA,SSAAGPGACM	ACC
C11orf30	c.3331C>T	p.R1111C	KQTASQVEQPIITQGSSVTKITFEG[p.R1111C]CQPPTVTKITGGSSVPKLTSPVTSIS	FEGCQPPTV	CRC
C11orf68	c.403G>T	p.V135L	PGSPNSEPVGWIAVYGQGYSPNSGD[p.V135L]LQGLQAAWEALQTSGRPITPGTLRQL	GDLQGLQAA,SPNSGDLQGL,GDLQGLQAAW	LUAD
C11orf9	c.782_783insC	p.S261fs	QLLQQHGAELPTHPSKKRKHSESPP[p.S261fs]QHPQCPDAEWNDQTGAWDRDSPASAPHSSPIATLASPGSALPGPWFLASQHCPCPDTALAPARCPLPRPPAGQ*	SALPGPWFL,ALPGPWFLA,FLASQHCPC,ALAPARCPL,TLASPGSAL,ASAPHSSPI,ATLASPGSA,HSSPIATLA,APHSSPIAT,AEWNDQTGA,RDSPASAPH,GSALPGPWF,HPQCPDAEW,LPGPWFLAS,CPDTALAPA,ASAPHSSPIA,ATLASPGSAL,SALPGPWFLA,LAPARCPLPR,APHSSPIATL,TALAPARCPL,RKHSESPPQH,AEWNDQTGAW,SQHCPCPDTA,SPIATLASPG,SPGSALPGPW	STAD
C12orf32	c.179A>T	p.D60V	LPITHTRQVPSKPIDHSTITSWVSP[p.D60V]VFDTAAGSLFPAYQKHQNRARHSSRK	TITSWVSPV,WVSPVFDTA,ITSWVSPVF,SPVFDTAAG,STITSWVSPV,WVSPVFDTAA,VFDTAAGSLF,TITSWVSPVF	TGCT
C12orf4	c.1004G>A	p.R335Q	KLHRLQTALSLYSTSLCGLVLLVDN[p.R335Q]QINSYSGIKRDFATVCQECTDFHFPR	LVDNQINSY,NQINSYSGI,QINSYSGIK,GLVLLVDNQI,LLVDNQINSY,QINSYSGIKR	UCEC
C12orf43	c.82G>C	p.E28Q	APSGTVSDSESSNSSSDAEELERCR[p.E28Q]QAAMPAWGLEQRPHVAGKPRAGAANS	RCRQAAMPA,QAAMPAWGL,LERCRQAAM,CRQAAMPAW,RQAAMPAWG,EELERCRQA,RQAAMPAWGL,ELERCRQAAM,RCRQAAMPAW,EELERCRQAA,AEELERCRQA	CESC
C12orf65	c.428A>C	p.K143T	VFYNGENSPVHKEKREAAKKKQERK[p.K143T]TRAKETLEKKKLLKELWESSKKVH*	KQERKTRAK,KTRAKETLE,RKTRAKETL,KTRAKETLEK,ERKTRAKETL	TGCT
C13orf33	c.200delG	p.R67fs	QPGAFQLSGDQLVVARPGEPAAARG[p.R67fs]ASTSSVTASCASTGSSTASAATSRGMWN*	STASAATSR,STGSSTASA,ASAATSRGM,SAATSRGMW,GEPAAARGA,SSTASAATSR,AARGASTSSV,STSSVTASCA,EPAAARGAST,RGASTSSVTA,TASAATSRGM,ASAATSRGMW	STAD
C14orf101	c.883G>A	p.E295K	FSLAKSEIGSSMSEILLSQVTNMRT[p.E295K]KLSFNIQALAVCANICLATKDRQNPS	KLSFNIQAL,RTKLSFNIQ,TNMRTKLSF,KLSFNIQALA,NMRTKLSFNI,LSQVTNMRTK,RTKLSFNIQA,SQVTNMRTKL,VTNMRTKLSF,TKLSFNIQAL	CRC
C14orf102	c.268delA	p.R90fs	SSDESDTNKKLKQTSRKKKKEKKKK[p.R90fs]GSISIIRKQRGSMGRRVAAGLRQTPILKRTNLPEALEAVKRNLRNRIKEIMLQLILDIALFGLRTFRL*	NLPEALEAV,IMLQLILDI,MLQLILDIA,ILDIALFGL,RIKEIMLQL,GLRQTPILK,ALFGLRTFR,KGSISIIRK,IALFGLRTF,LFGLRTFRL,IIRKQRGSM,KQRGSMGRR,RGSMGRRVA,GSMGRRVAA,MGRRVAAGL,AVKRNLRNR,KRNLRNRIK,RNRIKEIML,SISIIRKQR,TPILKRTNL,SMGRRVAAG,NLRNRIKEI,QLILDIALF,KKKKGSISI,KKKGSISII,KRTNLPEAL,LRNRIKEIM,KEIMLQLIL,LQLILDIAL,SMGRRVAAGL,IMLQLILDIA,MLQLILDIAL,LILDIALFGL,ALFGLRTFRL,ILKRTNLPEA,RIKEIMLQLI,AGLRQTPILK,IALFGLRTFR,KQRGSMGRRV,RGSMGRRVAA,MGRRVAAGLR,GLRQTPILKR,RTNLPEALEA,AVKRNLRNRI,EAVKRNLRNR,EIMLQLILDI,SIIRKQRGSM,NLRNRIKEIM,LQLILDIALF,DIALFGLRTF,KKKKGSISII,RRVAAGLRQT,VAAGLRQTPI,LKRTNLPEAL,IKEIMLQLIL	STAD
C14orf102	c.343G>A	p.D115N	RKHQHHKKTKRKHGPSSSSRSETDT[p.D115N]NSEKDKPSRGVGGSKKESEEPNQGNN	RSETDTNSEK	CRC
C14orf105	c.299G>T	p.R100I	ASRDMYFDIPLEHRETSIIKRHPPQ[p.R100I]ILQKLEPIDLPRVITSGRLLSQREAR	IIKRHPPQI,IKRHPPQIL,SIIKRHPPQI,IIKRHPPQIL,KRHPPQILQK	CRC
C14orf118	c.836G>T	p.R279I	GECVPGFTVPNLLPKWAPDHCSEVE[p.R279I]IMDSGLDKFSDSTFLLPSRPAQRGYH	EIMDSGLDK,IMDSGLDKF,EIMDSGLDKF,SEVEIMDSGL	UCEC
C14orf126	c.16C>T	p.R6W	MAEGS[p.R6W]WIPQARALLQQCLHARLQIRPADGDV	EGSWIPQAR,SWIPQARAL,AEGSWIPQA,SWIPQARALL,GSWIPQARAL	KIRP

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C14orf166B	c.690C>A	p.F230L	DSAALLCQALSTNYQIKKLDLSHNQ[p.F230L]LSDVGGEHLGQMLAINVGLTSLDLSW	KLDLSHNQL,QLSDVGGEHL,KKLDLSHNQL	UCEC
C14orf177	c.269G>T	p.G90V	CCGECSTCFCTEEKSECQRHEETSP[p.G90V]VSCNHQIMSASTISAFCATPRFKQLF	SPVSCNHQI,CQRHEETSPV,SPVSCNHQIM	CLL
C14orf43	c.939delC	p.P313fs	GLQPAGPLGQSHLAHHSMAPYPFPP[p.P313fs]TQI*	PYPFPPTQI,MAPYPFPPT,SMAPYPFPPT,APYPFPPTQI	STAD
C15orf2	c.1462G>A	p.V488I	LALPADLVPILGDQSNEKGGSYNSV[p.V488I]IGAAPLTSDPPTPPSSTPSFKPPVTR	NSVIGAAPL,KGGSYNSVI,GSYNSVIGAA,YNSVIGAAPL	CRC
C15orf2	c.2257G>T	p.V753F	PGSGNTQPSGNTASVQGSTSLPAQS[p.V753F]FRAPATASNHPLNPGATPQPKFGAPD	SLPAQSFRA,TSLPAQSFR,QSFRAPATA,LPAQSFRAP,STSLPAQSF,AQSFRAPAT,STSLPAQSFR,SFRAPATASN,LPAQSFRAPA,GSTSLPAQSF,AQSFRAPATA	LUAD
C15orf2	c.2716G>T	p.G906W	RRPTTTSSHPLNTGSISHSTLGATD[p.G906W]WQQKSDSSFILGNPATPAPVIGLTSP	WQQKSDSSF,TLGATDWQQK,WQQKSDSSFI	LUAD
C15orf23	c.71C>T	p.S24F	MAAPEAPPLDRVFRTTWLSTECD[p.S24F]FHPLPPSYRKFLFETQAADLAGGTTV	TWLSTECDF,DFHPLPPSY,STECDFHPL,DFHPLPPSYR,LSTECDFHPL,CDFHPLPPSY	SKCM
C15orf33	c.1018G>A	p.D340N	GSKKAPAKSVKERIADSQEHISTSI[p.D340N]NFNIIKILNNPRAYTLPISKEESRLS	SINFNIIKI,TSINFNIIK,ISTSINFNI,STSINFNII,EHISTSINF,INFNIIKIL,HISTSINFNI,STSINFNIIK,TSINFNIIKI,QEHISTSINF,ISTSINFNII	CRC
C15orf52	c.294delG	p.G98fs	RKKNQALLRRYQEIQEDRRQAEQGG[p.G98fs]WL*	RQAEQGGWL	STAD
C16orf3	c.193G>A	p.G65S	RACPVACPVGCPIACPVSCPVACPV[p.G65S]SCPVGSMATAPQGLSPQEWEADRETG	VACPVSCPV,PVACPVSCPV,CPVSCPVGSM	CESC
C16orf55	c.353A>C	p.D118A	RASNETLVSCSSSGSDQQRTIREPE[p.D118A]AWGPYRRHRNPSTADAYNSHLKE*	REPEAWGPY,RTIREPEAW,EAWGPYRRHR,IREPEAWGPY	KIRC
C16orf62	c.730C>A	p.L244I	SDTSVIQFYPSKFVLITDILDTFGK[p.L244I]IVYERIFSMCVDSRSVLPDHFSPENA	IVYERIFSM,TFGKIVYER,DILDTFGKI,LDTFGKIVY,GKIVYERI,F,ILDTFGKIVY,TFGKIVYERI,KIVYERIFSM,DTFGKIVYER,FGKIVYERIF	TGCT
C16orf74	c.61_63delAGC	p.S21del	MGLKMSCLKGFQMCVSSSSS[p.S21del]HDEAPVLNDKHLDVPDIIITPPTPTGMM	MCVSSSSSH,QMCVSSSSSH	PRAD
C16orf87	c.452G>T	p.R151I	ANLSDEKAFVFSVALAEINRKIINQ[p.R151I]LIL*	KIINQILIL,NRKIINQIL,RKIINQILI,EINRKIINQI,RKIINQILIL	CRC
C17orf96	c.187C>G	p.L63V	LCLRALAFCALAKPRASSLGPGPGE[p.L63V]VAARSPVLRGPQAPLRPGGWAPDGLK	SLGPGPGEV,VAARSPVLR,EVAARSPVL,GEVAARSPV,EVAARSPVLR,GEVAARSPVL	ACC
C19orf10	c.34G>C	p.G12R	MAAPSGGWNGV[p.G12R]RASLWAALLLGAVALRPAEAVSEPTT	GVRASLWAA,RASLWAALL,VRASLWAAL,GVRASLWAAL,GWNGVRASLW,RASLWAALLL,GGWNGVRASL,VRASLWAALL	ACC
C19orf21	c.784C>T	p.R262C	PHLANGHVVPIKPQVKGVVREENKV[p.R262C]CAVPTWASVQVVDDPGSLASVESPGT	CAVPTWASV,REENKVCAV,NKVCAVPTW,EENKVCAVPT	STAD
C19orf70	c.150delC	p.P50fs	YDQELLGPSDKSQAALQKAGEVVPP[p.P50fs]PCTSSASTCVSRQACRYPSSQPLQRFTFPSVTPGMQAS*	CVSRQACRY,LQRFTFPSV,SSASTCVSR,SQPLQRFTF,TFPSVTPGM,RQACRYPSS,CTSSASTCV,FTFPSVTPG,VPPPCTSSA,CRYPSSQPL,GEVVPPPCT,PLQRFTFPSV,FTFPSVTPGM,TSSASTCVSR,STCVSRQACR,SSQPLQRFTF,YPSSQPLQRF,FPSVTPGMQA,RQACRYPSSQ,LQRFTFPSVT	STAD
C1QBP	c.674C>T	p.T225I	ESDIFSIREVSFQSTGESEWKDTNY[p.T225I]ILNTDSLDWALYDHLMDFLADRGVDN	NYILNTDSL,SEWKDTNYI,ILNTDSLDW,ILNTDSLDWA,SEWKDTNYIL,YILNTDSLDW	TGCT
C1QTNF5	c.582_583insG	p.G194fs	CVWHIQVATDHAIQLKIEALSIESV[p.G194fs]GLLPF*	ALSIESVGL,IESVGLLPF,LSIESVGLL,ALSIESVGLL,EALSIESVGL,SIESVGLLPF	STAD
C1QTNF5	c.924delC	p.P308fs	NCADGSDETNCSAKFSGSVEQSHPP[p.P308fs]PRLLAP*	QSHPPPRLLA,VEQSHPPPRL	STAD

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C1R	c.647delC	p.P216fs	AECSSELYTEASGYISSLEYPRSYP[p.P216fs]LTCAATTASGWSGASPCTSSSWSLLILMTTSKYTAPMTSYRSMPTGRTLASSVGSKGPPTSTPAAMLWICCSSQMSRGTAGAGSCATPPRSSSAPSPRP*	TSSSWSLLI,ILMTTSKYT,SMPTGRTLA,QMSRGTAGA,LLILMTTSK,TLASSVGSK,YTAPMTSYR,RSSSAPSPR,RSYPLTCAA,TTSKYTAPM,MTSYRSMPT,SYRSMPTGR,RSMPTGRTL,RTLASSVGS,SSQMSRGTA,AGSCATPPR,ATPPRSSSA,LILMTTSKY,KYTAPMTSY,TTASGWSGA,CTSSSWSLL,STPAAMLWI,YPRSYPLTC,APMTSYRSM,MPTGRTLAS,LEYPRSYPL,CAATTASGW,SSSWSLLIL,SSWSLLILM,LMTTSKYTA,SKYTAPMTS,LWICCSSQM,SQMSRGTAG,YPLTCAATT,PPTSTPAAM,TSTPAAMLW,TPAAMLWIC,CTSSSWSLLI,SLEYPRSYPL,ILMTTSKYTA,MLWICCSSQM,SQMSRGTAGA,SLLILMTTSK,RTLASSVGSK,TSYRSMPTGR,RSYPLTCAAT,MTTSKYTAPM,KYTAPMTSYR,RSMPTGRTLA,LLILMTTSKY,SKYTAPMTSY,WICCSSQMSR,TTASGWSGAS,YTAPMTSYRS,YPRSYPLTCA,YPLTCAATTA,SPCTSSSWSL,MPTGRTLASS,GPPTSTPAAM,LEYPRSYPLT,GASPCTSSSW,TSSSWSLLIL,SSSWSLLILM,YRSMPTGRTL,SKGPPTSTPA	STAD
C1RL	c.1051delC	p.L351fs	PDYRQNESHNFSGDIALLELQHSIP[p.L351fs]WAPTSSRSVCPIMRPSTAAACWATSVGLAWRWAG*	AAACWATSV,ELQHSIPWA,IMRPSTAAA,ATSVGLAWR,SSRSVCPIM,IPWAPTSSR,STAAACWAT,APTSSRSVC,CPIMRPSTA,LELQHSIPW,LQHSIPWAP,WATSVGLAW,RPSTAAACW,TSVGLAWRW,TAAACWATSV,CWATSVGLAW,SSRSVCPIMR,IMRPSTAAAC,SIPWAPTSSR,WATSVGLAWR,STAAACWATS,CPIMRPSTAA,RPSTAAACWA,LLELQHSIPW,LELQHSIPWA,LQHSIPWAPT,TSSRSVCPIM,AACWATSVGL	CRC
C1orf106	c.1612C>T	p.R538C	PPGYFPAGRYVVVAESPLPPGEWEL[p.R538C]CRAAPGPAYEEEGTPLRYQRLVPSRS	GEWELCRAA,CRAAPGPAY,WELCRAAPG,LCRAAPGPAY,WELCRAAPGP,GEWELCRAAP	ACC
C1orf167	c.367A>G	p.S123G	WWHLRALGPDATSSCTKTPSALEPL[p.S123G]GSSTLQDSLEKVPRAPTLPDTLQGSL	LEPLGSSTL,ALEPLGSSTL	TGCT
C1orf173	c.2063C>A	p.S688Y	ESFENVLKEGTEKGTQEIAEGLSEK[p.S688Y]YGKHVSAEEKEKDKSKLWEESTAQVK	IAEGLSEKY,GLSEKYGKHV,YGKHVSAEEK,EIAEGLSEKY,SEKYGKHVSA	LUAD
C1orf173	c.4360G>A	p.G1454S	AGVGTPGALERKTSGLGQEQEEGSE[p.G1454S]SQEAATGSGDGRQETGAAEKFRLGLS	EEGSESQEA,QEEGSESQEA,EEGSESQEAA	LUAD
C1orf74	c.760G>A	p.D254N	PGLRDILNTWEKDLRTRFRTQNDFA[p.D254N]NLSISSEIVTLPAVAL*	NLSISSEIV,RTQNDFANL,FANLSISSEI,RFRTQNDFAN,FRTQNDFANL,TQNDFANLSI	LUSC
C1orf87	c.1622G>T	p.R541L	LSPQKIDQALRRFRSGENMLLEPAL[p.R541L]LYLKEL*	MLLEPALLY,NMLLEPALL,LLEPALLYL,MLLEPALLYL,LLEPALLYLK,NMLLEPALLY,EPALLYLKEL	LUAD
C20orf132	c.1146A>C	p.E382D	LKLPLRFQRLGHLVALMALLCGDPQ[p.E382D]DKVAEEAAEGIHSLLHITLRLKYITH	LLCGDPQDKV	KIRC
C20orf160	c.136delC	p.P46fs	KAGRRAACRSSVSRRPLHSMPLYPP[p.P46fs]TTSSTPRFCCVTTWRKRSSSWATLPG*	HSMPLYPPT,SSTPRFCCV,RFCCVTTWR,RKRSSSWAT,KRSSSWATL,MPLYPPTTS,RFCCVTTWRK,TWRKRSSSWA,RKRSSSWATL,RSSSWATLPG,TSSTPRFCCV,MPLYPPTTSS,HSMPLYPPTT,TTWRKRSSSW,TPRFCCVTTW	STAD
C20orf26	c.3263G>A	p.R1088Q	LEVQMAQPNYGLELVTGSAKNGTYF[p.R1088Q]QIHINKYKMVETITCLSREPFPASNY	TYFQIHINK,FQIHINKYK,YFQIHINKY,AKNGTYFQI,GTYFQIHINK,TYFQIHINKY,SAKNGTYFQI,YFQIHINKYK,FQIHINKYKM,AKNGTYFQIH	CRC
C22orf26	c.83C>T	p.P28L	ASATAAWHCPPLCLPPLPASAPTSP[p.P28L]LNPATRPAPGPGRRARCPQSAHPAPT	APTSPLNPA,LPASAPTSPL,SPLNPATRPA	ACC

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C22orf40	c.96_97insC	p.P32fs	RPLGVFECELCTLTAPYSYVGQKPP[p.P32fs]QHPVDGPPGGKLCHEGSLHLRQGQIPGPRLVLQFVQQAGVCGPGMQFILLQEILPPLCPGEHQCFSSGNSARLGEKESSIKEDPQPARFSDVSATGARSSGGTLHRAPGPACARDAAELGAAMPGLVSGPLGAALQPRGAGVQLGAATGPGSCSKRVVQRQMPDKTQPGTRPGPPTCPSGPRPE*	LQFVQQAGV,MQFILLQEI,LLQEILPPL,RLGEKESSI,ALQPRGAGV,GQIPGPRLV,TLHRAPGPA,GLVSGPLGA,LVSGPLGAA,ATGPGSCSK,RSSGGTLHR,VVQRQMPDK,GQKPPQHPV,HLRQGQIPG,GNSARLGEK,KTQPGTRPG,GTRPGPPTC,CFSSGNSAR,FSSGNSARL,DAAELGAAM,GPRLVLQFV,GARSSGGTL,GPACARDAA,MPGLVSGPL,QPRGAGVQL,SLHLRQGQI,GKLCHEGSL,LCHEGSLHL,GVCGPGMQF,GEHQCFSSG,KEDPQPARF,ARFSDVSAT,LHRAPGPAC,VSGPLGAAL,SKRVVQRQM,RQMPDKTQP,AELGAAMPG,KLCHEGSLHL,VLQFVQQAGV,GMQFILLQEI,MQFILLQEIL,ILLQEILPPL,LLQEILPPLC,AMPGLVSGPL,RLVLQFVQQA,ELGAAMPGLV,GLVSGPLGAA,LVSGPLGAAL,RLGEKESSIK,RVVQRQMPDK,AATGPGSCSK,SGNSARLGEK,SIKEDPQPAR,RSSGGTLHRA,GTLHRAPGPA,IPGPRLVLQF,QQAGVCGPGM,RQGQIPGPRL,GQIPGPRLVL,LQFVQQAGVC,AGVCGPGMQF,HQCFSSGNSA,IKEDPQPARF,RDAAELGAAM,AELGAAMPGL,LQPRGAGVQL,VQLGAATGPG,CSKRVVQRQM,RQMPDKTQPG,GEHQCFSSGN	CRC
C22orf43	c.55A>G	p.K19E	MGNILTCCINSHCGWPRG[p.K19E]EDAPCYESDTDIYETVAAATSESTTV	WPRGEDAPC,GEDAPCYES,WPRGEDAPCY	TGCT
C2orf44	c.1368T>A	p.N456K	IMLEEEPSITSGESQTTYSTFSAPL[p.N456K]KKANRKKLIESLSPDFCHQNKGLLLT	YSTFSAPLK,STFSAPLKK,PLKKANRKK,SAPLKKANR,TYSTFSAPLK,YSTFSAPLKK,STFSAPLKKA,SAPLKKANRK,FSAPLKKANR	CLL
C2orf53	c.815C>A	p.P272H	VEYPICLVCLRPRSPSCPLPRYRTG[p.P272H]HRLLAFPQLLPCVQGQESGPLRIGIG	RYRTGHRLL,RTGHRLLAF,HRLLAFPQL,RYRTGHRLLA,LPRYRTGHRL,YRTGHRLLAF,GHRLLAFPQL,HRLLAFPQLL	LUAD
C2orf71	c.3675_3676insAGC	p.1225_1226insS	GRPQPPTLDPTSTSYESQLGQNSSS[p.1225_1226insS]SEESPKKDTEPGSSPCSPELQGGTRRAS	SSSSEESPK,SSSSEESPKK,SQLGQNSSSS	KIRC
C2orf81	c.943A>C	p.T315P	LELRSEGVPCIASGVLVSYPSVGGA[p.T315P]PRPSASCQQQRAGHSDVRLSAHHHRM	YPSVGGAPR,SYPSVGGAPR	ACC
C3	c.2670delC	p.P890fs	LLHNPAFCSLATTKRRHQQTVTIPP[p.P890fs]SPRCPFHMSSCR*	TVTIPPSPR,IPPSPRCPF,QTVTIPPSPR,SPRCPFHMSS,HQQTVTIPPS	STAD
C3orf15	c.1655G>A	p.R552Q	RTCHALQEDEKLVKKAEKQVTLALQ[p.R552Q]QQRNLHEHKVSLVENHLAGLEGRALA	VTLALQQQR,QQRNLHEHK,KQVTLALQQ,QQQRNLHEH,QVTLALQQQR,KQVTLALQQQ,LQQQRNLHEH,QQRNLHEHKV	CLL
C3orf20	c.2219G>T	p.R740L	IISSQNYTSTGQLQWLLNTLYNHQQ[p.R740L]LGRGSPCIQCRYDSYRLLQYDLDSPL	LYNHQQLGR,QQLGRGSPC,TLYNHQQLGR,HQQLGRGSPC,QQLGRGSPCI	LUAD
C3orf23	c.649C>T	p.R217C	SWLDNNGKSAVKKLKNSLPLRKELD[p.R217C]CLKDELSHQLQLSDIRWQRSWGIAHR	CLKDELSHQL,KELDCLKDEL,LPLRKELDCL	UCEC
C3orf30	c.681C>A	p.D227E	AERRTSEQITHRLSKLSERRPSVQI[p.D227E]ESGSSVPSDQSPSVQIDSGSSVPSDQ	VQIESGSSV,IESGSSVPS,SVQIESGSSV,VQIESGSSVP	LUSC
C3orf39	c.997C>T	p.R333W	LALAQEFQMKTVTVSLEDHTFADVV[p.R333W]WLVSNASMLVSMHGAQLVTTLFLPRG	TFADVVWLV,WLVSNASML,HTFADVVWL,DVVWLVSNA,VWLVSNASM,HTFADVVWLV,WLVSNASMLV,VWLVSNASML,VVWLVSNASM	CRC
C3orf62	c.554G>A	p.R185Q	SNMPLNNSSQEVTKDLLDMIDHTSI[p.R185Q]QTIEELAGKIEFENELNHMCGHCQDS	QTIEELAGK,IDHTSIQTI,TSIQTIEEL,MIDHTSIQTI,HTSIQTIEEL,QTIEELAGKI	UCEC
C3orf70	c.17C>T	p.S6L	MSAAA[p.S6L]LPASERGWKSEKLDEAQALARSCAAR	AAALPASER,SAAALPASER,AALPASERGW	BLCA,CESC
C4orf21	c.2398G>C	p.E800Q	SKDTEAHISEPEDLGKIRSPPPDHV[p.E800Q]QVETAREGKQYWNPRNSSELSGLVNT	VQVETAREG	CESC
C5orf30	c.10G>A	p.D4N	MEV[p.D4N]NINGESRSTLTTLPFPGAEANSPGKA	EVNINGESR	CRC

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C5orf4	c.341G>A	p.R114Q	LFFWSFNGLLLVVDTTGKPNFISRY[p.R114Q]QIQVGKNEPVDPVKLRQSIRTVLFNQ	FISRYQIQV,ISRYQIQVGK,KPNFISRYQI,YQIQVGKNEP	CRC
C5orf65	c.734A>G	p.Q245R	PRAAGAPRPRLLLRTGSLDESLGPL[p.Q245R]RAAAGFVQTALARKLSPEAPAPSSAT	SLGPLRAAA,GPLRAAAGF,RAAAGFVQTA,ESLGPLRAAA,DESLGPLRAA	ACC
C6orf170	c.2171A>C	p.K724T	RTGAINECVTFIFNRYAKKLQVSRH[p.K724T]TKFGYGVLVTRVASTAAGGIALKKSG	KLQVSRHTK,VSRHTKFGY,HTKFGYGVL,LQVSRHTKF,RHTKFGYGV,TKFGYGVLV,KLQVSRHTKF,KKLQVSRHTK,VSRHTKFGYG,HTKFGYGVLV,QVSRHTKFGY,RHTKFGYGVL,TKFGYGVLVT	CRC
C6orf89	c.172_173insC	p.P58fs	GMSEKAIEKFIRQLLEKNEPQRPPP[p.P58fs]AVSSPYSCV*	AVSSPYSCV,EPQRPPPAV,PPPAVSSPY,RPPPAVSSPY	STAD
C7	c.2059C>A	p.R687S	GMSLEGPSAFLCGSSLKWSPEMKNA[p.R687S]SCVQKENPLTQAVPKCQRWEKLQNSR	EMKNASCVQK,SPEMKNASCV	LUAD
C7orf49	c.389delG	p.G130fs	GSSSEEEDSGKQALAPGLSPSQRPG[p.G130fs]VPALPVAGALRRRRKRMC*	SQRPGVPAL,AGALRRRRK,GALRRRRKR,ALRRRRKRM,RPGVPALPV,GLSPSQRPGV,VAGALRRRRK,SPSQRPGVPA,RPGVPALPVA,VPALPVAGAL,ALRRRRKRMC,SQRPGVPALP	STAD
C7orf50	c.535delC	p.L179fs	RARELTVQKAEALMRELDEEGSDPP[p.L179fs]CRGGPSASDRCCSCSPSGFSAGRGRCPVQGCLRPHRVQLLRRWGPGSPAGQRLSKGFQLLRWWGPGSPAPEPRKGPFPPPDPPWPVTAVTVMAGSVPSAQSVDALESPGPLALEGPSSPRNLLWREMSIFLPGIF*	RLSKGFQLL,VMAGSVPSA,NLLWREMSI,CLRPHRVQL,EMSIFLPGI,LSKGFQLLR,MSIFLPGIF,RPHRVQLLR,RVQLLRRWG,RWWGPGSPA,LWREMSIFL,TVMAGSVPS,APEPRKGPF,WPVTAVTVM,GPSSPRNLL,LLWREMSIF,RRWGPGSPA,QRLSKGFQL,SKGFQLLRW,KGFQLLRWW,LESPGPLAL,REMSIFLPG,DPPWPVTAV,TVMAGSVPSA,LLWREMSIFL,FSAGRGRCPV,CLRPHRVQLL,RLSKGFQLLR,REMSIFLPGI,RGRCPVQGCL,RPHRVQLLRR,GSPAGQRLSK,CSPSGFSAGR,LALEGPSSPR,FPPPDPPWPV,TAVTVMAGSV,GPGSPAGQRL,VPSAQSVDAL,SPRNLLWREM,EMSIFLPGIF,RCCSCSPSGF,LRRWGPGSPA,RRWGPGSPAG,GQRLSKGFQL,QRLSKGFQLL,LSKGFQLLRW,FQLLRWWGPG,LRWWGPGSPA,ALESPGPLAL,LEGPSSPRNL,RNLLWREMSI,NLLWREMSIF,CPVQGCLRPH,WPVTAVTVMA,PPWPVTAVTV,GPFPPPDPPW,GPSSPRNLLW	STAD
C7orf57	c.88G>A	p.E30K	SKELQGATHRYAPCDWYYHVPVKRS[p.E30K]KKAVDAPPASQIPGLSNLGDSHSENL	HVPVKRSKK,KKAVDAPPA,YYHVPVKRSK,RSKKAVDAPP,VPVKRSKKAV	HNSC
C7orf58	c.418G>T	p.G140W	HQHILTQHGYTVVIAEERLNAGLGP[p.G140W]WLLEQGDLGSWDLLICLSSKKAEGTP	RLNAGLGPW,RLNAGLGPWL	LUAD
C7orf58	c.713G>T	p.R238L	PSVCLDQGMQLKPSTSSHLLKTVKP[p.R238L]LVWKPGDWSREQLNETTVLAPHETIF	LLKTVKPLV,KTVKPLVWK,HLLKTVKPL,LKTVKPLVW,HLLKTVKPLV,LVWKPGDWSR,SHLLKTVKPL,LLKTVKPLVW	LUAD
C7orf63	c.28G>A	p.A10T	MWTEEAGAT[p.A10T]TEAQESGIRNKSSSSSQIPVVGVVTE	EEAGATTEA,TEEAGATTEA	CRC
C9orf131	c.1024delC	p.P342fs	GYETHLETTGHKKMPQAFEPPMPPP[p.P342fs]ANPQLLCQNPEKLALKEDLLYLRTSGEPWDTERNLRPLSLQCQSLALP*	LALKEDLLY,ALKEDLLYL,SLQCQSLAL,KLALKEDLL,QLLCQNPEK,MPPPANPQL,ERNLRPLSL,YLRTSGEPW,CQNPEKLAL,FEPPMPPPA,QLLCQNPEKL,KLALKEDLLY,CQNPEKLALK,LYLRTSGEPW,ALKEDLLYLR,MPPPANPQLL,RPLSLQCQSL,LALKEDLLYL,TERNLRPLSL,LSLQCQSLAL,GEPWDTERNL	STAD
C9orf174	c.406C>T	p.R136W	ITNHREKKLQQSTKYWCLNQSAESL[p.R136W]WICAMRGGENRPPARVQSSSEELELR	ESLWICAMR,NQSAESLWI,AESLWICAM,QSAESLWICA,CLNQSAESLW,SAESLWICAM	BRCA
CABP5	c.433delC	p.R145fs	NGDGEITLVELQQAMQRLLGERLTP[p.R145fs]GRSLRLSGRLMLMETAQLTLKSL*	RLSGRLMLM,LMLMETAQL,MLMETAQLT,RLTPGRSLR,RSLRLSGRL,SLRLSGRLM,ERLTPGRSL,LRLSGRLML,LMETAQLTL,RLMLMETAQL,MLMETAQLTL,RLTPGRSLRL,LMETAQLTLK,RSLRLSGRLM,SLRLSGRLML,SGRLMLMETA,ETAQLTLKSL,GERLTPGRSL,LRLSGRLMLM	STAD
CACHD1	c.2159C>A	p.S720Y	SLMDKAFDPTRRQWYLHAVANPGLI[p.S720Y]YLTGPYLDVGGAGYVVTISHTIHSSS	AVANPGLIY,LIYLTGPYL,YLTGPYLDV,GLIYLTGPY,VANPGLIYL,AVANPGLIYL,GLIYLTGPYL,IYLTGPYLDV,HAVANPGLIY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CACNA1A	c.1994C>T	p.T665M	NFDEGTPPTNFDTFPAAIMTVFQIL[p.T665M]MGEDWNEVMYDGIKSQGGVQGGMVFS	LMGEDWNEV,IMTVFQILM,FQILMGEDW,MGEDWNEVM,MGEDWNEVMY,ILMGEDWNEV,LMGEDWNEVM,VFQILMGEDW,AIMTVFQILM	CRC
CACNA1A	c.2315C>A	p.S772Y	EVSPLSAANMSIAVKEQQKNQKPAK[p.S772Y]YVWEQRTSEMRKQNLLASREALYNEM	PAKYVWEQR,NQKPAKYVW,YVWEQRTSEM,QQKNQKPAKY	LUAD
CACNA1C	c.2129C>T	p.S710L	RRSTFDNFPQSLLTVFQILTGEDWN[p.S710L]LVMYDGIMAYGGPSFPGMLVCIYFII	ILTGEDWNL,LTGEDWNLV,GEDWNLVMY,NLVMYDGIM,TGEDWNLVMY,ILTGEDWNLV,LVMYDGIMAY,LTGEDWNLVM	UCEC
CACNA1D	c.3218G>T	p.R1073L	AKSNPEECRGLFILYKDGDVDSPVV[p.R1073L]LERIWQNSDFNFDNVLSAMMALFTVS	SPVVLERIW,DVDSPVVLER,LERIWQNSDF	LUAD
CACNA2D1	c.1055C>A	p.A352E	AKGITDYKKGFSFAFEQLLNYNVSR[p.A352E]ENCNKIIMLFTDGGEERAQEIFNKYN	RENCNKIIM,RENCNKIIML	LUAD
CACNA2D3	c.994G>A	p.A332T	CLNGTLVQADRTNKEHFREHLDKLF[p.A332T]TKGIGMLDIALNEAFNILSDFNHTGQ	KLFTKGIGM,REHLDKLFT,KLFTKGIGML	CRC
CACNB2	c.1823G>A	p.R608H	ASHRDHNHRDETHGSSDHRHRESRH[p.R608H]HSRDVDREQDHNECNKQRSRHKSKDR	RHRESRHHSR,RESRHHSRDV	CRC
CACNG3	c.400G>A	p.V134I	ILSVTLLFFGGLCVAASEFHRSRHN[p.V134I]IILSAGIFFVSAGLSNIIGIIVYISA	RSRHNIILS,FHRSRHNII,HRSRHNIIL,SRHNIILSA,RSRHNIILSA,EFHRSRHNII,FHRSRHNIIL,SEFHRSRHNI	CRC
CACNG3	c.413C>T	p.A138V	TLLFFGGLCVAASEFHRSRHNVILS[p.A138V]VGIFFVSAGLSNIIGIIVYISANAGD	ILSVGIFFV,VILSVGIFF,NVILSVGIF,SRHNVILSV,VILSVGIFFV,RSRHNVILSV,LSVGIFFVSA,NVILSVGIFF,RHNVILSVGI,HNVILSVGIF	CRC
CACNG3	c.694C>T	p.R232W	LRAKSHSEFLKKSTFARLPPYRYRF[p.R232W]WRRSSSRSTEPRSRDLSPISKGFHTI	RYRFWRRSS,RFWRRSSSR,PPYRYRFWR,PYRYRFWRR,YRFWRRSSS,LPPYRYRFW,RLPPYRYRFW,RYRFWRRSSS,RFWRRSSSRS,LPPYRYRFWR,PPYRYRFWRR,YRYRFWRRSS	LUAD
CACNG5	c.361G>A	p.G121R	MIRSATPFPLVSLFFMFIGFILNNI[p.G121R]RHIRPHRTILAFVSGIFFILSGLSLV	FILNNIRHI,NIRHIRPHR,ILNNIRHIR,RHIRPHRTI,GFILNNIRHI,FIGFILNNIR,FILNNIRHIR,NNIRHIRPHR,RHIRPHRTIL	CRC
CACNG8	c.437T>G	p.V146G	LRVVRASSIFPILSAILLLLGGVCV[p.V146G]GASRVYKSKRNIILGAGILFVAAGLS	LLGGVCVGA,CVGASRVYK,GASRVYKSK,VCVGASRVY,LLLGGVCVGA,VGASRVYKSK,GVCVGASRVY	BLCA
CADM1	c.569C>T	p.S190L	NCTAMASKPATTIRWFKGNTELKGK[p.S190L]LEVEEWSDMYTVTSQLMLKVHKEDDG	LEVEEWSDM,TELKGKLEV,LEVEEWSDMY	CRC
CADPS	c.2875C>A	p.R959S	DAALEVQPPDTWDSFPLFQLLNDFL[p.R959S]STDYNLCNGKFHKHLQDLFAPLVVRY	LNDFLSTDY,FLSTDYNLC,DFLSTDYNL,LLNDFLSTDY,STDYNLCNGK,FQLLNDFLST,NDFLSTDYNL	LUAD
CADPS	c.3217G>A	p.A1073T	PSWMAAIYDADNGSGTSEDLFWKLD[p.A1073T]TLQTFIRDLHWPEEEFGKHLEQRLKL	KLDTLQTFI,WKLDTLQTF,KLDTLQTFIR,FWKLDTLQTF,WKLDTLQTFI	CRC
CALB2	c.180G>C	p.K60N	YIEGKELENFFQELEKARKGSGMMS[p.K60N]NSDNFGEKMKEFMQKYDKNSDGKIEM	NSDNFGEKM,GMMSNSDNF,SNSDNFGEK,MSNSDNFGEK,SGMMSNSDNF	CESC
CALB2	c.772C>T	p.R258C	KEMNIQQLTNYRKSVMSLAEAGKLY[p.R258C]CKDLEIVLCSEPPM*	KLYCKDLEI,KLYCKDLEIV,LYCKDLEIVL	LUAD
CALCB	c.242G>C	p.R81T	DYVQMKASELKQEQETQGSSSAAQK[p.R81T]TACNTATCVTHRLAGLLSRSGGMVKS	AQKTACNTA,KTACNTATCV,AQKTACNTAT	CESC
CALD1	c.1018G>A	p.E340K	ERMREEEKRAAEERQRIKEEEKRAA[p.E340K]KERQRIKEEEKRAAEERQRIKEEEKR	AAKERQRIK,RAAKERQRI,RAAKERQRIK	CLL
CALN1	c.691G>A	p.V231I	LNETSGNCQTEFEGVHSQKQNRQTC[p.V231I]IRKSLICAFAMAFIISVMLIAANQIL	KQNRQTCIR,QNRQTCIRK,CIRKSLICA,RQTCIRKSL,IRKSLICAF,KQNRQTCIRK,SQKQNRQTCI,CIRKSLICAF,RQTCIRKSLI	GBM
CAMK2B	c.392G>T	p.G131V	EYYSEADASHCIQQILEAVLHCHQM[p.G131V]VVVHRDLKPENLLLASKCKGAAVKLA	AVLHCHQMV,VLHCHQMVV,MVVVHRDLK,AVLHCHQMVV,VLHCHQMVVV,QMVVVHRDLK,EAVLHCHQMV,HQMVVVHRDL	LUAD
CAMSAP1	c.1396_1397insA	p.T466fs	RHRSNSLTRVDGQPRGAAIAWPEKK[p.T466fs]NQACVPANTFCSTSRCEL*	VPANTFCST,QACVPANTF,KKNQACVPA,WPEKKNQACV,NQACVPANTF	BLCA

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CAMSAP1	c.1396delA	p.T466fs	RHRSNSLTRVDGQPRGAAIAWPEKK[p.T466fs]PGLRPSQHLLLYITLRVVKWIPALATASAWPAPSAKTVWHPTLLI*	LLLYITLRV,LLYITLRVV,RVVKWIPAL,GLRPSQHLL,VVKWIPALA,SAWPAPSAK,HLLLYITLR,KWIPALATA,LYITLRVVK,ASAWPAPSA,SAKTVWHPT,KTVWHPTLL,RPSQHLLLY,LATASAWPA,TVWHPTLLI,IPALATASA,WPAPSAKTV,SQHLLLYIT,VKWIPALAT,AKTVWHPTL,HLLLYITLRV,LLLYITLRVV,ALATASAWPA,GLRPSQHLLL,YITLRVVKWI,RVVKWIPALA,WIPALATASA,LLYITLRVVK,ASAWPAPSAK,LYITLRVVKW,TLRVVKWIPA,SAKTVWHPTL,KTVWHPTLLI,LRPSQHLLLY,TASAWPAPSA,KPGLRPSQHL,RPSQHLLLYI,IPALATASAW,WPAPSAKTVW,SQHLLLYITL,LRVVKWIPAL,VKWIPALATA,AKTVWHPTLL	KICH
CANT1	c.392A>G	p.K131R	RIAVIADLDTESRAQEENTWFSYLK[p.K131R]RGYLTLSDSGDKVAVEWDKDHGVLES	YLKRGYLTL,NTWFSYLKR,SYLKRGYLT,WFSYLKRGY,FSYLKRGYL,YLKRGYLTLS,SYLKRGYLTL,TWFSYLKRGY,ENTWFSYLKR	PRAD
CAPNS1	c.906_911delGCTGGT	p.LV303del	LHTSSELQSPSSYFASRPWVRAKGL[p.LV303del]LGFPVLTLHPPLPSGCS*	GLLGFPVLT,WVRAKGLLG,VRAKGLLGF,AKGLLGFPV,KGLLGFPVL,GLLGFPVLTL,RAKGLLGFPV,WVRAKGLLGF,RPWVRAKGLL,AKGLLGFPVL	TGCT
CAPRIN2	c.37G>A	p.E13K	MEVQVSQASLGF[p.E13K]KLTSVEKSLREWSRLSREVIAWLCPS	SLGFKLTSV,VSQASLGFK,GFKLTSVEK,SQASLGFKL,QVSQASLGFK,LGFKLTSVEK,KLTSVEKSLR,SQASLGFKLT,FKLTSVEKSL	CRC
CARD11	c.1268G>A	p.R423Q	IEKDKYRKQIRELEEKNDEMRIEMV[p.R423Q]QREACIVNLESKLRRLSKDSNNLDQS	EMRIEMVQR,DEMRIEMVQ,IEMVQREAC,MRIEMVQREA,IEMVQREACI,VQREACIVNL	CRC
CARD11	c.1876G>A	p.E626K	LDDDSHERYSFGPSSIHSSSSSHQS[p.E626K]KGLDAYDLEQVNLMFRKFSLERPFRP	SSSSSHQSK,HQSKGLDAY,HSSSSSHQSK,SHQSKGLDAY	DLBCL
CARD11	c.279G>C	p.E93D	SKINRAGRLLDILHTKGQRGYVVFL[p.E93D]DSLEFYYPELYKLVTGKEPTRRFSTI	FLDSLEFYY,GYVVFLDSL,VVFLDSLEF,VFLDSLEFY,FLDSLEFYYP,VVFLDSLEFY,YVVFLDSLEF,RGYVVFLDSL,VFLDSLEFYY,DSLEFYYPEL	DLBCL
CARD11	c.3195C>G	p.I1065M	ANIEAVAAKNKHCLLEAGIGCTRDL[p.I1065M]MKSNIYPIVLFIRVCEKNIKRFRKLL	LMKSNIYPI,RDLMKSNIY,MKSNIYPIV,DLMKSNIYPI,LMKSNIYPIV,GIGCTRDLMK,CTRDLMKSNI,MKSNIYPIVL	LUAD
CARM1	c.605C>T	p.A202V	LQNHTDFKDKIVLDVGCGSGILSFF[p.A202V]VAQAGARKIYAVEASTMAQHAEVLVK	ILSFFVAQA,FVAQAGARK,SFFVAQAGA,FFVAQAGAR,LSFFVAQAG,GILSFFVAQA,FVAQAGARKI,SFFVAQAGAR,VAQAGARKIY,CGSGILSFFV,LSFFVAQAGA	GBM
CASC1	c.161G>A	p.R54Q	ERRLKEEEEARLKYEKEEMERLEIQ[p.R54Q]QIEKEKWHRLEAKDLERRNEELEELY	RLEIQQIEK,MERLEIQQI	CRC
CASC3	c.1808C>T	p.P603L	MNLPHPGLHPHQTPAPLPNPGLYPP[p.P603L]LVSMSPGQPPPQQLLAPTYFSAPGVM	GLYPPLVSM,NPGLYPPLV,GLYPPLVSMS,LPNPGLYPPL	STAD
CASC3	c.1934C>T	p.P645L	TYFSAPGVMNFGNPSYPYAPGALPP[p.P645L]LPPPHLYPNTQAPSQVYGGVTYYNPA	YAPGALPPL,LPPLPPPHL,ALPPLPPPHL,PYAPGALPPL,LPPLPPPHLY	STAD
CASC3	c.1973C>T	p.S658L	PSYPYAPGALPPPPPHLYPNTQAP[p.S658L]LQVYGGVTYYNPAQQQVQPKPSPPRR	NTQAPLQVY,LYPNTQAPL,LQVYGGVTY,APLQVYGGV,HLYPNTQAPL,LQVYGGVTYY,QAPLQVYGGV,YPNTQAPLQV	STAD
CASC3	c.695C>T	p.S232F	RQRKLWKDEGRWEHDKFREDEQAPK[p.S232F]FRQELIALYGYDIRSAHNPDDIKPRR	KFRQELIAL,APKFRQELI,REDEQAPKF,FRQELIALY,KFRQELIALY,EQAPKFRQEL	STAD
CASD1	c.2341delT	p.F781fs	DLAQIIIPKDNSSLLKRLACIAAFF[p.F781fs]VDSSSYHPFKINQNIRFQKF*	DSSSYHPFK,INQNIRFQK,AFFVDSSSY,LACIAAFFV,HPFKINQNI,VDSSSYHPF,FKINQNIRF,NQNIRFQKF,FVDSSSYHPF,RLACIAAFFV,KINQNIRFQK,INQNIRFQKF,AAFFVDSSSY,HPFKINQNIR,DSSSYHPFKI	STAD
CASP14	c.13C>T	p.R5W	MSNP[p.R5W]WSLEEEKYDMSGARLALILCVTKARE	NPWSLEEEKY	CRC
CASP5	c.67delA	p.R23fs	MAAVPRVEGVFIFLIEDSGKKK[p.R23fs]GVRILKLCSKVSFRVDWITS*	RILKLCSKV,KVSFRVDWI,KLCSKVSFR,KKKGVRILK,GKKKGVRIL,KKGVRILKL,LKLCSKVSF,SKVSFRVDW,KLCSKVSFRV,GVRILKLCSK,SGKKKGVRIL,ILKLCSKVSF,KKKGVRILKL,SKVSFRVDWI	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CASP8	c.1413delA	p.R471fs	YEVSNKDDKKNMGKQMPQPTFTLRK[p.R471fs]NLSSLLIDGAILFVLFCFVFLRQNLALSPRLECSGVISAHRKLRLPGSGHSPASASRVAGTTGARHHTWLIF*	LLIDGAILF,LIDGAILFV,ILFVLFCFV,FVLFCFVFL,TLRKNLSSL,FVFLRQNLA,VLFCFVFLR,CSGVISAHR,SGVISAHRK,RVAGTTGAR,DGAILFVLF,AILFVLFCF,LFVLFCFVF,CFVFLRQNL,VFLRQNLAL,RQNLALSPR,VISAHRKLR,KLRLPGSGH,GARHHTWLI,LPGSGHSPA,LRKNLSSLL,RKNLSSLLI,ARHHTWLIF,IDGAILFVL,FTLRKNLSSL,NLSSLLIDGA,LLIDGAILFV,LIDGAILFVL,AILFVLFCFV,FVFLRQNLAL,TLRKNLSSLL,RLECSGVISA,RLPGSGHSPA,FVLFCFVFLR,CSGVISAHRK,IDGAILFVLF,GAILFVLFCF,ILFVLFCFVF,RQNLALSPRL,KLRLPGSGHS,SGHSPASASR,ASRVAGTTGA,GARHHTWLIF,RVAGTTGARH,ECSGVISAHR,GVISAHRKLR,QPTFTLRKNL,SLLIDGAILF	STAD
CAST	c.1917T>A	p.D639E	DDALDKLSDSLGQRQPDPDENKPME[p.D639E]EKVKEKAKAEHRDKLGERDDTIPPEY	MEEKVKEKA	CLL
CATSPER4	c.1274C>T	p.T425M	MIVEEVRAIRFNQEQESEVLNRRSS[p.T425M]MSGSLETTSSKDIRQMSQQQDLLSAL	SMSGSLETT,EVLNRRSSM,RRSSMSGSL,NRRSSMSGSL,SEVLNRRSSM	KIRC
CBFB	c.454G>A	p.E152K	FDEERAQQEDALAQQAFEEARRRTR[p.E152K]KFEDRDRSHREEMEVRVSQLLAVTGK	EARRRTRKF,RTRKFEDRDR,RKFEDRDRSH,EEARRRTRKF	CRC
CBLL1	c.413delA	p.E138fs	PIKIYGRMIPCKHVFCYDCAILHEK[p.E138fs]REIRCVQAVVILCSELSSVHEVLSSCVALFKGAREHICLRETYRLISTIAI*	ILCSELSSV,VLSSCVALF,CLRETYRLI,LSSCVALFK,CVALFKGAR,HICLRETYR,GAREHICLR,TYRLISTIA,ILHEKREIR,EIRCVQAVV,ELSSVHEVL,EVLSSCVAL,ETYRLISTI,REIRCVQAV,RCVQAVVIL,SELSSVHEV,HEVLSSCVA,ALFKGAREH,EHICLRETY,RETYRLIST,YRLISTIAI,REHICLRET,HEKREIRCV,VILCSELSSV,SVHEVLSSCV,ALFKGAREHI,VLSSCVALFK,TYRLISTIAI,EHICLRETYR,ETYRLISTIA,EVLSSCVALF,REIRCVQAVV,SELSSVHEVL,HEVLSSCVAL,REHICLRETY,RETYRLISTI	STAD
CBLN3	c.206delC	p.P69fs	ECLVVCEPGRAAAGGPGGAALGEAP[p.P69fs]LGEWHLLRSEATTMSQQGKPAMAPVGPSTSTRSW*	AMAPVGPST,ATTMSQQGK,QGKPAMAPV,APLGEWHLL,MSQQGKPAM,APVGPSTST,LLRSEATTM,GAALGEAPL,GEWHLLRSE,GPSTSTRSW,EAPLGEWHLL,TTMSQQGKPA,KPAMAPVGPS,TMSQQGKPAM,HLLRSEATTM,GEAPLGEWHL,GEWHLLRSEA,QQGKPAMAPV,AMAPVGPSTS	STAD
CBWD6	c.304_305insG	p.E102fs	ESGEGSALEKSLAVSQGGELYEEWL[p.E102fs]GT*	GELYEEWLGT	KICH
CC2D2A	c.3850C>T	p.R1284C	ESQEDEKLLQATEKFQAECALKFPN[p.R1284C]CQCLTTVIDISGKTVFITRYLKPLNP	LKFPNCQCL,FPNCQCLTT,ALKFPNCQCL,CQCLTTVID,FPNCQCLTTV,AECALKFPNC	CRC
CCDC108	c.3492delC	p.P1164fs	LERDPTPCELTYKVPTRHSMSQIPP[p.P1164fs]SSPL*	SQIPPSSPL,MSQIPPSSPL	STAD
CCDC111	c.1250G>T	p.R417L	GIKGGIRRWNYFFPEELLVYDICKY[p.R417L]LWCENIGRAHKSNNIMILVDLKNEVW	LVYDICKYL,VYDICKYLW,YLWCENIGR,CKYLWCENI,LLVYDICKYL,YLWCENIGRA,LVYDICKYLW	LUAD
CCDC120	c.22A>G	p.I8V	MEVKGQL[p.I8V]VSSPTFNAPAALFGEAAPQVKSERLR	LVSSPTFNA,GQLVSSPTF,MEVKGQLVS,QLVSSPTFNA,MEVKGQLVSS,KGQLVSSPTF	KIRC
CCDC121	c.1190G>T	p.W397L	IEQAQKLTATQSHLENRKQQLQQEQ[p.W397L]LYLESLIQARQRLQGSHNQCLNRQDV	QQLQQEQLY,KQQLQQEQL,QEQLYLESL,QLYLESLIQA,KQQLQQEQLY,LYLESLIQAR,RKQQLQQEQL,QQLQQEQLYL,QQEQLYLESL,QEQLYLESLI	LUSC
CCDC132	c.2512C>T	p.R838C	NIYVDALLKEFEQFNRRLNEVSKRV[p.R838C]CIPLPVSNILWEHCIRLANRTIVEGY	CIPLPVSNI,VSKRVCIPL,KRVCIPLPV,NEVSKRVCI,EVSKRVCIPL,SKRVCIPLPV	UCEC
CCDC135	c.937G>A	p.E313K	AEKAKPDALHGLRVHSWVLVLSGKR[p.E313K]KVPENFFIDPFTGHSYSTQDEHFLGI	GKRKVPENF,RKVPENFFI,WVLVLSGKRK,KRKVPENFF,GKRKVPENFF	HNSC
CCDC144A	c.3791C>T	p.S1264L	NTTSIKTQMELTIKDLESEISRIKT[p.S1264L]LQADFNKTELERYKELYLEEVKVRES	KTLQADFNK,ISRIKTLQA,RIKTLQADF,SEISRIKTL,LQADFNKTEL,RIKTLQADFN,EISRIKTLQA,SRIKTLQADF	UCEC
CCDC148	c.1260delA	p.K420fs	KEEEKEKLWKKKELLQRAEKKKKIK[p.K420fs]NTGPRKNRSGKKWK*	KIKNTGPRK,KNRSGKKWK,RKNRSGKKW	STAD

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CCDC15	c.1463C>A	p.P488H	ILPKYQDQNFLPKDQNFLSRDQHVL[p.P488H]HKDQDILPKYQDQNFLPKDQNFLSRD	LSRDQHVLH,LSRDQHVLHK	CLL
CCDC152	c.457G>C	p.E153Q	GYKKEISKLYQDMQRKVELNEEKHK[p.E153Q]QLIEKKEMEISELNAKLRSQEKEKQN	KHKQLIEKK,KQLIEKKEM,QLIEKKEMEI,HKQLIEKKEM	CESC
CCDC153	c.598_599insC	p.P200fs	QWDGAALRLHARHKEQQRQFGLTPP[p.P200fs]WIFEATSP*	LTPPWIFEA,RQFGLTPPW,QFGLTPPWI,FGLTPPWIF,RQFGLTPPWI,GLTPPWIFEA,QFGLTPPWIF,QRQFGLTPPW	STAD
CCDC153	c.599delC	p.P200fs	QQWDGAALRLHARHKEQQRQFGLTP[p.P200fs]LDL*	QRQFGLTPL,RQFGLTPLD,RQFGLTPLDL,QQRQFGLTPL	STAD
CCDC159	c.994G>T	p.A332S	KELSDIWSAVHVLQNSIDSLTLCSG[p.A332S]SCPKASSLRGHKGHQCLSPPLPSWDS	TLCSGSCPK,TLCSGSCPKA,LTLCSGSCPK,GSCPKASSLR	TGCT
CCDC168	c.15058G>T	p.D5020Y	GYTLSNSKGPVQPTAQGEEKGGLRI[p.D5020Y]YMEDKMLPKCTDLKAKQLLLSDILNT	YMEDKMLPK,GLRIYMEDK,EEKGGLRIY,LRIYMEDKM,RIYMEDKML,IYMEDKMLPK,GEEKGGLRIY,EEKGGLRIYM	UCEC
CCDC169-SOHLH2	c.485A>G	p.K162R	LDDCIFNMVLLKVPSSLSAEELEAI[p.K162R]RLIRFGKKKNTHSLFVFIIPENFKGC	AIRLIRFGK,RLIRFGKKK,ELEAIRLIR,LEAIRLIRF,EELEAIRLI,AEELEAIRL,AIRLIRFGKK,EAIRLIRFGK,EELEAIRLIR,AEELEAIRLI	STAD
CCDC19	c.620G>T	p.R207L	KLRMEQEEELKDMSKIILNAKCHAI[p.R207L]LDAQILEKQQIQKELDTEEKRLDQMM	ILDAQILEK,LNAKCHAIL,HAILDAQIL,ILNAKCHAIL,AILDAQILEK	LUAD
CCDC19	c.836G>T	p.R279L	RIRGRRQIVEQMEKNQEERSLLAEQ[p.R279L]LEQEKEQMLEYMEQLQEEDLKDMERR	LEQEKEQML,EERSLLAEQL	LUAD
CCDC36	c.626G>T	p.R209I	AQNDLVFEAVQDKGNMEQAILEMKK[p.R209I]IFEARQGEFIEMKSNLKHLEVLVAQQ	IFEARQGEF,EMKKIFEAR,AILEMKKIF,LEMKKIFEA,KIFEARQGEF,QAILEMKKIF	UCEC
CCDC53	c.172C>T	p.R58C	FVVHTVQFLNRFSTVCEEKLADLSL[p.R58C]CIQQIETTLNILDAKLSSIPGLDDVT	KLADLSLCI,ADLSLCIQQI	CESC
CCDC60	c.689G>A	p.R230H	GQKWEHFITAPKTKKFKIPTMRVTN[p.R230H]HKPSRRGSTLSLSRASGGSSPQSSMI	PTMRVTNHK,RVTNHKPSR,VTNHKPSRR,RVTNHKPSRR	CRC
CCDC79	c.1319A>C	p.N440T	IEQLEREGNEEEIQRENYQDNISSM[p.N440T]TISIQNTWKHLHADRIGRGSKAEDED	NISSMTISI,TISIQNTWK,MTISIQNTW,YQDNISSMT,YQDNISSMTI,MTISIQNTWK,SMTISIQNTW	CLL
CCDC81	c.776G>T	p.R259I	NRERKCKLKDQSDKEEGTRDISSPK[p.R259I]ILRDRQALFPAKVTNVSLLEKFERSE	ILRDRQALF,DISSPKILR,RDISSPKIL,KILRDRQAL,GTRDISSPKI,KILRDRQALF	CRC
CCDC88A	c.2031_2032insA	p.K677fs	ITCEKIEALEQENSELERENRKLKK[p.K677fs]NIG*	RENRKLKKNI	STAD
CCDC88C	c.5553_5554insC	p.P1851fs	QKLGAPEALGGRETGSHTLQSPAPP[p.P1851fs]QLP*	LQSPAPPQL,TLQSPAPPQL	CRC
CCKAR	c.811C>A	p.L271M	QKKSAKERKPSTTSSGKYEDSDGCY[p.L271M]MQKTRPPRKLELRQLSTGSSSRANRI	YMQKTRPPR,MQKTRPPRK,YEDSDGCYM,YMQKTRPPRK,MQKTRPPRKL,CYMQKTRPPR	LUAD
CCKBR	c.706G>A	p.V236M	SARVRQTWSVLLLLLLFFIPGVVMA[p.V236M]MAYGLISRELYLGLRFDGDSDSDSQS	FIPGVVMAM,VVMAMAYGL,VMAMAYGLI,AMAYGLISR,MAMAYGLIS,FIPGVVMAMA,VVMAMAYGLI,MAMAYGLISR,FFIPGVVMAM,MAYGLISREL,IPGVVMAMAY	CRC
CCNB3	c.2794G>A	p.A932T	ETLLKKPLALKMSTINEAVLFEDMI[p.A932T]TLNEKPTTGKELSFKEPLALQESPTY	VLFEDMITL	CLL
CCR5	c.554G>T	p.S185I	SLPGIIFTRSQKEGLHYTCSSHFPY[p.S185I]IQYQFWKNFQTLKIVILGLVLPLLVM	SSHFPYIQY,HFPYIQYQF,IQYQFWKNF,FPYIQYQFW,CSSHFPYIQY,YTCSSHFPYI,SHFPYIQYQF,HFPYIQYQFW,YIQYQFWKNF	KIRC
CCZ1	c.642G>C	p.E214D	IFGGISFFPLDKMTYLKIQSFINRM[p.E214D]DESLNIVKYTAFLYNDQLIWSGLEQD	FINRMDESL,RMDESLNIV,DESLNIVKY,RMDESLNIVK,SFINRMDESL,MDESLNIVKY	KIRC
CD101	c.1781G>A	p.R594Q	SDLKVPLTVTWQFQPASSHIFHQLI[p.R594Q]QITHNGTIEWGNFLSRFQKKTKVSQS	HIFHQLIQI,IQITHNGTI,SHIFHQLIQI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CD101	c.847G>T	p.D283Y	PDETWMFITKKQTDQTTLRIQPAVK[p.D283Y]YFQVNITADSLFAEGKPLELVCLVVS	RIQPAVKYF,KYFQVNITA,AVKYFQVNI,LRIQPAVKY,QPAVKYFQV,IQPAVKYFQV,TLRIQPAVKY,LRIQPAVKYF,VKYFQVNITA	CRC
CD109	c.1409T>A	p.L470Q	AYFLGSKSSMAVHSLFKSPSKTYIQ[p.L470Q]QKTRDENIKVGSPFELVVSGNKRLKE	KTYIQQKTR,PSKTYIQQK,QQKTRDENIK,IQQKTRDENI	CLL
CD163L1	c.2161G>A	p.V721M	SDMELRLVGGSSRCAGKVEVNVQGA[p.V721M]MGILCANGWGMNIAEVVCRQLECGSA	VEVNVQGAM,MGILCANGW,EVNVQGAMGI,KVEVNVQGAM,VQGAMGILCA,AMGILCANGW	GBM
CD180	c.683A>C	p.N228T	SLNFNGNNVKGIELGAFDSTIFQSL[p.N228T]TFGGTPNLSVIFNGLQNSTTQSLWLG	LTFGGTPNL,STIFQSLTF,SLTFGGTPNL,FQSLTFGGTP	CRC
CD1B	c.122G>T	p.W41L	GNSEHAFQGPTSFHVIQTSSFTNST[p.W41L]LAQTQGSGWLDDLQIHGWDSDSGTAI	FTNSTLAQT,SSFTNSTLA,TSSFTNSTL,LAQTQGSGW,QTSSFTNSTL,TSSFTNSTLA,TLAQTQGSGW	LUAD
CD1C	c.265C>T	p.R89C	TIIFLHNWSKGNFSNEELSDLELLF[p.R89C]CFYLFGLTREIQDHASQDYSKYPFEV	LSDLELLFC,ELLFCFYLF,LFCFYLFGL,CFYLFGLTR,SDLELLFCF,LELLFCFYL,LSDLELLFCF,LLFCFYLFGL,SDLELLFCFY,FCFYLFGLTR,LELLFCFYLF	SKCM
CD1D	c.74delT	p.L25fs	MGCLLFLLLWALLQAWGSAEVPQRL[p.L25fs]SPSAASRSRPSPIAAGRAPTAWRGWGSCRRTAGATTRTPSAL*	RLSPSAASR,ASRSRPSPI,RSRPSPIAA,AGRAPTAWR,VPQRLSPSA,SPIAAGRAP,AAGRAPTAW,AASRSRPSPI,ASRSRPSPIA,RSRPSPIAAG,AWRGWGSCRR,TAWRGWGSCR,EVPQRLSPSA,VPQRLSPSAA,RPSPIAAGRA,SPIAAGRAPT,AEVPQRLSPS,IAAGRAPTAW	GBM
CD1E	c.253T>G	p.F85V	GDLQTHGWDTVLGTIRFLKPWSHGN[p.F85V]VSKQELKNLQSLFQLYFHSFIQIVQA	KPWSHGNVS,FLKPWSHGNV,KPWSHGNVSK,HGNVSKQELK	STAD
CD209	c.847G>A	p.A283T	WEWTFFQGNCYFMSNSQRNWHDSIT[p.A283T]TCKEVGAQLVVIKSAEEQNFLQLQSS	DSITTCKEV	GBM
CD4	c.492delG	p.Q164fs	TLESPPGSSPSVQCRSPRGKNIQGG[p.Q164fs]RPSPCLSWSSRIVAPGHALSCRTRRRWSSK*	CLSWSSRIV,RIVAPGHAL,RTRRRWSSK,RGKNIQGGR,SSRIVAPGH,HALSCRTRR,LSWSSRIVA,SSRIVAPGHA,HALSCRTRRR,IQGGRPSPCL,GGRPSPCLSW,SRIVAPGHAL,SPCLSWSSRI	STAD
CD55	c.466G>A	p.E156K	PGYRREPSLSPKLTCLQNLKWSTAV[p.E156K]KFCKKKSCPNPGEIRNGQIDVPGGIL	NLKWSTAVK,STAVKFCKK,WSTAVKFCK,TAVKFCKKK,LKWSTAVKF,KWSTAVKFCK,WSTAVKFCKK,STAVKFCKKK,NLKWSTAVKF	UCEC
CD7	c.521delC	p.P174fs	ASALPAPPTGSALPDPQTASALPDP[p.P174fs]QQPLPSLRPWR*	ALPDPQQPL,DPQQPLPSL,QPLPSLRPW,SALPDPQQPL,QQPLPSLRPW	KIRC
CD79B	c.589T>C	p.Y197H	LFIIVPIFLLLDKDDSKAGMEEDHT[p.Y197H]HEGLDIDQTATYEDIVTLRTGEVKWS	EEDHTHEGL,MEEDHTHEGL,HEGLDIDQTA	DLBCL
CD79B	c.589T>G	p.Y197D	LFIIVPIFLLLDKDDSKAGMEEDHT[p.Y197D]DEGLDIDQTATYEDIVTLRTGEVKWS	MEEDHTDEGL	DLBCL
CD93	c.838delG	p.D280fs	PLCVSPKYGCNFNNGGCHQDCFEGG[p.D280fs]MAPSSAAADQDSGCWMTW*	GMAPSSAAA,HQDCFEGGM,FEGGMAPSS,FEGGMAPSSA	STAD
CDAN1	c.1936_1937insC	p.L646fs	GERKQFAVVLLSLRLLAKFLGFVAF[p.L646fs]PAIPGA*	FLGFVAFPA,FVAFPAIPG,LGFVAFPAI,FLGFVAFPAI,FVAFPAIPGA,KFLGFVAFPA	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CDC14A	c.369delC	p.N123fs	AYAVIYLKKTPEEAYRALLSGSNPP[p.N123fs]IFHSGMLPLEIALTISPFSTVCRESERDYNMDFLTLRHLMWMNMNIMSELKMVTSTGLFQENF*	NMDFLTLRH,LLSGSNPPI,GMLPLEIAL,MLPLEIALT,LTISPFSTV,HLMWMNMNI,NIMSELKMV,IMSELKMVT,STVCRESER,NMNIMSELK,IFHSGMLPL,DYNMDFLTL,KMVTSTGLF,YNMDFLTLR,EIALTISPF,MNMNIMSEL,PPIFHSGML,LPLEIALTI,LMWMNMNIM,LSGSNPPIF,LEIALTISP,RESERDYNM,SERDYNMDF,MDFLTLRHL,LRHLMWMNM,MNIMSELKM,SELKMVTST,LKMVTSTGL,RDYNMDFLT,ALLSGSNPPI,MLPLEIALTI,ALTISPFSTV,NMDFLTLRHL,FLTLRHLMWM,HLMWMNMNIM,WMNMNIMSEL,TISPFSTVCR,MNMNIMSELK,DFLTLRHLMW,RHLMWMNMNI,TLRHLMWMNM,FSTVCRESER,DYNMDFLTLR,EIALTISPFS,NPPIFHSGML,ELKMVTSTGL,LLSGSNPPIF,LEIALTISPF,LKMVTSTGLF,FHSGMLPLEI,SGMLPLEIAL,SERDYNMDFL,RDYNMDFLTL,YNMDFLTLRH,MDFLTLRHLM,NMNIMSELKM,TSTGLFQENF,LPLEIALTIS	STAD
CDC14B	c.1123C>T	p.R375C	GSVIGPQQQFLVMKQTNLWLEGDYF[p.R375C]CQKLKGQENGQHRAAFSKLLSGVDDI	LEGDYFCQKL	CRC
CDC25C	c.965delA	p.K322fs	ENLNRPRLKQVEKFKDNTIPDKVKK[p.K322fs]SIFLAKESSGRAYV*	KVKKSIFLA,IPDKVKKSI,AKESSGRAY,KESSGRAYV,FLAKESSGRA,KVKKSIFLAK,LAKESSGRAY,IFLAKESSGR,IPDKVKKSIF	STAD
CDC27	c.1379delT	p.L460fs	ITKLDSSIISEGKISTITPQIQAFN[p.L460fs]HKKQQQKV*	QIQAFNHKK,AFNHKKQQQK	UCS
CDC27	c.1665T>G	p.D555E	EVRRIENYRVEGMEIYSTTLWHLQK[p.D555E]EVALSVLSKDLTDMDKNSPEAWCAAG	TLWHLQKEV,LQKEVALSV,EVALSVLSK,WHLQKEVAL,QKEVALSVL,KEVALSVLS,HLQKEVALSV,LQKEVALSVL,TTLWHLQKEV,KEVALSVLSK	CRC
CDC27	c.1712A>T	p.N571I	STTLWHLQKDVALSVLSKDLTDMDK[p.N571I]ISPEAWCAAGNCFSLQREHDIAIKFF	MDKISPEAW,KISPEAWCAA	TGCT
CDC27	c.271delA	p.I91fs	CTTPQCKYLLAKCCVDLSKLAEGEQ[p.I91fs]SYLVECLISRKAMMILLLSLVIQLALLFHCWDMYIARQIGLPKDQNVTKRALV*	AMMILLLSL,MMILLLSLV,LLLSLVIQL,LLSLVIQLA,SLVIQLALL,ALLFHCWDM,CLISRKAMM,LISRKAMMI,LVECLISRK,IARQIGLPK,LVIQLALLF,LFHCWDMYI,MYIARQIGL,ISRKAMMIL,KLAEGEQSY,LLFHCWDMY,YLVECLISR,HCWDMYIAR,SRKAMMILL,RKAMMILLL,MILLLSLVI,LSLVIQLAL,DQNVTKRAL,AEGEQSYLV,GEQSYLVEC,VECLISRKA,WDMYIARQI,KLAEGEQSYL,CLISRKAMMI,KAMMILLLSL,AMMILLLSLV,MMILLLSLVI,ILLLSLVIQL,LLLSLVIQLA,LLSLVIQLAL,LLFHCWDMYI,YIARQIGLPK,YLVECLISRK,SLVIQLALLF,IQLALLFHCW,ISRKAMMILL,ALLFHCWDMY,SKLAEGEQSY,GEQSYLVECL,VECLISRKAM,SRKAMMILLL,LALLFHCWDM	BLCA
CDC27	c.724C>T	p.P242S	LESSNSKYSLNTDSSVSYIDSAVIS[p.P242S]SDTVPLGTGTSILSKQVQNKPKTGRS	VISSDTVPL,AVISSDTVPL,DSAVISSDTV	CESC,TGCT
CDC42BPA	c.2023C>A	p.P675T	EQSEHYSKQLENELEGLKQKQISYS[p.P675T]TGVCSIEHQQEITKLKTDLEKKSIFY	KQISYSTGV,SYSTGVCSI,KQKQISYST,KQKQISYSTG,KQISYSTGVC,ISYSTGVCSI	BRCA
CDCA7L	c.1215delC	p.P405fs	GPCLRNRYGEDVRSALLDPDWVCPP[p.P405fs]VVGSAIAATVGSVTAAVPQESSFIWPSFMVMTMLRNIWRAYKRSW*	AIAATVGSV,FIWPSFMVM,MVMTMLRNI,TMLRNIWRA,ATVGSVTAA,TVGSVTAAV,MTMLRNIWR,SSFIWPSFM,SFMVMTMLR,SFIWPSFMV,MLRNIWRAY,LRNIWRAYK,RNIWRAYKR,CPPVVGSAI,WPSFMVMTM,AAVPQESSF,ESSFIWPSF,VMTMLRNIW,QESSFIWPS,VPQESSFIW,DPDWVCPPV,VVGSAIAATV,ATVGSVTAAV,SSFIWPSFMV,FIWPSFMVMT,FMVMTMLRNI,MTMLRNIWRA,SAIAATVGSV,MLRNIWRAYK,PSFMVMTMLR,SFIWPSFMVM,IWPSFMVMTM,MVMTMLRNIW,TMLRNIWRAY,VMTMLRNIWR,WVCPPVVGSA,ESSFIWPSFM,WPSFMVMTML,TAAVPQESSF,IAATVGSVTA,QESSFIWPSF,DPDWVCPPVV,CPPVVGSAIA	CRC
CDH1	c.727G>A	p.E243K	EPLDRERIATYTLFSHAVSSNGNAV[p.E243K]KDPMEILITVTDQNDNKPEFTQEVFK	VSSNGNAVK,AVSSNGNAVK,AVKDPMEILI	BRCA

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CDH1	c.760G>T	p.D254Y	TLFSHAVSSNGNAVEDPMEILITVT[p.D254Y]YQNDNKPEFTQEVFKGSVMEGALPGT	TVTYQNDNK,MEILITVTY,YQNDNKPEF,ITVTYQNDNK,TYQNDNKPEF	STAD
CDH10	c.1045G>A	p.E349K	DTQEGIITVKKPLDYESRRLYTLKV[p.E349K]KAENTHVDPRFYYLGPFKDTTIVKIS	RLYTLKVKA,KVKAENTHV,LKVKAENTH,LKVKAENTHV	CRC
CDH10	c.1414C>T	p.R472C	LDRELSQWHNLTVIAAEINNPKETT[p.R472C]CVAVFVRILDVNDNAPQFAVFYDTFV	TTCVAVFVR,ETTCVAVFV,KETTCVAVF,ETTCVAVFVR,TTCVAVFVRI,NPKETTCVAV,KETTCVAVFV	LUAD
CDH10	c.1731C>G	p.S577R	NGFNRHEISTYLLPVVISDNDYPIQ[p.S577R]RSTGTLTIRVCACDSQGNMQSCSAEA	YPIQRSTGT,IQRSTGTLT,QRSTGTLTI,IQRSTGTLTI,YPIQRSTGTL	LUAD
CDH10	c.382C>A	p.R128S	IIDEKTGDIHATRRIDREEKAFYTL[p.R128S]SAQAINRRTLRPVEPESEFVIKIHDI	TLSAQAINR,FYTLSAQAI,EKAFYTLSA,KAFYTLSAQ,YTLSAQAINR,AFYTLSAQAI,KAFYTLSAQA,TLSAQAINRR,SAQAINRRTL,EEKAFYTLSA,REEKAFYTLS	LUAD
CDH11	c.1070A>C	p.K357T	KKPVDFETKRAYSLKVEAANVHIDP[p.K357T]TFISNGPFKDTVTVKISVEDADEPPM	TFISNGPFK,NVHIDPTFI,ANVHIDPTF,PTFISNGPFK,PTFISNGPF,PTFISNGPFK,EAANVHIDPT,AANVHIDPTF,DPTFISNGPF	STAD
CDH12	c.2020G>A	p.D674N	SKEDIRDNVIHYDDEGGGEEDTQAF[p.D674N]NIGALRNPKVIEENKIRRDIKPDSLC	TQAFNIGAL,QAFNIGALR,NIGALRNPK,DTQAFNIGA,EEDTQAFNI,TQAFNIGALR,DTQAFNIGAL,GEEDTQAFNI	CRC
CDH12	c.2116C>A	p.P706T	PKVIEENKIRRDIKPDSLCLPRQRP[p.P706T]TMEDNTDIRDFIHQRLQENDVDPTAP	LCLPRQRPTM,RQRPTMEDNT	HNSC
CDH18	c.2161G>T	p.A721S	KLTPRHQTSSTLESIDVQEFIKQRL[p.A721S]SEADLDPSVPPYDSLQTYAYEGQRSE	FIKQRLSEA,KQRLSEADL,SEADLDPSV	LUAD
CDH18	c.583G>A	p.A195T	EMSDMGTSVLQVTATDADDPTYGNS[p.A195T]TRVVYSILQGQPYFSVDPKTGVIRTA	STRVVYSIL,YGNSTRVVY,NSTRVVYSI,STRVVYSILQ	GBM
CDH2	c.1639G>T	p.D547Y	QDPDRYMQQNIRYTKLSDPANWLKI[p.D547Y]YPVNGQITTIAVLDRESPNVKNNIYN	KIYPVNGQI,DPANWLKIY,YPVNGQITT,YPVNGQITTI,LKIYPVNGQI	CRC
CDH20	c.1298C>A	p.P433H	IQIISAKDPDVTNNSIRYSIDRSSD[p.P433H]HGRFFYVDITTGALMTARPLDREEFS	SSDHGRFFY,RSSDHGRFF,HGRFFYVDI,RSSDHGRFFY,SSDHGRFFYV,IDRSSDHGRF	LUAD
CDH20	c.401C>T	p.A134V	IDDTTGDIHAIQRLDREERAQYTLR[p.A134V]VQALDRRTGRPMEPESEFIIKIQDIN	QYTLRVQAL,AQYTLRVQA,AQYTLRVQAL,YTLRVQALDR,RAQYTLRVQA,TLRVQALDRR	CRC
CDH23	c.1207G>A	p.V403I	EGLNSMFEVYLVGNNSHHFIISPTS[p.V403I]IQGKADIRIRVAIPLDYETVDRYDFD	HFIISPTSI,IQGKADIRI,IISPTSIQGK,HHFIISPTSI	STAD
CDH23	c.3395T>A	p.F1132Y	ASVPEDIPEGHSILQLKATDADEGE[p.F1132Y]YGRVWYRILHGNHGNNFRIHVSNGLL	ATDADEGEY,EYGRVWYRI,YGRVWYRIL,DEGEYGRVW,EYGRVWYRIL,KATDADEGEY,EGEYGRVWYR,GEYGRVWYRI,DEGEYGRVWY	KIRC
CDH23	c.531C>A	p.F177L	FIVNATDPDLGAGGSVLYSFQPPSQ[p.F177L]LFAIDSARGIVTVIRELDYETTQAYQ	FQPPSQLFA,SFQPPSQLF,QLFAIDSAR,YSFQPPSQL,SQLFAIDSA,QPPSQLFAI,FQPPSQLFAI,LYSFQPPSQL,YSFQPPSQLF,SFQPPSQLFA,SQLFAIDSAR	CRC
CDH6	c.709C>A	p.Q237K	SETGIIKTALLNMDRENREQYQVVI[p.Q237K]KAKDMGGQMGGLSGTTTVNITLTDVN	KAKDMGGQM,REQYQVVIKA,YQVVIKAKDM,IKAKDMGGQM	LUAD
CDH7	c.673C>A	p.Q225K	PYFSVEPKTGVIKTALPNMDREAKD[p.Q225K]KYLLVIQAKDMVGQNGGLSGTTSVTV	KYLLVIQAK,EAKDKYLLV,REAKDKYLL,AKDKYLLVI,NMDREAKDKY,EAKDKYLLVI,REAKDKYLLV	HNSC
CDH9	c.1569C>A	p.F523L	ENAKPGQLIQTVSVMDKDDPPRGHK[p.F523L]LFFEPVPEFTLNPNFTIVDNKDNTAG	LFFEPVPEF,KLFFEPVPEF,RGHKLFFEPV	CRC
CDHR1	c.652A>G	p.R218G	QAGATLDYERSRTHYITVVAKDGGG[p.R218G]GLHGADVVFSATTTVTVNVEDVQDMA	GLHGADVVF,GGLHGADVVF	MM

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CDK11B	c.237_239delAGA	p.E79del	SPYRREDSMEDRGEEDDSLAIKPPQ[p.E79del]MSRKEKVHHRKDEKRKEKCRHHSHSAEG	SLAIKPPQM,AIKPPQMSR,AIKPPQMSRK,LAIKPPQMSR	HNSC
CDK13	c.2638C>A	p.R880S	DFGLARLYSSEESRPYTNKVITLWY[p.R880S]SPPELLLGEERYTPAIDVWSCGCILG	TLWYSPPEL,LWYSPPELL,WYSPPELLL,ITLWYSPPEL,TLWYSPPELL,LWYSPPELLL	LUAD
CDK16	c.322C>T	p.R108C	GSDGESDQASATSSDEVQSPVRVRM[p.R108C]CNHPPRKISTEDINKRLSLPADIRLP	RMCNHPPRK,RVRMCNHPP,RVRMCNHPPR,RMCNHPPRKI	CRC
CDK5RAP2	c.4776C>G	p.H1592Q	LDEEHRRLREASGEGWKGQDPFRDL[p.H1592Q]QSLLMEIQALRLQLERSIETSSTLQS	RDLQSLLMEI,LQSLLMEIQA,DPFRDLQSLL	KIRC
CDKAL1	c.1226_1227CA>TG	p.P409L	YKFPSLFINQFYPRPGTPAAKMEQV[p.P409L]LAQVKKQRTKDLSRVFHSYSPYDHKIG	KMEQVLAQV,AAKMEQVLA,AKMEQVLAQ,MEQVLAQVK,KMEQVLAQVK,LAQVKKQRTK,QVLAQVKKQR,TPAAKMEQVL,AKMEQVLAQV	TGCT
CDKN2A	c.247C>T	p.H83Y	RVAELLLLHGAEPNCADPATLTRPV[p.H83Y]YDAAREGFLDTLVVLHRAGARLDVRD	VYDAAREGF,LTRPVYDAA,TLTRPVYDAA,LTRPVYDAAR,DPATLTRPVY	HNSC
CDKN2A	c.322G>T	p.D108Y	HDAAREGFLDTLVVLHRAGARLDVR[p.D108Y]YAWGRLPVDLAEELGHRDVARYLRAA	RYAWGRLPV,GARLDVRYA,AGARLDVRY,ARLDVRYAW,RAGARLDVRY,RLDVRYAWGR,GARLDVRYAW,VRYAWGRLPV,YAWGRLPVDL	LUSC
CDR1	c.92T>C	p.V31A	DVDFLEDVPLLEDIPLLEDVPLLED[p.V31A]APLLEDTSRLEDINLMEDMALLEDVD	PLLEDAPLL,VPLLEDAPL,APLLEDTSRL,LEDVPLLEDA,VPLLEDAPLL	KIRP
CDYL	c.179C>G	p.A60G	VSAPDGPSDPSISVSSEQSGAQQPP[p.A60G]GLQVERIVDKRKNKKGKTEYLVRWKG	AQQPPGLQV,AQQPPGLQVE	TGCT
CEACAM5	c.1918C>A	p.L640I	CHSASNPSPQYSWRINGIPQQHTQV[p.L640I]IFIAKITPNNNGTYACFVSNLATGRN	HTQVIFIAK,IPQQHTQVI,PQQHTQVIF,QQHTQVIFI,TQVIFIAKI,HTQVIFIAKI,IPQQHTQVIF,QQHTQVIFIA	CRC
CELF4	c.925G>C	p.A309P	YLNPMAAFAAAQMQQMAALNMNGLA[p.A309P]PAPMTPTSGGSTPPGITAPAVPSIPS	APAPMTPTS,LNMNGLAPA,MNGLAPAPM,ALNMNGLAPA,GLAPAPMTPT,NMNGLAPAPM	LUAD
CELSR1	c.1841delG	p.G614fs	AVDADSGENARLHYRLVDTASTFLG[p.G614fs]AAALGLRILPPPLTSPSRSTTAPVGSQCVPSWTARRWSTTASGWRRWTTARPP*	FLGAAALGL,STFLGAAAL,STTASGWRR,GLRILPPPL,PSRSTTAPV,TARRWSTTA,SGWRRWTTA,GWRRWTTAR,CVPSWTARR,DTASTFLGA,TASTFLGAA,GAAALGLRI,AAALGLRIL,VGSQCVPSW,SQCVPSWTA,RRWSTTASG,RWSTTASGW,RRWTTARPP,VPSWTARRW,ILPPPLTSPS,TFLGAAALGL,RWSTTASGWR,ASGWRRWTTA,SGWRRWTTAR,SQCVPSWTAR,DTASTFLGAA,TASTFLGAAA,TTAPVGSQCV,WTARRWSTTA,SPSRSTTAPV,ASTFLGAAAL,GAAALGLRIL,RRWSTTASGW	STAD
CELSR2	c.34_35insCGC	p.16_17insP	MRSPATGVPLPTPPPP[p.16_17insP]PLLLLLLLLLPPPLLGDQVGPCRSLGSR	LPTPPPPPL,TPPPPPLLL,LPTPPPPPLL,TPPPPPLLLL	ACC
CELSR2	c.50T>C	p.L17P	MRSPATGVPLPTPPPP[p.L17P]PLLLLLLLPPPLLGDQVGPCRSLGS	LPTPPPPPL,TPPPPPLLL,LPTPPPPPLL,TPPPPPLLLL	TGCT
CEP152	c.61G>A	p.E21K	MSLDFGSVALPVQNEDEEYD[p.E21K]KEDYEREKELQQLLTDLPHDMLDDDL	KEDYEREKEL	CRC
CEP192	c.6173C>T	p.S2058L	TEVYDLPQRPNDVQLFYGSMCKIIL[p.S2058L]LVIGEFRDCISSREFLQPSSKASLES	SMCKIILLV,ILLVIGEFR,IILLVIGEF,GSMCKIILLV,SMCKIILLVI,IILLVIGEFR,KIILLVIGEF	BLCA
CEP44	c.758C>T	p.S253L	VNVNPEITALQTMLAECQENLKKLT[p.S253L]LIEKRLDCLEQKMKGKVMVDENTWTN	QENLKKLTL,TLIEKRLDCL,NLKKLTLIEK,CQENLKKLTL,KKLTLIEKRL,QENLKKLTLI	UCEC

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CERCAM	c.254_260delCGGCTGT	p.A85fs	RARMALWCATDHNVDNTTEMLQEWL[p.A85fs]GAMTMLLWSGGLRASPGSTQMKRVPSTGPKKGTSF*	MLQEWLGAM,WLGAMTMLL,TMLLWSGGL,LLWSGGLRA,MLLWSGGLR,RVPSTGPKK,RASPGSTQM,STQMKRVPS,MTMLLWSGG,TQMKRVPST,LQEWLGAMT,QEWLGAMTM,LGAMTMLLW,MLQEWLGAMT,MTMLLWSGGL,MLLWSGGLRA,TMLLWSGGLR,RASPGSTQMK,EWLGAMTML,WLGAMTMLLW,MKRVPSTGPK,EMLQEWLGAM,LQEWLGAMTM,QEWLGAMTML,LRASPGSTQM,TQMKRVPSTG,TEMLQEWLGA	KIRC
CERS3	c.285G>T	p.E95D	FVASPLAKSFGIKETVRKVTPNTVL[p.E95D]DNFFKHSTRQPLQTDIYGLAKKCNLT	NTVLDNFFK,TVLDNFFKH,DNFFKHSTR,TPNTVLDNF,VTPNTVLDNF,TPNTVLDNFF	CRC
CETN3	c.189delA	p.K63fs	TDKDEAIDYHELKVAMRALGFDVKK[p.K63fs]LMY*	GFDVKKLMY,LGFDVKKLM,LGFDVKKLMY,RALGFDVKKL	STAD
CFB	c.940_941CG>AT	p.R314M	INVSVAIITFASEPKVLMSVLNDNS[p.R314M]MDMTEVISSLENANAYKDHENGTGTNTY	VLNDNSMDM,NSMDMTEVI,MSVLNDNSM,LMSVLNDNSM,VLNDNSMDMT,MDMTEVISSL	SKCM
CFDP1	c.386_387insC	p.P129fs	ARKKKEDELWASFLNDVGPKSKVPP[p.P129fs]KYTS*	GPKSKVPPK,KSKVPPKYT,KSKVPPKYTS	LUAD
CFHR5	c.1322G>A	p.R441H	LCKENYLLPEAKEIVCKDGRWQSLP[p.R441H]HCVESTAYCGPPPSINNGDTTSFPLS	SLPHCVEST,RWQSLPHCV,LPHCVESTA,SLPHCVESTA,LPHCVESTAY,GRWQSLPHCV,WQSLPHCVES	CESC
CFI	c.111delA	p.K37fs	CFHLRFCKVTYTSQEDLVEKKCLAK[p.K37fs]NILTSPAIKSSASHGRDALRAPVFVNYRISAQRMALQCVQLTGEASQHTVNKRVWNVFIQGQSF*	RMALQCVQL,TVNKRVWNV,AQRMALQCV,NILTSPAIK,ASHGRDALR,RAPVFVNYR,RISAQRMAL,LRAPVFVNY,VNYRISAQR,DALRAPVFV,SPAIKSSAS,SASHGRDAL,APVFVNYRI,NVFIQGQSF,KKCLAKNIL,AKNILTSPA,KNILTSPAI,RDALRAPVF,YRISAQRMA,SQHTVNKRV,VNKRVWNVF,RMALQCVQLT,ALRAPVFVNY,FVNYRISAQR,RAPVFVNYRI,TVNKRVWNVF,LAKNILTSPA,KNILTSPAIK,AIKSSASHGR,KSSASHGRDA,HGRDALRAPV,SASHGRDALR,EASQHTVNKR,LTSPAIKSSA,LTGEASQHTV,HTVNKRVWNV,SPAIKSSASH,SSASHGRDAL,AKNILTSPAI,GRDALRAPVF,VNYRISAQRM,YRISAQRMAL,QRMALQCVQL,VQLTGEASQH,SQHTVNKRVW,WNVFIQGQSF,VEKKCLAKNI	STAD
CGB8	c.52A>G	p.T18A	MEMFQGLLLLLLLSMGG[p.T18A]AWASREMLRPRCRPINATLAVEKEGC	AWASREMLR,GGAWASREM,GAWASREML,GAWASREMLR,MGGAWASREM	BLCA
CHCHD4	c.236C>T	p.T79M	PCLGGMASGPCGEQFKSAFSCFHYS[p.T79M]MEEIKGSDCVDQFRAMQECMQKYPDL	AFSCFHYSM,SAFSCFHYSM,CFHYSMEEIK,MEEIKGSDCV	HNSC
CHD3	c.1789delC	p.P597fs	WRWGEPPVAVPAPQQADGNPDVPPP[p.P597fs]VLFKADQSESSLSSG*	NPDVPPPVL,KADQSESSL,VPPPVLFKA,DVPPPVLFKA,FKADQSESSL,NPDVPPPVLF	STAD
CHD4	c.2924G>A	p.R975H	LGPHMLRRLKADVFKNMPSKTELIV[p.R975H]HVELSPMQKKYYKYILTRNFEALNAR	HVELSPMQK,IVHVELSPM,TELIVHVEL,HVELSPMQKK,LIVHVELSPM,MPSKTELIVH,TELIVHVELS	CRC,UCEC
CHD5	c.2401G>A	p.A801T	YVVTYTGDKESRSVIRENEFSFEDN[p.A801T]TIRSGKKVFRMKKEVQIKFHVLLTSY	FSFEDNTIR,NTIRSGKKV,TIRSGKKVFR,EFSFEDNTIR,NTIRSGKKVF,NEFSFEDNTI	CRC
CHDH	c.119A>C	p.E40A	ARGALGQQQSLGARALASAGSESRD[p.E40A]AYSYVVVGAGSAGCVLAGRLTEDPAE	AGSESRDAY,SESRDAYSY,ESRDAYSYV,RDAYSYVVV,GSESRDAYSY,ESRDAYSYVV,DAYSYVVVGA,SAGSESRDAY,SESRDAYSYV	ACC
CHEK2	c.1116_1117CA>TG	p.K373E	LKPENVLLSSQEEDCLIKITDFGHS[p.K373E]EILGETSLMRTLCGTPTYLAPEVLVSV	ITDFGHSEI,EILGETSLM,SEILGETSL,TDFGHSEIL,KITDFGHSEI,EILGETSLMR,SEILGETSLM	GBM
CHEK2	c.1117A>G	p.K373E	LKPENVLLSSQEEDCLIKITDFGHS[p.K373E]EILGETSLMRTLCGTPTYLAPEVLVS	ITDFGHSEI,EILGETSLM,SEILGETSL,TDFGHSEIL,KITDFGHSEI,EILGETSLMR,SEILGETSLM	KIRC,PRAD,UCS
CHIT1	c.851_852insC	p.P284fs	LILGMPTYGRSFTLASSSDTRVGAP[p.P284fs]SHRVWHSRPLHQGRRDAGLL*	RVWHSRPLH,RVGAPSHRV,HSRPLHQGR,PSHRVWHSR,HRVWHSRPL,VGAPSHRVW,HQGRRDAGL,RVWHSRPLHQ,HSRPLHQGRR,DTRVGAPSHR,RPLHQGRRDA,SHRVWHSRPL,RVGAPSHRVW,HQGRRDAGLL	KIRC
CHN1	c.792G>C	p.K264N	CGLNVHKQCSKMVPNDCKPDLKHVK[p.K264N]NVYSCDLTTLVKAHTTKRPMVVDMCI	DLKHVKNVY,VKNVYSCDL,NVYSCDLTTL,HVKNVYSCDL	LUAD

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CHN2	c.129C>G	p.I43M	AEEYQPPIWKSYLYQLQQEAPRPKR[p.I43M]MICPREVENRPKYYGREFHGIISREQ	RPKRMICPR,APRPKRMIC,QEAPRPKRM,KRMICPREV,RMICPREVE,MICPREVENR,QQEAPRPKRM	LUSC
CHRNA3	c.67_69delCTG	p.L23del	MGSGPLSLPLALSPPRLLLLLL[p.L23del]SLLPVARASEAEHRLFERLFEDYNEIIR	RLLLLLLSL,RLLLLLLSLL	BLCA
CHRNA4	c.1188C>G	p.S396R	LIESMHKMASAPRFWPEPEGEPPAT[p.S396R]RGTQSLHPPSPSFCVPLDVPAEPGPS	ATRGTQSLH,PPATRGTQSL	LUAD
CHRNA9	c.1082C>A	p.P361Q	WARVVILKYMSRVLFVYDVGESCLS[p.P361Q]QHHSRERDHLTKVYSKLPESNLKAAR	ESCLSQHHSR,CLSQHHSRER,SQHHSRERDH,GESCLSQHHS	LUAD
CIC	c.1521delC	p.R507fs	PEGNKGFGRKVFSPVIRSSFTHCRP[p.R507fs]HWTLSPQGPRILL*	TLSPQGPRI,WTLSPQGPR,SFTHCRPHW,SSFTHCRPH,RPHWTLSPQ,SPQGPRILL,FTHCRPHWTL,RSSFTHCRPH,HWTLSPQGPR,WTLSPQGPRI,SSFTHCRPHW	STAD
CIC	c.3341_3342insC	p.A1114fs	ITAFYSGSPAPTSSAPLAQPSQAPP[p.A1114fs]KPGLHCGHQHNPTCSHHSAQGPASPCHCHPSPD*	AQPSQAPPK,SQAPPKPGL,HQHNPTCSH,SHHSAQGPA,AQGPASPCH,NPTCSHHSA,LAQPSQAPPK,SQAPPKPGLH,HQHNPTCSHH	STAD
CIC	c.3341delC	p.A1114fs	VITAFYSGSPAPTSSAPLAQPSQAP[p.A1114fs]QAWSTLWPPAQPHLQPPFCPRARQPLPLPPQPRLALSPAPQQVP*	ALSPAPQQV,HLQPPFCPR,LWPPAQPHL,AWSTLWPPA,RARQPLPLP,LPLPPQPRL,LPPQPRLAL,QPRLALSPA,AQPHLQPPF,SQAPQAWST,TLWPPAQPH,QPSQAPQAW,APQAWSTLW,TLWPPAQPHL,SQAPQAWSTL,HLQPPFCPRA,RARQPLPLPP,CPRARQPLPL,AQPSQAPQAW,QAWSTLWPPA,LPLPPQPRLA,LALSPAPQQV	STAD
CIITA	c.2182G>A	p.E728K	AESELAFPSFLLQCFLGALWLALSG[p.E728K]KIKDKELPQYLALTPRKKRPYDNWLE	ALWLALSGK,LWLALSGKI,ALWLALSGKI,GALWLALSGK,LWLALSGKIK,KIKDKELPQY	UCEC
CILP2	c.1657G>A	p.V553M	VTFVDPSGEFMDAVRVLPFDPRGAG[p.V553M]MYHEVKAMRKKAPVILHTSQSNTIPL	GMYHEVKAM,MYHEVKAMR,RGAGMYHEVK,MYHEVKAMRK,GMYHEVKAMR,LPFDPRGAGM,AGMYHEVKAM	GBM
CIRH1A	c.749G>T	p.S250I	TGTLVKSHLIANADVQSIAVADQED[p.S250I]IFVVGTAEGTVFHFQLVPVTSNSSEK	AVADQEDIFV,IAVADQEDIF,QEDIFVVGTA	HNSC
CIZ1	c.2003T>C	p.V668A	SEPQHQQRLGEIQHMSQACLLSLLP[p.V668A]APRDVLETEDEEPPPRRWCNTCQLYY	SLLPAPRDV,LLSLLPAPR,CLLSLLPAPR,SLLPAPRDVL,LPAPRDVLET	CRC
CIZ1	c.266T>C	p.L89P	QLLQLQQLLQQSPPQAPLPMAVSRG[p.L89P]PPPQQPQQPLLNLQGTNSASLLNGSM	LPMAVSRGPP	GBM
CKAP2	c.2050T>A	p.*684K	GRETDAFVCRPNAALCRVYYEADTT[p.*684K]KEK*	RVYYEADTTK	CLL
CKAP5	c.1727G>C	p.G576A	AGGPPKKGKPAAPGGAGNTGTKNKK[p.G576A]ALETKEIVEPELSIEVCEEKASAVLP	KNKKALETK,KKALETKEI	TGCT
CLCN2	c.1934_1935insCCG	p.645_645R>RR	ILLGSIERSQVVALLGAQLSPARRR[p.645_645R>RR]RQHMQERRATQTSPLSDQEGPPTPEASV	QLSPARRRR,SPARRRRQH,RRRRQHMQER,SPARRRRQHM	KIRC
CLCNKA	c.371C>A	p.P124Q	YPVALVSFSSGFSQSITPSSGGSGI[p.P124Q]QELKTMLAGVILEDYLDIKNFGAKVV	SGIQELKTM,QELKTMLAG,QELKTMLAGV	LUAD
CLDN23	c.628G>A	p.V210M	CDERCRRRRKGPSAGPRRSSVSTIQ[p.V210M]MEWPEPDLAPAIKYYSDGQHRPPPAQ	RSSVSTIQM,IQMEWPEPD,MEWPEPDLA,IQMEWPEPDL,RRSSVSTIQM,SSVSTIQMEW,MEWPEPDLAP	ACC
CLDN7	c.514T>G	p.S172A	DFYNPLIPTNIKYEFGPAIFIGWAG[p.S172A]AALVILGGALLSCSCPGNESKAGYRV	AIFIGWAGA,FIGWAGAAL,GWAGAALVI,FIGWAGAALV,AIFIGWAGAA,IFIGWAGAAL,GWAGAALVIL,IGWAGAALVI	KIRP
CLEC12B	c.650G>T	p.W217L	MSQPLLMFSFFWLGLSWDSSGRSWF[p.W217L]LEDGSVPSPSLFSTKELDQINGSKGC	FLEDGSVPS,DSSGRSWFL,RSWFLEDGSV	LUAD
CLEC18A	c.1268G>A	p.R423H	GQPDNHGFGNCVELQASAAFNWNNQ[p.R423H]HCKTRNRYICQFAQEHISRWGPGS*	NQHCKTRNR,AAFNWNNQH,AFNWNNQHCK,NWNNQHCKTR,NQHCKTRNRY	CRC

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CLEC4A	c.626G>A	p.R209H	YNESSTFWHPREPSDPNERCVVLNF[p.R209H]HKSPKRWGWNDVNCLGPQRSVCEMMK	VLNFHKSPK,RCVVLNFHK,LNFHKSPKR,VVLNFHKSPK,VLNFHKSPKR,LNFHKSPKRW,NERCVVLNFH	PRAD
CLEC4C	c.536G>T	p.R179L	QWVDQTPYNENVTFWHSGEPNNLDE[p.R179L]LCAIINFRSSEEWGWNDIHCHVPQKS	NLDELCAII,ELCAIINFR,DELCAIINF,GEPNNLDEL	LUSC
CLIC6	c.892C>G	p.Q298E	EGPAGDSMDAEGPAGRARRVSGEPQ[p.Q298E]ESGDGSLSPQAEAIEVAAGESAGRSP	EPQESGDGSL	ACC
CLIP1	c.3052_3053insA	p.S1018fs	AAKKHEEEKKELERKLSDLEKKMET[p.S1018fs]KPQPVSGAESQV*	KMETKPQPV,METKPQPVS,ETKPQPVSGA,KKMETKPQPV	BLCA,KIRP
CLK4	c.203G>T	p.R68L	CKPHHQFKESDCHYLEARSLNERDY[p.R68L]LDRRYVDEYRNDYCEGYVPRHYHRDI	RSLNERDYL,LDRRYVDEY,RDYLDRRYV,YLDRRYVDEY,SLNERDYLDR,NERDYLDRRY	LUAD
CLN3	c.616G>A	p.G206S	ISWWSSGTGGAGLLGALSYLGLTQA[p.G206S]SLSPQQTLLSMLGIPALLLASYFLLL	YLGLTQASL,SLSPQQTLL,ASLSPQQTL,SYLGLTQASL,LSYLGLTQAS,ASLSPQQTLL	LUSC
CLSTN1	c.1844C>T	p.T615M	LEGEDLGELDKAMQHISYLNSRQFP[p.T615M]MPGIRRLKITSTIKCFNEATCISVPP	YLNSRQFPM,RQFPMPGIR,QFPMPGIRR,FPMPGIRRL,MPGIRRLKI,RQFPMPGIRR,SYLNSRQFPM,NSRQFPMPGI	STAD
CLSTN2	c.2276C>T	p.P759L	YSIYGVGSMSRYEQVLHHIRYRNWR[p.P759L]LASLEARRFRIKCSELNGRYTSNEFN	HIRYRNWRL,RYRNWRLAS,RLASLEARR,YRNWRLASL,LASLEARRF,RYRNWRLASL,HIRYRNWRLA,RLASLEARRF,NWRLASLEAR,LASLEARRFR,HHIRYRNWRL,RNWRLASLEA	HNSC
CLUL1	c.1387G>C	p.G463R	SELANQAPETEIIFNSIQVVPRIHE[p.G463R]RNISKQDETMMTDLSILPSSNFTLKI	RIHERNISK,QVVPRIHER,VPRIHERNI,RNISKQDETM	KIRC
CMA1	c.242T>A	p.I81K	IRRNFVLTAAHCAGRSITVTLGAHN[p.I81K]KTEEEDTWQKLEVIKQFRHPKYNTST	TVTLGAHNK,ITVTLGAHNK,KTEEEDTWQK	CLL
CMAS	c.329G>A	p.R110Q	FQSVWVSTDHDEIENVAKQFGAQVH[p.R110Q]QRSSEVSKDSSTSLDAIIEFLNYHNE	HQRSSEVSK,QFGAQVHQR,KQFGAQVHQ,AQVHQRSSEV,KQFGAQVHQR	CRC
CMIP	c.688G>A	p.A230T	EIVSKLLSENTNLTTQEHENIIVAI[p.A230T]TPLLENNHPPPDLCEFFCKHCRERPR	IIVAITPLL,NIIVAITPL,HENIIVAIT,NIIVAITPLL	CLL
CMTM8	c.77G>C	p.S26T	MEEPQRARSHTVTTTASSFAENFST[p.S26T]TSSSFAYDREFLRTLPGFLIVAEIVL	STTSSSFAY,TSSSFAYDR,FSTTSSSFA,AENFSTTSS,NFSTTSSSF,FSTTSSSFAY,TTSSSFAYDR,ENFSTTSSSF,SSFAENFSTT,AENFSTTSSS	TGCT
CNBD1	c.1187T>C	p.L396P	RSIIGFVKLRSNKVKRSQKLVYMGK[p.L396P]PKEKESFGEISVLLQVPFTCTIITKK	KLVYMGKPK,LVYMGKPKEK,MGKPKEKESF	STAD
CNGA4	c.1529A>C	p.K510T	AEIALQEATESRLRGLDQQLDDLQT[p.K510T]TFARLLAELESSALKIAYRIERLEWQ	TFARLLAEL,QLDDLQTTF,LQTTFARLL,QLDDLQTTFA,TTFARLLAEL,QQLDDLQTTF,LQTTFARLLA	STAD
CNKSR2	c.746C>T	p.P249L	SEGLGMYIKSTYDGLHVITGTTENS[p.P249L]LADRCKKIHAGDEVIQVNHQTVVGWQ	SLADRCKKI,NSLADRCKK	TGCT
CNOT3	c.58G>A	p.E20K	MADKRKLQGEIDRCLKKVS[p.E20K]KGVEQFEDIWQKLHNAANANQKEKYE	CLKKVSKGV,KVSKGVEQF,KKVSKGVEQF	PRAD
CNOT6	c.744delT	p.S248fs	QEILSCNADIVSLQEVETEQYYSFF[p.S248fs]W*	TEQYYSFFW	STAD
CNRIP1	c.304C>T	p.R102W	EPDGDRVVYTGTYDTEGVTPTKSGE[p.R102W]WQPIQITMPFTDIGTFETVWQVKFYN	EWQPIQITM,TKSGEWQPI,GEWQPIQIT,WQPIQITMPF,GEWQPIQITM	CRC
CNTFR	c.754G>T	p.D252Y	QTPSTWPDPESFPLKFFLRYRPLIL[p.D252Y]YQWQHVELSDGTAHTITDAYAGKEYI	LILYQWQHV,YRPLILYQW,LYQWQHVEL,RYRPLILYQ,LRYRPLILY,YQWQHVELS,ILYQWQHVEL,PLILYQWQHV,FLRYRPLILY,RYRPLILYQW,YQWQHVELSD	LUAD
CNTN5	c.1136C>T	p.S379F	LEIPNVQLDDAGIYECRAENSRGKN[p.S379F]FFRGQLQVYTYPHWVEKLNDTQLDSG	NSRGKNFFR,FFRGQLQVY,AENSRGKNF,GKNFFRGQL,RGKNFFRGQL,KNFFRGQLQV,NFFRGQLQVY,ENSRGKNFFR,RAENSRGKNF,AENSRGKNFF	SKCM
CNTN5	c.533C>A	p.T178N	IDGTFIISNPSEAKDSGHYQCLATN[p.T178N]NVGSILSREATLQFAYLGNFSGRTRS	YQCLATNNV,LATNNVGSI,CLATNNVGSI,HYQCLATNNV,YQCLATNNVG,LATNNVGSIL	LUSC

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CNTN6	c.2420G>T	p.R807M	NNEGEGSLSTVTIVYSGEDEPQLAP[p.R807M]MGTSLQSFSASEMEVSWNAIAWNRNT	QLAPMGTSL,PMGTSLQSF,APMGTSLQSF,GEDEPQLAPM,PQLAPMGTSL	LUAD
CNTNAP1	c.3086G>T	p.S1029I	EPGTWMRYNLQSALRSAAREFSHML[p.S1029I]IRPVPGYEPGYIPGYDTPGYVPGYHG	FSHMLIRPV,MLIRPVPGY,REFSHMLIR,AAREFSHMLI,HMLIRPVPGY,EFSHMLIRPV,REFSHMLIRP	PRAD
CNTNAP2	c.1185C>A	p.F395L	EPYTVPVFFNATSYLEVPGRLNQDL[p.F395L]LSVSFQFRTWNPNGLLVFSHFADNLG	RLNQDLLSV,LLSVSFQFR,DLLSVSFQF,NQDLLSVSF,LLSVSFQFRT,DLLSVSFQFR,LNQDLLSVSF,QDLLSVSFQF	LUAD
CNTNAP4	c.1307A>C	p.Y436S	LFSELQLISGGILLFLSDGKLKSNL[p.Y436S]SQPGKLPSDITAGVELNDGQWHSVSL	KSNLSQPGK,KLKSNLSQPG,KSNLSQPGKL	KIRC
CNTNAP4	c.34A>T	p.I12F	MLLFYLLVVLS[p.I12F]FDSTKASALTNPNVALFLLADDCDDP	VLSFDSTKA,VVLSFDSTK,FYLLVVLSF,FDSTKASAL,LVVLSFDSTK,LFYLLVVLSF,LSFDSTKASA	CLL
CNTRL	c.553C>T	p.P185S	SKIEGIENMCNLQKLNLAGNEIEHI[p.P185S]SVWLGKKLKSLRVLNLKGNKISSLQD	HISVWLGKK,SVWLGKKLK,EIEHISVWL,NEIEHISVW,ISVWLGKKL,ISVWLGKKLK,NEIEHISVWL	CESC
CNTROB	c.2759_2760insG	p.R920fs	PKTEKPPARKKSGHPAPSSMRSRGG[p.R920fs]SLEMSPPTLSPLCSLIVVILINAH*	TLSPLCSLI,SMRSRGGSL,MSPPTLSPL,RSRGGSLEM,SPLCSLIVV,SLEMSPPTL,LEMSPPTLS,TLSPLCSLIV,SLIVVILINA,EMSPPTLSPL,SSMRSRGGSL,SMRSRGGSLE,RSRGGSLEMS,SPLCSLIVVI,MRSRGGSLEM,GSLEMSPPTL,LEMSPPTLSP	STAD
COBLL1	c.2196A>C	p.K732N	DPLTVKDPICAHGNDDLLPPVDRID[p.K732N]NNSTASYLKNYPLYRQDYNPKPKPSN	IDNNSTASY,RIDNNSTASY,IDNNSTASYL	CRC
COG5	c.1850A>G	p.H617R	TKVVSSQSSFPLAAEQTIISALKAI[p.H617R]RALMENAVQPLLTSVGDAIEAIIITM	ALKAIRALM,AIRALMENA,IISALKAIR,SALKAIRAL,AIRALMENAV,SALKAIRALM,TIISALKAIR,ISALKAIRAL	TGCT
COL14A1	c.3245G>T	p.R1082I	STVGALNKIGTDGTQVAMVQFTDDP[p.R1082I]ITEFKLNAYKTKETLLDAIKHISYKG	FTDDPITEF,ITEFKLNAY,MVQFTDDPI,VQFTDDPIT,FTDDPITEFK,AMVQFTDDPI,ITEFKLNAYK,QFTDDPITEF	CRC
COL15A1	c.2123A>G	p.K708R	ARGPNGSVGEKGDPGNRGLPGPPGK[p.K708R]RGQAGPPGVMGPPGPPGPPGPPGPGC	RGQAGPPGVM	TGCT
COL18A1	c.2652delC	p.G884fs	DRGSRGEKGDPGKDGVGQPGLPGPP[p.G884fs]DPRDLWSTCRSRTDPS*	DLWSTCRSR	KIRP
COL19A1	c.1613C>A	p.P538Q	GPPGLIGSPGLKGQQGSAGSMGPRG[p.P538Q]QPGDVGLPGEHGIPGKQGIKGEKGDP	GPRGQPGDV	LUAD
COL4A6	c.1648C>A	p.L550I	GPAGAPGLVGPLGPSGPKGKKGEPI[p.L550I]ISTIQGMPGDRGDSGSQGFRGVIGEP	KGKKGEPII,KKGEPIISTI,EPIISTIQGM	CRC
COL5A2	c.1546G>T	p.G516W	QGPIGPPGEEGKRGPRGDPGTVGPP[p.G516W]WPVGERGAPGNRGFPGSDGLPGPKGA	GTVGPPWPV,DPGTVGPPW	LUAD
COL5A2	c.1834G>T	p.G612W	LGPLGAPGEDGRPGPPGSIGIRGQP[p.G612W]WSMGLPGPKGSSGDPGKPGEAGNAGV	WSMGLPGPK,SIGIRGQPW,RGQPWSMGL,QPWSMGLPG,GSIGIRGQPW,IGIRGQPWSM	LUAD
COL6A3	c.7133C>A	p.A2378D	GQKGDPGYPGPAGPKGNRGDSIDQC[p.A2378D]DLIQSIKDKCPCCYGPLECPVFPTEL	DSIDQCDLI	TGCT
COL6A3	c.8374G>A	p.D2792N	YFFVVLGIGRKVNIKEVYTFASEPN[p.D2792N]NVFFKLVDKSTELNEEPLMREGRLLP	NVFFKLVDK,FASEPNNVF,ASEPNNVFF,EPNNVFFKL,YTFASEPNNV,ASEPNNVFFK,TFASEPNNVF,FASEPNNVFF,EPNNVFFKLV,SEPNNVFFKL	CRC
COL6A5	c.6671C>T	p.T2224M	QEDFLGGNGFIGQELNSGRESPFVK[p.T2224M]MEDNGSDYLVYLPSQMFEPQKLMINY	KMEDNGSDY,MEDNGSDYL,KMEDNGSDYL,SGRESPFVKM,VKMEDNGSDY,MEDNGSDYLV	GBM
COL9A1	c.632C>A	p.P211Q	GVERSSATLFVDCNRIESLPIKPRG[p.P211Q]QIDIDGFAVLGKLADNPQVSVPFELQ	QIDIDGFAV,GQIDIDGFA,LPIKPRGQI,GQIDIDGFAV	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
COL9A1	c.848delC	p.P283fs	RITPSQTTDERGPPGEQGPPGPPGP[p.P283fs]LEFQASMASTVTEVLRAPRAPRVLQVNRESQELQASLAHLALMD*	FQASMASTV,SMASTVTEV,ELQASLAHL,LQASLAHLA,VLRAPRAPR,ASLAHLALM,VTEVLRAPR,MASTVTEVL,ESQELQASL,GPLEFQASM,LEFQASMAS,RESQELQAS,QELQASLAH,QASLAHLAL,TEVLRAPRA,ASMASTVTEV,SMASTVTEVL,LQASLAHLAL,FQASMASTVT,VLRAPRAPRV,ELQASLAHLA,MASTVTEVLR,TVTEVLRAPR,EVLRAPRAPR,ESQELQASLA,APRAPRVLQV,LEFQASMAST,LRAPRAPRVL,LQVNRESQEL,RESQELQASL,SQELQASLAH,QELQASLAHL,QASLAHLALM	STAD
COPB1	c.1273C>T	p.R425C	NVIPVLMEFLSDNNEAAAADVLEFV[p.R425C]CEAIQRFDNLRMLIVEKMLEVFHAIK	EFVCEAIQR,DVLEFVCEA,FVCEAIQRF,EFVCEAIQRF,DVLEFVCEAI,CEAIQRFDNL	CRC
COQ2	c.196G>T	p.V66L	SFALARAAGAPHGGDLQPPACPEPR[p.V66L]WRQLSLSAAAVVDSAPRPLQPYLRLM	RWRQLSLSA,CPEPRWRQL,EPRWRQLSL,WRQLSLSAA,RWRQLSLSAA,WRQLSLSAAA,QPPACPEPRW	ACC
CORO2A	c.1576T>A	p.*526R	LTQREVQAKQLELEIKNLRMGSEQL[p.*526R]RAETSALLTLRDTTRLHGEV*	QLRAETSAL,TLRDTTRLH,ETSALLTLR,LLTLRDTTR,DTTRLHGEV,LRAETSALL,AETSALLTL,SEQLRAETS,QLRAETSALL,LLTLRDTTRL,NLRMGSEQLR,SEQLRAETSA,EQLRAETSAL,RAETSALLTL	CRC
COX15	c.256C>A	p.L86I	PSKAAERVVGRWLLVCSGTVAGAVI[p.L86I]IGGVTRLTESGLSMVDWHLIKEMKPP	VIIGGVTRL	CRC
COX6A1	c.23C>T	p.S8L	MAVVGVS[p.S8L]LVSRLLGRSRPQLGRPMSSGAHGEEG	MAVVGVSLV,SLVSRLLGR,AVVGVSLVSR,VSLVSRLLGR,LVSRLLGRSR	BLCA
CPAMD8	c.2352delC	p.P784fs	TDEAVPAFQPHTGSLVAVAPSRHPP[p.P784fs]EQRREKGLSSPKHGFGIVSTSVTHLVRGHSV*	IVSTSVTHL,STSVTHLVR,REKGLSSPK,VSTSVTHLV,SPKHGFGIV,GLSSPKHGF,IVSTSVTHLV,GIVSTSVTHL,VSTSVTHLVR,VTHLVRGHSV,HGFGIVSTSV,KGLSSPKHGF,FGIVSTSVTH	STAD
CPE	c.869C>A	p.P290Q	SAHEYSSSPDDAIFQSLARAYSSFN[p.P290Q]QAMSDPNRPPCRKNDDDSSFVDGTTN	RAYSSFNQA,AYSSFNQAM,RAYSSFNQAM	LUAD
CPNE8	c.381G>T	p.Q127H	SKSPNLSKHDFLGQVFCTLGEIVGS[p.Q127H]HGSRLEKPIVGIPGKKCGTIILTAEE	GSHGSRLEK,EIVGSHGSR,GEIVGSHGS,VGSHGSRLEK,EIVGSHGSRL	LUAD
CPS1	c.2564C>A	p.T855K	TPRLPMNKEWPSNLDLRKELSEPSS[p.T855K]KRIYAIAKAIDDNMSLDEIEKLTYID	SSKRIYAIA,SKRIYAIAK,ELSEPSSKR,SEPSSKRIY,LSEPSSKRIY,SSKRIYAIAK,EPSSKRIYAI,KRIYAIAKAI	LUSC
CPSF4	c.656C>A	p.P219Q	NPPLQRSSSLIQLTSQNSSPNQQRT[p.P219Q]QQVIGVMQSQNSSAGNRGPRPLEQVT	RTQQVIGVM,NQQRTQQVI,SPNQQRTQQV,QQRTQQVIGV,QRTQQVIGVM	LUAD
CR1L	c.237delA	p.L79fs	PIGTYLNYECRPGYSGRPFSIICLK[p.L79fs]TQSGQVLRTSANVNHVVILQIL*	CLKTQSGQV,QVLRTSANV,RTSANVNHV,KTQSGQVLR,TSANVNHVV,LKTQSGQVL,SANVNHVVI,ANVNHVVIL,GQVLRTSANV,RTSANVNHVV,TSANVNHVVI,NVNHVVILQI,CLKTQSGQVL,SANVNHVVIL	STAD
CR2	c.618delC	p.V206fs	ESGYLLVGEKIINCLSSGKWSAVPP[p.V206fs]HVKRHAVNL*	WSAVPPHVK,KWSAVPPHV,HVKRHAVNL,SAVPPHVKR,PPHVKRHAV,GKWSAVPPH,SGKWSAVPPH,KWSAVPPHVK,WSAVPPHVKR,VPPHVKRHAV,GKWSAVPPHV	STAD
CRB1	c.1883delT	p.L628fs	SICAFQNSFLGGLPVGMTSNGVALL[p.L628fs]TSIICHPHLRL*	SIICHPHLR,SIICHPHLRL,TSIICHPHLR,MTSNGVALLT,LTSIICHPHL	HNSC
CRB1	c.1888T>G	p.F630V	ICAFQNSFLGGLPVGMTSNGVALLN[p.F630V]VYNMPSTPSFVGCLQDIKIDWNHITL	NGVALLNVY,VALLNVYNM,LLNVYNMPST,VYNMPSTPSF,SNGVALLNVY,TSNGVALLNV	STAD
CRB2	c.3329C>T	p.T1110M	GWEGPRCEAHVDPCHSAPCARGRCH[p.T1110M]MHPDGRFECRCPPGFGGPRCRLPVPS	RGRCHMHPD,CHMHPDGRF,RGRCHMHPDG,APCARGRCHM,RCHMHPDGRF,HMHPDGRFEC	ACC
CREBBP	c.4303G>C	p.D1435H	FGMHVQEYGSDCPPPNTRRVYISYL[p.D1435H]HSIHFFRPRCLRTAVYHEILIGYLEY	YLHSIHFFR,HSIHFFRPR,VYISYLHSI,ISYLHSIHF,SYLHSIHFF,RVYISYLHS,YISYLHSIH,RVYISYLHSI,SYLHSIHFFR,YISYLHSIHF,ISYLHSIHFF	BLCA
CREBBP	c.4337G>A	p.R1446H	CPPPNTRRVYISYLDSIHFFRPRCL[p.R1446H]HTAVYHEILIGYLEYVKKLGYVTGHI	HFFRPRCLH,HTAVYHEIL,RPRCLHTAV,FFRPRCLHT,CLHTAVYHEI,FFRPRCLHTA,RPRCLHTAVY,HTAVYHEILI	DLBCL

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CREBBP	c.6281C>T	p.P2094L	DLLRTLKSPSSPQQQQQVLNILKSN[p.P2094L]LQLMAAFIKQRTAKYVANQPGMQPQP	VLNILKSNL,ILKSNLQLM,NLQLMAAFI,LQLMAAFIK,KSNLQLMAA,SNLQLMAAF,LKSNLQLMA,ILKSNLQLMA,NLQLMAAFIK,KSNLQLMAAF,LKSNLQLMAA	UCEC
CRIPAK	c.142_143insCG	p.M48fs	PACSCAHVECPPAHTCRCGVPACSH[p.M48fs]TCPCGVPACSHVPMWSARLLTHVSMWSAHLLMCPCGVPTCSHVPMWSATCSHTCPCGVPACSRAHVECPPAHTCRCGVPACSHVPMRSARLLTRAHAECPPAHTCPCGVPACSHVPTWSARLLTRAHVECPPAHTCQRGVPA*	SMWSAHLLM,HLLMCPCGV,WSARLLTHV,HVSMWSAHL,RLLTHVSMW,LTHVSMWSA,HTCQRGVPA,MWSARLLTH,TWSARLLTR,VPTCSHVPM,VPACSRAHV,VPTWSARLL,ARLLTHVSM,THVSMWSAH,VSMWSAHLL,LMCPCGVPT,SHVPMWSAT,LLTHVSMWSA,SMWSAHLLMC,LLMCPCGVPT,HVSMWSAHLL,GVPACSRAHV,SARLLTHVSM,PTWSARLLTR,HVPTWSARLL,ARLLTHVSMW,LTHVSMWSAH,THVSMWSAHL,VSMWSAHLLM,VPTCSHVPMW,VPMWSATCSH	BLCA
CRIPAK	c.427T>C	p.C143R	SHVPMRSARLLTRAHAECPPAHTCP[p.C143R]RGVPACSHVPMRSARLLTRADVECPP	HTCPRGVPA,CPPAHTCPR,RGVPACSHV	ACC
CRIPAK	c.520T>C	p.C174R	SHVPMRSARLLTRADVECPPAHTCP[p.C174R]RGVPACSHVPTWSARLITRAHVECSP	HTCPRGVPA,CPPAHTCPR,RGVPACSHV	ACC
CRIPAK	c.538_568delTCACACGTGCCAACGTGGAGTGCCCGCCTGA	p.S180fs	LTRADVECPPAHTCPCGVPACSHVP[p.S180fs]MWSARLLTRADVECLPAHTCPCGVFACSHVPMRSARLLTRADAECPPAHTCPCGVPACSRADVECPPAHTCPCGVPACSRADVGCPPAHMCRCGVPACSHVPMWSARLLTRADVECPPAHVPIWSARLLTRAIVECPPAHTHADVECPPAHTCPCGVPACSHVPMWSARLLTHVPMWSARLLTRAHVECLPAHTRAHVECPPAHTKPWHGGSVGFLSCRPSQTLLPYILLMVAF*	FLSCRPSQT,TLLPYILLM,LLPYILLMV,CLPAHTCPC,HMCRCGVPA,WSARLLTHV,GSVGFLSCR,VFACSHVPM,RLLTHVPMW,PWHGGSVGF,PYILLMVAF,HTCPCGVFA,SARLLTRAI,LTRAHVECL,RAHVECLPA,MWSARLLTH,RPSQTLLPY,FACSHVPMR,IWSARLLTR,DVECPPAHV,HVPIWSARL,QTLLPYILL,VPACSRADV,VPIWSARLL,LPAHTRAHV,AHTCPCGVF,RAIVECPPA,ARLLTHVPM,AHVECLPAH,LSCRPSQTL,SQTLLPYIL,LPYILLMVA,CPPAHVPIW,CPPAHTKPW,LLTRAHVECL,CLPAHTRAHV,FLSCRPSQTL,TLLPYILLMV,LLPYILLMVA,LLTRADVECL,HVECPPAHTK,GVFACSHVPM,SARLLTRADA,SARLLTRAIV,SARLLTHVPM,HTKPWHGGSV,VFACSHVPMR,PAHVPIWSAR,PIWSARLLTR,HVECLPAHTR,HVPIWSARLL,WSARLLTRAI,KPWHGGSVGF,RPSQTLLPYI,LPYILLMVAF,SRADVGCPPA,ADVGCPPAHM,AHMCRCGVPA,VECPPAHVPI,AHVPIWSARL,RAIVECPPAH,ARLLTHVPMW,RAHVECLPAH,LSCRPSQTLL,CRPSQTLLPY,SQTLLPYILL,VECLPAHTRA,VECPPAHTHA,LPAHTCPCGV,CPPAHTHADV	LUAD
CRIPAK	c.568A>C	p.I190L	ECPPAHTCPCGVPACSHVPTWSARL[p.I190L]LTRAHVECSPAHTCRCGVPACSHVPM	TWSARLLTR,VPTWSARLL,PTWSARLLTR,HVPTWSARLL	ACC
CRISPLD1	c.664C>T	p.R222W	PKAVYLVCNYSPKGNWWGHAPYKHG[p.R222W]WPCSACPPSFGGGCRENLCYKEGSDR	APYKHGWPC,YKHGWPCSA,WPCSACPPS,WPCSACPPSF,YKHGWPCSAC	BRCA
CROCC	c.1063G>C	p.A355P	RTSRAVQEAGLGLSTGLRLAESRAE[p.A355P]PALEKQALLQAQLEEQLRDKVLREKD	EPALEKQAL,AESRAEPAL,RLAESRAEPA,ESRAEPALEK,AEPALEKQAL	KIRP
CROT	c.1740G>T	p.Q580H	DPLFSKSGGGGNFVLSTSLVGYLRV[p.Q580H]HGVVVPMVHNGYGFFYHIRDDRFVVA	YLRVHGVVV,GYLRVHGVV,RVHGVVVPM,RVHGVVVPMV,LVGYLRVHGV,GYLRVHGVVV,LRVHGVVVPM	LUAD
CROT	c.96delA	p.L32fs	TEERTFQYQDSLPSLPVPSLEESLK[p.L32fs]NTLNQSPEHATR*	LEESLKNTL	STAD
CRTC3	c.1088C>T	p.S363L	NKTVLSSSLNNHPQTSVPNASALHP[p.S363L]LLRLFSLSNPSLSTTNLSGPSRRRQP	ASALHPLLR,ALHPLLRLF,NASALHPLL,HPLLRLFSL,SALHPLLRLF,NASALHPLLR,VPNASALHPL	LUAD
CRYGB	c.427A>G	p.R143G	HLTEIHSLNVLEGSWILYEMPNYRG[p.R143G]GQYLLRPGEYRRFLDWGAPNAKVGSL	NYRGGQYLL,MPNYRGGQY,YEMPNYRGG,EMPNYRGGQY,GQYLLRPGEY,NYRGGQYLLR,MPNYRGGQYL	TGCT
CRYGD	c.476delG	p.G159fs	YEMPNYRGRQYLLRPGDYRRYHDWG[p.G159fs]VQMPKSAL*	RYHDWGVQM,GVQMPKSAL,RRYHDWGVQM,WGVQMPKSAL	STAD
CRYM	c.943T>A	p.*315K	FKSLGMAVEDTVAAKLIYDSWSSGK[p.*315K]KNKGT*	SWSSGKKNK	CLL

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CSDE1	c.658C>T	p.R220C	NVQLETGDKINFVIDNNKHTGAVSA[p.R220C]CNIMLLKKKQARCQGVVCAMKEAFGF	SACNIMLLK,GAVSACNIM,AVSACNIMLL,VSACNIMLLK,SACNIMLLKK,HTGAVSACNI	UCEC
CSF2RB	c.892G>A	p.G298S	SFGLFYKPSPDAGEEECSPVLREGL[p.G298S]SSLHTRHHCQIPVPDPATHGQYIVSV	VLREGLSSL,EGLSSLHTR,REGLSSLHT	GBM
CSF3R	c.1404delC	p.P468fs	SLWVGWEPPNPWPQGYVIEWGLGPP[p.P468fs]ARAIATRPGGWNRMGEPRGFC*	ATRPGGWNR,RAIATRPGG,EWGLGPPAR,IEWGLGPPA,ATRPGGWNRM,IATRPGGWNR,RAIATRPGGW,IEWGLGPPAR	STAD
CSGALNACT2	c.1086G>T	p.L362F	VSLNEEFNRGRGLNVGARAWDKGEV[p.L362F]FMFFCDVDIYFSAEFLNSCRLNAEPG	FMFFCDVDI,EVFMFFCDV,RAWDKGEVF,GEVFMFFCD,AWDKGEVFMF,VFMFFCDVDI,RAWDKGEVFM,FMFFCDVDIY,ARAWDKGEVF,GEVFMFFCDV	ACC,KIRP,TGCT
CSHL1	c.350G>A	p.R117Q	SSNMEETQQKSNLELLHISLLLIES[p.R117Q]QLEPVRFLRSTFTNNLVYDTSDSDDY	SLLLIESQL,LIESQLEPV,SQLEPVRFL,QLEPVRFLR,LLIESQLEPV,SQLEPVRFLR,ISLLLIESQL,IESQLEPVRF	CESC
CSMD2	c.5564C>A	p.P1855Q	PTCVVPCGGNLTERRGTILSPGFPE[p.P1855Q]QYLNSLNCVWKIVVPEGAGIQIQVVS	QYLNSLNCV,FPEQYLNSL,GFPEQYLNSL,QYLNSLNCVW,ILSPGFPEQY,EQYLNSLNCV	LUAD
CSMD3	c.2071C>A	p.Q691K	DPGTPLYGIREGDGFSNRDVLRFEC[p.Q691K]KFGFELIGEKSIVCQENNQWSANIPI	LRFECKFGF,FECKFGFEL,RFECKFGFEL,VLRFECKFGF,RDVLRFECKF,FECKFGFELI	LUSC
CSMD3	c.2854C>T	p.H952Y	AEPGHSIKITFERFQTELNYDVLEV[p.H952Y]YDGPNLLSPLLGSYNGTQVPQFLFSS	LNYDVLEVY,EVYDGPNLL,LEVYDGPNL,ELNYDVLEVY,EVYDGPNLLS,LEVYDGPNLL,YDGPNLLSPL	CESC
CSMD3	c.3281C>A	p.T1094K	GDVRGPSGTILSPGYPEFYPNSLNC[p.T1094K]KWTVDVTHGKGVQFNFHTFHLEDHHD	NSLNCKWTV,YPNSLNCKW,SLNCKWTVDV,FYPNSLNCKW,KWTVDVTHGK,EFYPNSLNCK	LUSC
CSMD3	c.511G>A	p.E171K	STKSVFSLRLTSDFAVSAHGFKVYY[p.E171K]KELQSSSCGNPGVPPKGVLYGTRFDV	AHGFKVYYK,SAHGFKVYYK,HGFKVYYKEL	GBM
CSMD3	c.522G>T	p.Q174H	SVFSLRLTSDFAVSAHGFKVYYEEL[p.Q174H]HSSSCGNPGVPPKGVLYGTRFDVGDK	YEELHSSSC,HSSSCGNPGV	LUAD
CSMD3	c.7149_7150insT	p.F2383fs	LESVYSTSNQILIKFHSDFTTSGFF[p.F2383fs]CAQLSRLSTKGVPTSTTCAQC*	FTTSGFFCA,AQLSRLSTK,GFFCAQLSR,LSRLSTKGV,QLSRLSTKGV,SGFFCAQLSR,CAQLSRLSTK,TTSGFFCAQL,AQLSRLSTKG	LIHC
CSMD3	c.8179C>A	p.P2727T	LEHGRWRIVNGSHYEYKTKVVFSCD[p.P2727T]TGYHGLGPASIECLPNGTWSWRNERP	VVFSCDTGY,VVFSCDTGYH,KTKVVFSCDT,KVVFSCDTGY,FSCDTGYHGL,DTGYHGLGPA	LUAD
CSMD3	c.8429C>A	p.T2810N	CDLGFMLVGSAVRECLSSGLWSESE[p.T2810N]NRCLAGHCGIPELIVNGQVIGENYGY	SESENRCLA,SENRCLAGH	LUAD
CSPG5	c.355G>A	p.D119N	AVTGTAWLEADSPGLGGVTAEAGSG[p.D119N]NAQALPATLQAPHEVLGQSIMPPAIP	VTAEAGSGNA,AEAGSGNAQA	BLCA
CT47B1	c.702_728delGAAGCTCACAGAGGAGGCCACAGAGGA	p.234_243EKLTEEATEE>E	DLAEMAREPAEEAADEKPPEEAAEE[p.234_243EKLTEEATEE>E]PAAEEPTSEEAVAPEEVTKSQPEKWDEEAQDAAGEEEKEQEKEKDVENKVKN	EEAAEEPAA,AEEPAAEEPT	BRCA
CTAGE15P	c.1091C>T	p.A364V	IIQLSEVDKTKEELTEHIKNLQTQQ[p.A364V]VSLQSENIYFESENQKLQQKLKIMTE	VSLQSENIY,NLQTQQVSL,HIKNLQTQQV,QVSLQSENIY,KNLQTQQVSL,QQVSLQSENI,VSLQSENIYF	KIRP
CTCF	c.604_605insAA	p.K202fs	EQGELPPQEDPSWQKDPDYQPPAKK[p.K202fs]KQRKPKRANCVIQRRAKM*	RANCVIQRR,KPKRANCVI,KQRKPKRANC,RANCVIQRRA	STAD
CTCF	c.604delA	p.K202fs	EQGELPPQEDPSWQKDPDYQPPAKK[p.K202fs]QRKPKRANCVIQRRAKM*	RANCVIQRR,KPKRANCVI,KQRKPKRANC,RANCVIQRRA	STAD
CTCFL	c.1267G>A	p.E423K	YECHICHTRFTQSGTMKIHILQKHG[p.E423K]KNVPKYQCPHCATIIARKSDLRVHMR	ILQKHGKNV,KHGKNVPKY,KIHILQKHGK,LQKHGKNVPK,QKHGKNVPKY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CTDNEP1	c.376G>A	p.E126K	KHPVRFFVHKRPHVDFFLEVVSQWY[p.E126K]KLVVFTASMEIYGSAVADKLDNSRSI	KLVVFTASM,VVSQWYKLV,SQWYKLVVF,WYKLVVFTA,EVVSQWYKL,YKLVVFTAS,FLEVVSQWYK,VSQWYKLVVF,EVVSQWYKLV,YKLVVFTASM,LEVVSQWYKL,SQWYKLVVFT	CRC
CTNNA3	c.2567_2568insAA	p.K856fs	IIRIQSPAGPRHPVVMWRMKAPAKK[p.K856fs]NP*	RMKAPAKKNP	STAD
CTNNB1	c.1004A>T	p.K335I	ESKLIILASGGPQALVNIMRTYTYE[p.K335I]ILLWTTSRVLKVLSVCSSNKPAIVEA	IMRTYTYEI,YTYEILLWT,ILLWTTSRV,TYTYEILLW,TYEILLWTT,RTYTYEILL,EILLWTTSR,MRTYTYEIL,YEILLWTTS,NIMRTYTYEI,YTYEILLWTT,ILLWTTSRVL,IMRTYTYEIL,RTYTYEILLW,EILLWTTSRV,MRTYTYEILL,YEILLWTTSR	LIHC
CTNNB1	c.100G>A	p.G34R	ELDMAMEPDRKAAVSHWQQQSYLDS[p.G34R]RIHSGATTTAPSLSGKGNPEEEDVDT	QQSYLDSRI,RIHSGATTT,YLDSRIHSGA,RIHSGATTTA,QQQSYLDSRI,QQSYLDSRIH	UCEC
CTNNB1	c.101G>T	p.G34V	ELDMAMEPDRKAAVSHWQQQSYLDS[p.G34V]VIHSGATTTAPSLSGKGNPEEEDVDT	QQQSYLDSV,YLDSVIHSG,QQSYLDSVI,WQQQSYLDSV,YLDSVIHSGA,VIHSGATTTA,QQQSYLDSVI,QQSYLDSVIH	LIHC
CTNNB1	c.107A>C	p.H36P	DMAMEPDRKAAVSHWQQQSYLDSGI[p.H36P]PSGATTTAPSLSGKGNPEEEDVDTSQ	YLDSGIPSG,IPSGATTTA,YLDSGIPSGA	LIHC
CTNNB1	c.109T>G	p.S37A	MAMEPDRKAAVSHWQQQSYLDSGIH[p.S37A]AGATTTAPSLSGKGNPEEEDVDTSQV	YLDSGIHAG,IHAGATTTA,YLDSGIHAGA,GIHAGATTTA,AGATTTAPSL	UCEC
CTNNB1	c.110C>G	p.S37C	MAMEPDRKAAVSHWQQQSYLDSGIH[p.S37C]CGATTTAPSLSGKGNPEEEDVDTSQV	YLDSGIHCGA,GIHCGATTTA	UCEC
CTNNB1	c.110C>T	p.S37F	MAMEPDRKAAVSHWQQQSYLDSGIH[p.S37F]FGATTTAPSLSGKGNPEEEDVDTSQV	YLDSGIHFG,SYLDSGIHF,IHFGATTTA,YLDSGIHFGA,GIHFGATTTA,QSYLDSGIHF,IHFGATTTAP,FGATTTAPSL	LUAD,UCEC
CTNNB1	c.1161T>A	p.N387K	GMQALGLHLTDPSQRLVQNCLWTLR[p.N387K]KLSDAATKQEGMEGLLGTLVQLLGSD	VQNCLWTLRK	LIHC
CTNNB1	c.121A>G	p.T41A	PDRKAAVSHWQQQSYLDSGIHSGAT[p.T41A]ATAPSLSGKGNPEEEDVDTSQVLYEW	ATAPSLSGK,GATATAPSL,GIHSGATATA,TATAPSLSGK,SGATATAPSL	PRAD
CTNNB1	c.122C>T	p.T41I	PDRKAAVSHWQQQSYLDSGIHSGAT[p.T41I]ITAPSLSGKGNPEEEDVDTSQVLYEW	ITAPSLSGK,SGIHSGATI,TITAPSLSGK,SGATITAPSL	UCEC
CTNNB1	c.133T>C	p.S45P	AAVSHWQQQSYLDSGIHSGATTTAP[p.S45P]PLSGKGNPEEEDVDTSQVLYEWEQGF	TTAPPLSGK,GATTTAPPL,TTTAPPLSGK,SGATTTAPPL	ACC,LIHC
CTNNB1	c.94G>A	p.D32N	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32N]NSGIHSGATTTAPSLSGKGNPEEEDV	YLNSGIHSG,QQSYLNSGI,WQQQSYLNS,QQQSYLNSG,YLNSGIHSGA,QQQSYLNSGI,WQQQSYLNSG,QQSYLNSGIH	LIHC,UCEC
CTNNB1	c.94G>T	p.D32Y	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32Y]YSGIHSGATTTAPSLSGKGNPEEEDV	YLYSGIHSG,QQSYLYSGI,HWQQQSYLY,WQQQSYLYS,QQQSYLYSG,QSYLYSGIH,YLYSGIHSGA,QQQSYLYSGI,SHWQQQSYLY,WQQQSYLYSG,QQSYLYSGIH	UCEC
CTNNB1	c.95A>G	p.D32G	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32G]GSGIHSGATTTAPSLSGKGNPEEEDV	YLGSGIHSG,WQQQSYLGS,QQQSYLGSG,QQSYLGSGI,QSYLGSGIH,YLGSGIHSGA,WQQQSYLGSG,QQQSYLGSGI,QQSYLGSGIH	CESC,LIHC
CTNNB1	c.95A>T	p.D32V	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32V]VSGIHSGATTTAPSLSGKGNPEEEDV	QQSYLVSGI,YLVSGIHSG,LVSGIHSGA,HWQQQSYLV,WQQQSYLVS,QQQSYLVSG,QSYLVSGIH,YLVSGIHSGA,QQQSYLVSGI,SHWQQQSYLV,WQQQSYLVSG,QQSYLVSGIH	LIHC
CTNNB1	c.97T>C	p.S33P	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33P]PGIHSGATTTAPSLSGKGNPEEEDVD	YLDPGIHSG,WQQQSYLDP,QQQSYLDPG,QQSYLDPGI,YLDPGIHSGA,WQQQSYLDPG,QQQSYLDPGI,QQSYLDPGIH	LIHC
CTNNB1	c.98C>A	p.S33Y	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33Y]YGIHSGATTTAPSLSGKGNPEEEDVD	YLDYGIHSG,WQQQSYLDY,QQSYLDYGI,YLDYGIHSGA,HWQQQSYLDY,QQQSYLDYGI,QQSYLDYGIH	UCEC
CTNNB1	c.98C>G	p.S33C	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33C]CGIHSGATTTAPSLSGKGNPEEEDVD	YLDCGIHSG,WQQQSYLDC,QQSYLDCGI,YLDCGIHSGA,QQQSYLDCGI,QQSYLDCGIH	LIHC,UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CTNNB1	c.98C>T	p.S33F	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33F]FGIHSGATTTAPSLSGKGNPEEEDVD	YLDFGIHSG,WQQQSYLDF,QQSYLDFGI,QSYLDFGIH,YLDFGIHSGA,HWQQQSYLDF,QQQSYLDFGI,QQSYLDFGIH	UCEC
CTNND1	c.1341delA	p.I447fs	VHLGACGALKNISFGRDQDNKIAIK[p.I447fs]TVMVCLPLCDCFERLVIWTLLKLLPEPCGIFHPMTQSKWRLWTMHCMP*	KIAIKTVMV,KLLPEPCGI,AIKTVMVCL,LVIWTLLKL,RLVIWTLLK,KTVMVCLPL,IFHPMTQSK,QSKWRLWTM,KWRLWTMHC,EPCGIFHPM,NKIAIKTVM,FERLVIWTL,LLPEPCGIF,SKWRLWTMH,WRLWTMHCM,LPEPCGIFH,RLVIWTLLKL,LVIWTLLKLL,GIFHPMTQSK,CFERLVIWTL,KLLPEPCGIF,IFHPMTQSKW,KWRLWTMHCM,HPMTQSKWRL,TQSKWRLWTM,IAIKTVMVCL,IKTVMVCLPL,FERLVIWTLL,LPLCDCFERL,PEPCGIFHPM	STAD
CTSC	c.315delT	p.F105fs	NSGHFTIIYNQGFEIVLNDYKWFAF[p.F105fs]LSIKKRAAR*	FLSIKKRAA,KWFAFLSIK,WFAFLSIKK,LSIKKRAAR,FAFLSIKKR,YKWFAFLSI,NDYKWFAFL,KWFAFLSIKK,DYKWFAFLSI,WFAFLSIKKR,FLSIKKRAAR	STAD
CTSD	c.267_268insC	p.P89fs	GPIPEVLKNYMDAQYYGEIGIGTPP[p.P89fs]PVLHSRLRHGLLQPVGPLHPLQTAGHRLLDPPQVQQRQVQHLREEWYLV*	GLLQPVGPL,HLREEWYLV,HSRLRHGLL,RLRHGLLQP,QQRQVQHLR,VQHLREEWY,QPVGPLHPL,IGIGTPPPV,LRHGLLQPV,LQTAGHRLL,VQQRQVQHL,RQVQHLREE,RLRHGLLQPV,VLHSRLRHGL,HSRLRHGLLQ,QVQHLREEWY,EIGIGTPPPV,TPPPVLHSRL,HPLQTAGHRL,IGIGTPPPVL,LQPVGPLHPL,RQVQHLREEW,VQHLREEWYL,GEIGIGTPPP	STAD
CTTNBP2	c.1259C>T	p.S420L	TSSTPPLPSNAAPPTAQTPGIAPQN[p.S420L]LQAPPMHSLHSPCANTSLHPGLNPRI	LQAPPMHSL,PQNLQAPPM,NLQAPPMHSL,QTPGIAPQNL,APQNLQAPPM,LQAPPMHSLH	UCEC
CTTNBP2	c.490C>T	p.R164C	LEMEKLQLQALEQEHKKLAARLEEE[p.R164C]CGKNKQVVLMLVKECKQLSGKVIEEA	CGKNKQVVL,KLAARLEEEC,AARLEEECGK	CRC
CUBN	c.1786G>T	p.G596C	EHLRNGRGFTVRWETQQPECGGILT[p.G596C]CPYGSIKSPGYPGNYPPGRDCVWIVV	ILTCPYGSI,LTCPYGSIK,CGGILTCPY,ILTCPYGSIK	LUAD
CUBN	c.8448C>G	p.I2816M	GGGFYATWNTQTLGCGGIFHSDNGT[p.I2816M]MRSPHWPQNFPENSRCSWTAITHKSK	TMRSPHWPQ,IFHSDNGTM,TMRSPHWPQN,IFHSDNGTMR,GIFHSDNGTM,MRSPHWPQNF	KIRP
CUL1	c.1453G>A	p.E485K	DVFQKFYAKMLAKRLVHQNSASDDA[p.E485K]KASMISKLKQACGFEYTSKLQRMFQD	KASMISKLK,DAKASMISK,AKASMISKL,SASDDAKASM	BLCA
CUL7	c.1113G>C	p.L371F	QAQPSFRRSRRFRPRSEFASGNTYA[p.L371F]FYVRDTLQPGMRVRMLDDYEEISAGD	ASGNTYAFY,FASGNTYAF,YAFYVRDTL,FASGNTYAFY,EFASGNTYAF,TYAFYVRDTL,SGNTYAFYVR	LUAD
CUL9	c.5178T>G	p.D1726E	SPRCWPVSPLCYLYHPRKCLPTEFC[p.D1726E]EALDRFSSFYSQSQNHPVLDMGPHRR	CLPTEFCEA,LPTEFCEAL,EALDRFSSF,CEALDRFSS,CLPTEFCEAL,EALDRFSSFY,TEFCEALDRF,CEALDRFSSF	KIRC
CUX1	c.1316_1317insC	p.A439fs	LSGSARRKGKDQPESRRPGSLPAPP[p.A439fs]SFSVAPQPGGAGFQY*	LPAPPSFSV,APQPGGAGF,GSLPAPPSF,QPGGAGFQY,SLPAPPSFSV,FSVAPQPGGA,LPAPPSFSVA	STAD
CWC25	c.1090A>G	p.K364E	EELERKRQEMMENAKWREEERLNIL[p.K364E]ERHAKDEEREQRLEKLDSRDGKFIHR	RLNILERHAK	KIRC
CXCL9	c.366G>C	p.K122N	KKQKNGKKHQKKKVLKVRKSQRSRQ[p.K122N]NKTT*	KSQRSRQNK	LUAD
CXCR4	c.1033G>C	p.E345Q	VSRGSSLKILSKGKRGGHSSVSTES[p.E345Q]QSSSFHSS*	STESQSSSF,SQSSSFHSS,VSTESQSSSF	LUAD
CXXC1	c.468G>C	p.Q156H	MLARGSASPHKSSPQPLVATPSQHH[p.Q156H]HQQQQQQIKRSARMCGECEACRRTEDC	HHHQQQQQI	TGCT
CXorf51B	c.127G>A	p.V43I	QTPSTSSTKGRKKGKTPRQRRSRSG[p.V43I]IKGLKTTRKAKRPLRGSSSQKAGETN	RQRRSRSGI,QRRSRSGIK,RSRSGIKGL,RSRSGIKGLK,RQRRSRSGIK,GIKGLKTTRK,RRSRSGIKGL	KIRC
CXorf59	c.593G>T	p.R198M	LLHLSGKMPPGINSSQSLPVDNHEK[p.R198M]MVIQLHLQHSSLLDFLNAQGGCISHV	LPVDNHEKM,HEKMVIQLH,HEKMVIQLHL,LPVDNHEKMV	LUAD

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CYP11B1	c.1492C>G	p.R498G	LVRVFLYSLGRNPALFPRPERYNPQ[p.R498G]GWLDIRGSGRNFYHVPFGFGMRQCLG	RYNPQGWLDI	LUAD
CYP19A1	c.1216T>C	p.F406L	DVIDGYPVKKGTNIILNIGRMHRLE[p.F406L]LFPKPNEFTLENFAKNVPYRYFQPFG	IGRMHRLEL,MHRLELFPK,ELFPKPNEF,GRMHRLELF,RMHRLELFPK,LFPKPNEFTL,NIGRMHRLEL,IGRMHRLELF,LELFPKPNEF	TGCT
CYP19A1	c.338G>T	p.S113I	WISGEETLIISKSSSMFHIMKHNHY[p.S113I]ISRFGSKLGLQCIGMHEKGIIFNNNP	HIMKHNHYI,YISRFGSKL,HYISRFGSK,ISRFGSKLG,KHNHYISRF,HYISRFGSKL,IMKHNHYISR,NHYISRFGSK,ISRFGSKLGL,MKHNHYISRF,FHIMKHNHYI	THCA
CYP1A2	c.1447G>A	p.V483M	CIGEVLAKWEIFLFLAILLQQLEFS[p.V483M]MPPGVKVDLTPIYGLTMKHARCEHVQ	LLQQLEFSM,FSMPPGVKV,MPPGVKVDL,QQLEFSMPP,LEFSMPPGV,ILLQQLEFSM,QLEFSMPPGV,SMPPGVKVDL,LQQLEFSMPP,QQLEFSMPPG	BRCA
CYP27A1	c.335C>A	p.P112Q	LYKAKYGPMWMSYLGPQMHVNLASA[p.P112Q]QLLEQVMRQEGKYPVRNDMELWKEHR	ASAQLLEQV,HVNLASAQL,VNLASAQLL,SAQLLEQVM,LASAQLLEQV,HVNLASAQLL,MHVNLASAQL,ASAQLLEQVM	LUAD
CYP2B6	c.1331C>A	p.A444E	ALKKTEAFIPFSLGKRICLGEGIAR[p.A444E]EELFLFFTTILQNFSMASPVAPEDID	IAREELFLF,AREELFLFF,EELFLFFTT,GEGIAREEL,REELFLFFT,GIAREELFLF,IAREELFLFF,EELFLFFTTI,GEGIAREELF,REELFLFTT	LUAD
CYP2D6	c.1055A>G	p.H352R	VQRRVQQEIDDVIGQVRRPEMGDQA[p.H352R]RMPYTTAVIHEVQRFGDIVPLGVTHM	MGDQARMPY,RMPYTTAVI,QARMPYTTA,ARMPYTTAV,QARMPYTTAV,EMGDQARMPY,RPEMGDQARM,ARMPYTTAVI,RMPYTTAVIH	GBM
CYP4A11	c.553G>T	p.V185F	GLMADSVRVMLDKWEELLGQDSPLE[p.V185F]FFQHVSLMTLDTIMKCAFSHQGSIQV	LGQDSPLEF,GQDSPLEFF,LEFFQHVSL,EFFQHVSLM,SPLEFFQHV,FFQHVSLMTL,DSPLEFFQHV,LLGQDSPLEF,LEFFQHVSLM,LGQDSPLEFF	OV
CYP4B1	c.1302G>T	p.E434D	HIYALHRNSAVWPDPEVFDSLRFST[p.E434D]DNASKRHPFAFMPFSAGPRNCIGQQF	SLRFSTDNA,RFSTDNASK,TDNASKRHPF	CRC
CYP7B1	c.995A>C	p.K332T	YLLRHPEAMAAVRDEIDRLLQSTGQ[p.K332T]TKGSGFPIHLTREQLDSLICLESSIF	QTKGSGFPI,RLLQSTGQTK,GQTKGSGFPI,TKGSGFPIHL	STAD
DAB2IP	c.481G>A	p.E161K	ILGQDYCFEVTTSSGSKCFSCRSAA[p.E161K]KRDKWMENLRRAVHPNKDNSRRVEHI	CFSCRSAAK,FSCRSAAKR,RSAAKRDKW,KCFSCRSAAK,SCRSAAKRDK,CFSCRSAAKR,AKRDKWMENL	BRCA
DACH2	c.1615C>T	p.R539C	TMQKRLKKEKKTKRKLQEALEFESK[p.R539C]CREQVEQALKQATTSDSGLRMLKDTG	FESKCREQV,EALEFESKCR	CRC
DACH2	c.1616G>T	p.R539L	TMQKRLKKEKKTKRKLQEALEFESK[p.R539L]LREQVEQALKQATTSDSGLRMLKDTG	KLREQVEQA,EALEFESKL,FESKLREQV,KLREQVEQAL,EALEFESKLR,QEALEFESKL	LUAD
DBC1	c.646G>A	p.V216I	AIKVTETRTGPLGCNSYDNLDSVSS[p.V216I]ILLQSTESKLHLQGLQIIFPQYLQEK	NLDSVSSIL,ILLQSTESK,NLDSVSSILL,ILLQSTESKL,SILLQSTESK,YDNLDSVSSI	CRC
DBF4B	c.761C>A	p.S254Y	PFLKIEDESRKFRPFHHQFKSFPEI[p.S254Y]YFLGPKDASPFEAPTTLGSMHHTRES	KSFPEIYFL,SFPEIYFLG,QFKSFPEIY,FKSFPEIYF,QFKSFPEIYF,HQFKSFPEIY,FKSFPEIYFL	CRC
DCAF12L2	c.737G>A	p.R246H	RMDPDMFNGSIAWHSEVGLPVYAHI[p.R246H]HPRDVEAIPRASTNPSNRKVRALAFS	PVYAHIHPR,HIHPRDVEA,HIHPRDVEAI,VYAHIHPRDV,LPVYAHIHPR	GBM
DCC	c.1337G>A	p.R446H	AIPSSSVLPSAPRDVVPVLVSSRFV[p.R446H]HLSWRPPAEAKGNIQTFTVFFSREGD	LVSSRFVHL,SSRFVHLSW,VLVSSRFVH,VHLSWRPPA,VLVSSRFVHL,FVHLSWRPPA,HLSWRPPAEA,SSRFVHLSWR,VSSRFVHLSW	LUAD
DCHS1	c.703delC	p.R235fs	LDRENRSHYMLQLEAYDGGSPPRRA[p.R235fs]RPCWT*	SPPRRARPC	STAD
DCHS2	c.6447C>A	p.F2149L	TRENTYVEYSIISGNSQNNFHVETK[p.F2149L]LFHSEYPYKQVGYLVLLHSLDREASA	KLFHSEYPY,LFHSEYPYK,NFHVETKLF,ETKLFHSEY,KLFHSEYPYK,NNFHVETKLF,VETKLFHSEY,TKLFHSEYPY	CRC
DCLK2	c.1646C>A	p.S549Y	HGLSIVHRDIKPENLLVCEYPDGTK[p.S549Y]YLKLGDFGLATVVEGPLYTVCGTPTY	YLKLGDFGL,CEYPDGTKY,TKYLKLGDF,YLKLGDFGLA,KYLKLGDFGL,YPDGTKYLKL,CEYPDGTKYL	CRC
DCLRE1B	c.82T>A	p.F28I	GVLIPHTPIAVDFWSLRRAGTARLF[p.F28I]ILSHMHSDHTVGLSSTWARPLYCSPI	RLFILSHMH,RAGTARLFI,ARLFILSHM,ILSHMHSDHT,GTARLFILSH,RAGTARLFIL,TARLFILSHM,RRAGTARLFI	TGCT

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DCT	c.1595G>A	p.R532Q	LVVMGTLVALVGLFVLLAFLQYRRL[p.R532Q]QKGYTPLMETHLSSKRYTEEA*	RLQKGYTPL,FLQYRRLQK,LQKGYTPLM,QYRRLQKGY,LQYRRLQKG,RLQKGYTPLM,AFLQYRRLQK,LQYRRLQKGY,RRLQKGYTPL	UCEC
DCUN1D4	c.824T>C	p.L275P	EKDQRSLDINTAKCMLGLLLGKIWP[p.L275P]PFPVFHQFLEQSKYKVINKDQWCNVL	LLLGKIWPP,LLGKIWPPF,KIWPPFPVF,PFPVFHQFL,GKIWPPFPV,PPFPVFHQF,LLLGKIWPPF,LGKIWPPFPV,KIWPPFPVFH,GKIWPPFPVF,WPPFPVFHQF	THCA
DDC	c.1297delA	p.I433fs	LVCFRLKGSNKVNEALLQRINSAKK[p.I433fs]STWFHVTSGTSLSCALPSVLARWNLPMCSGPGNTSKSWRPTCCEQRGSRSEASCRNQKLKRDISENWNKKQINIILPSWNSAVCGFPCLSPKLSRGL*	SLSCALPSV,VLARWNLPM,ILPSWNSAV,CGFPCLSPK,CALPSVLAR,CSGPGNTSK,ASCRNQKLK,ALPSVLARW,SWNSAVCGF,SAKKSTWFH,GSRSEASCR,INSAKKSTW,AKKSTWFHV,KKSTWFHVT,FHVTSGTSL,SGTSLSCAL,LSCALPSVL,LKRDISENW,KQINIILPS,SAVCGFPCL,LPSWNSAVC,SLSCALPSVL,VLARWNLPMC,IILPSWNSAV,ILPSWNSAVC,CLSPKLSRGL,RSEASCRNQK,CALPSVLARW,KQINIILPSW,SAKKSTWFHV,SVLARWNLPM,SWRPTCCEQR,STWFHVTSGT,TSLSCALPSV,NIILPSWNSA,NSAVCGFPCL,LPSVLARWNL,WNKKQINIIL,RINSAKKSTW,INSAKKSTWF,WFHVTSGTSL,SEASCRNQKL,KLKRDISENW,CGFPCLSPKL,CEQRGSRSEA	STAD
DDI1	c.824G>A	p.R275Q	VNGHPLKAFVDSGAQMTIMSQACAE[p.R275Q]QCNIMRLVDRRWAGVAKGVGTQRIIG	AEQCNIMRL,SQACAEQCNI,AEQCNIMRLV	CRC
DDX11	c.1126G>A	p.A376T	PYYGSRLAIPAAQLVVLPYQMLLHA[p.A376T]TTRQAAGIRLQDQVVIIDEAHNLIDT	LLHATTRQA,TTRQAAGIR,QMLLHATTR,YQMLLHATT,LHATTRQAA,MLLHATTRQA,LLHATTRQAA,TTRQAAGIRL,YQMLLHATTR,LPYQMLLHAT	TGCT
DDX11	c.622delA	p.K208fs	AERLEQLESGEEELVLAEYESDEEK[p.K208fs]RWRAEWMRMRMTWRKNT*	MRMRMTWRK,RWRAEWMRM,EWMRMRMTW,RAEWMRMRM,WMRMRMTWR,RMRMTWRKN,EEKRWRAEW,AEWMRMRMT,WMRMRMTWRK,RWRAEWMRMR,RMRMTWRKNT,EWMRMRMTWR,KRWRAEWMRM,WRAEWMRMRM,AEWMRMRMTW,DEEKRWRAEW	TGCT
DDX11L2	c.382T>C	p.*128Q	CLFLSLEPPPPRDHISHCLLSAQFH[p.*128Q]QK*	LLSAQFHQK,CLLSAQFHQK	UCS
DDX17	c.488delG	p.G163fs	HPEVARLTPYEVDELRRKKEITVRG[p.G163fs]EMFVLNPCLPSIMLTSHNM*	VLNPCLPSI,SIMLTSHNM,ITVRGEMFV,KEITVRGEM,GEMFVLNPC,EMFVLNPCL,NPCLPSIML,LPSIMLTSH,FVLNPCLPSI,VLNPCLPSIM,EITVRGEMFV,KKEITVRGEM,KEITVRGEMF,GEMFVLNPCL	STAD
DDX39B	c.447_448insT	p.F149fs	LAFQISKEYERFSKYMPNVKVAVFF[p.F149fs]WWSVYQEG*	VAVFFWWSV,AVFFWWSVY,FWWSVYQEG,VKVAVFFWW,KVAVFFWWSV,VAVFFWWSVY	KIRC
DDX56	c.986G>T	p.R329L	FNQGFYDCVIATDAEVLGAPVKGKR[p.R329L]LGRGPKGDKASDPEAGVARGIDFHHV	LGRGPKGDK,KGKRLGRGPK,RLGRGPKGDK	LUAD
DEFA1	c.270G>T	p.W90C	DCYCRIPACIAGERRYGTCIYQGRL[p.W90C]CAFCC*	IYQGRLCAF,IYQGRLCAFC,CIYQGRLCAF	LUAD
DENND2A	c.1496G>T	p.R499L	GRKKRKIPKLVLRINAIYEVRRGKK[p.R499L]LVKRLSQSMESNSGKVTDENSESDSD	RGKKLVKRL,LVKRLSQSM,YEVRRGKKL,KLVKRLSQSM,EVRRGKKLVK,YEVRRGKKLV	LUAD
DENND2A	c.2063G>A	p.R688Q	EVYCIVSRLGCFSLFSRILDEVEKR[p.R688Q]QGISPALVQPLMRSVMEAPFPALGKT	KRQGISPAL,RQGISPALV,EKRQGISPAL,VEKRQGISPA	LUAD
DENND4A	c.1070C>A	p.P357H	LYRYSISGPHVLPIEKHISHFMHKV[p.P357H]HFPSPQRPRILVQLSPHDNLILSQPV	FMHKVHFPS,KVHFPSPQR,HFPSPQRPR,ISHFMHKVH,SHFMHKVHF,KVHFPSPQRP,ISHFMHKVHF,FMHKVHFPSP	CRC
DENND4C	c.3242G>A	p.R1081Q	ESEKSSPAVSRSKTFTGRFKQQTPS[p.R1081Q]QTHKERSTSLSALVRSSPHGSLGSVV	RFKQQTPSQ,KQQTPSQTH,RFKQQTPSQT,KQQTPSQTHK,FKQQTPSQTH	CRC
DENND5B	c.3068G>A	p.G1023E	GELGDTGVMQIPKNLLEMTFECQNL[p.G1023E]EKLTTVQIGHDNSGLLAKWLVDCVMV	FECQNLEKL,LEKLTTVQI,CQNLEKLTTV,MTFECQNLEK	HNSC
DGCR8	c.1552G>A	p.E518K	SVQDAPTKKEFVINPNGKSEVCILH[p.E518K]KYMQRVLKVRPVYNFFECENPSEPFG	ILHKYMQRV,KSEVCILHK,CILHKYMQR,KYMQRVLKV,HKYMQRVLK,SEVCILHKY,LHKYMQRVL,KSEVCILHKY,CILHKYMQRV,ILHKYMQRVL,LHKYMQRVLK,KYMQRVLKVR,SEVCILHKYM,HKYMQRVLKV	THCA

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DGKB	c.38C>T	p.S13L	MTNQEKWAHLSP[p.S13L]LEFSQLQK YAEYSTKKLKDVLEEFHG	EKWAHLSPL,WAHLSPLEF,LEFSQLQKY,HLSPLEFSQL,KW AHLSPLEF,QEKWAHLSPL,LEFSQLQKYA	BRCA
DHPS	c.147C>A	p.F49L	LPPESTQVRGYDFNRGVNYRALLEA[p.F 49L]LGTTGFQATNFGRAVQQVNAMIE KKL	ALLEALGTT,ALGTTGFQA,NYRALLEAL,LEALGTTGF,EALGT TGFQA,LLEALGTTGF,VNYRALLEAL	CESC
DHRS 4	c.653T>C	p.I218T	LGLNKTLAIELAPRNIRVNCLAPGL[p.I2 18T]TKTSFSRMLWMDKEKEESMKETL RIR	CLAPGLTKT,LTKTSFSRM,GLTKTSFSR,APGLTKTSF,TKTSFS RML,GLTKTSFSRM,LTKTSFSRML,LAPGLTKTSF,TKTSFSR MLW	LIHC
DHTK D1	c.1229G>A	p.R410 Q	DIGKLVGCAIIHVNGDSPEEVVRAT[p.R 410Q]QLAFEYQRQFRKDVIIDLLCYRQ WGH	TQLAFEYQR,VVRATQLAF,RATQLAFEY,EVVRATQLA,EEV VRATQL,ATQLAFEYQR,VVRATQLAFE,VRATQLAFEY,QLA FEYQRQF,EVVRATQLAF,EEVVRATQLA	CRC
DHX9	c.119T>G	p.V40G	RKMTPSYEIRAVGNKNRQKFMCEVQ[p .V40G]GEGYNYTGMGNSTNKKDAQS NAARDF	GEGYNYTGM,FMCEVQGEGY,CEVQGEGYNY	LUSC
DIAPH 2	c.361G>A	p.E121 K	ERSLNLSEKEVLDLFEKMMEDMNLN[p. E121K]KEKKAPLRNKDFTTKREMVVQY ISAT	MMEDMNLNK,LNKEKKAPL,KMMEDMNLNK,KEKKAPLR NK,NLNKEKKAPL	UCEC
DICER 1	c.5113G>A	p.E170 5K	KAYLLQAFTHASYHYNTITDCYQRL[p.E 1705K]KFLGDAILDYLITKHLYEDPRQH SPG	RLKFLGDAI,ITDCYQRLK,LKFLGDAIL,ITDCYQRLKF,RLKFLG DAIL,TITDCYQRLK,KFLGDAILDY,YQRLKFLGDA	CLL
DIRAS 1	c.235G>T	p.G79C	VCTLQITDTTGSHQFPAMQRLSISK[p.G 79C]CHAFILVFSVTSKQSLEELGPIYKLI	SISKCHAFI,RLSISKCHA,ISKCHAFIL,LSISKCHAF,MQRLSISK C,KCHAFILVF,SISKCHAFIL,ISKCHAFILV,LSISKCHAFI,RLSIS KCHAF,MQRLSISKCH,SKCHAFILVF	KIRC
DIS3	c.2339G>A	p.R780 K	CSGMDNDFHHYGLASPIYTHFTSPI[p.R 780K]KRYADVIVHRLLAVAIGADCTYPE LT	YTHFTSPIK,HFTSPIKRY,FTSPIKRYA,SPIKRYADV,IKRYADV IV,KRYADVIVH,YTHFTSPIKR,IYTHFTSPIK,SPIKRYADVI,TH FTSPIKRY,IKRYADVIVH	MM
DISP1	c.2194_219 5GG>TT	p.G732 L	EKVLPCIVIKFRYLWLFWFLALTVG[p.G 732L]LAYIVCINPKMKLPSLELSEFQVFR SS	FLALTVGLA,ALTVGLAYI,LTVGLAYIV,WFLALTVGL,LALTV GLAY,FLALTVGLAY,ALTVGLAYIV,LAYIVCINPK,FWFLALTV GL,LALTVGLAYI	SKCM
DISP1	c.2287C>T	p.R763 C	INPKMKLPSLELSEFQVFRSSHPFE[p.R7 63C]CYDAEYKKLFMFERVHHGEELHM PIT	RSSHPFECY,HPFECYDAE,CYDAEYKKLF,HPFECYDAEY,FRS SHPFECY	CRC
DISP2	c.3062T>C	p.F102 1S	VAGTVLLTVGLLVLLEWQLNTAEAL[p.F 1021S]SLSASVGLSVDFTVNYCISYHLCP HP	NTAEALSLS,EALSLSASV,LNTAEALSL,AEALSLSAS,LSLSAS VGL,ALSLSASVGL,SLSASVGLSV,QLNTAEALSL,NTAEALSL SA,WQLNTAEALS,AEALSLSASV	KIRC
DKK2	c.689G>A	p.R230 H	KPVLHQGEVCTKQRKKGSHGLEIFQ[p. R230H]HCDCAKGLSCKVWKDATYSSK ARLHV	EIFQHCDCA,FQHCDCAKGL,LEIFQHCDCA	CRC
DLC1	c.1049C>T	p.A350 V	LATQEPTDNQVRLRKRKEIREDRDR[p. A350V]VRLDSMVLLIMKLDQLDQDIEN ALST	RVRLDSMVL,RDRVRLDSM,VRLDSMVLL,REDRDRVRL,RV RLDSMVLL,EIREDRDRVR,KEIREDRDRV	CRC
DLC1	c.2222G>C	p.S741 T	ISALNGNRINVPMVRKRSVSNSTQT[p. S741T]TSSSSQSETSSAVSTPSPVTRTRS LS	RSVSNSTQTT	BLCA,PR AD,TGCT ,THCA
DLC1	c.666G>T	p.E222 D	ISLSEIKDAPKVNAVDTLNVKDIAP[p.E2 22D]DKQLLNSAVIAQQRRKPDPPKDE NER	NVKDIAPDK	CRC
DLEU7	c.248C>T	p.A83V	RARPGPGREERGGGVGTRSRRTAAR[p. A83V]VNSPEEEVVRGAEGGAELLPFPR DRG	RSRRTAARV,RTAARVNSP,RSRRTAARVN,RTAARVNSPE	ACC
DLG2	c.1871C>T	p.S624 L	KRRVERKERARLKTVKFNAKPGVID[p.S 624L]LKGSFNDKRKKSFIFSRKFPFYKNK E	GVIDLKGSF,NAKPGVIDLK,DLKGSFNDKR	UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
DLGAP3	c.1130delG	p.G377fs	GLLGPETKAKARTYHYLQVPQDDWG[p.G377fs]VTPPVARMGRSPAAGCGAAATSKPWGMRRAETQTAAPRHLPKQSPDASPPVAPPAWTRPGSTAVSHPGSTPGAPSLATAVPSPLDSSAMS*	WTRPGSTAV,TAAPRHLPK,ATSKPWGMR,VARMGRSPA,TSKPWGMRR,PVAPPAWTR,QVPQDDWGV,QSPDASPPV,STPGAPSLA,SPAAGCGAA,KPWGMRRAE,VPSPLDSSA,ARMGRSPAA,RMGRSPAAG,GAAATSKPW,MRRAETQTA,RRAETQTAA,TQTAAPRHL,KQSPDASPP,GSTPGAPSL,LATAVPSPL,SPPVAPPAW,LQVPQDDWGV,KQSPDASPPV,SLATAVPSPL,QTAAPRHLPK,ATSKPWGMRR,VARMGRSPAA,TSKPWGMRRA,GMRRAETQTA,RAETQTAAPR,VSHPGSTPGA,DWGVTPPVAR,VTPPVARMGR,DASPPVAPPA,SPAAGCGAAA,KPWGMRRAET,VPSPLDSSAM,WGVTPPVARM,CGAAATSKPW,MRRAETQTAA	STAD
DLL3	c.952G>C	p.D318H	PRSFECTCPRGFYGLRCEVSGVTCA[p.D318H]HGPCFNGGLCVGGADPDSAYICHCPP	VTCAHGPCF,CEVSGVTCAH,GVTCAHGPCF	BLCA
DMBT1	c.4562G>T	p.R1521L	SRASTAGSESTLALRLVNGGDRCRG[p.R1521L]LVEVLYQGSWGTVCDDYWDTNDANVV	GLVEVLYQGS,RCRGLVEVLY	LUAD
DMD	c.5316G>C	p.K1772N	DHCRKLVEPQISELNHRFAAISHRI[p.K1772N]NTGKASIPLKELEQFNSDIQKLLEPL	ISHRINTGK,RINTGKASI,NTGKASIPL,AISHRINTGK,NTGKASIPLK,HRINTGKASI	BRCA
DMD	c.9584G>A	p.R3195H	NVPLCVDMCLNWLLNVYDTGRTGRI[p.R3195H]HVLSFKTGIISLCKAHLEDKYRYLFK	TGRTGRIHV,HVLSFKTGI,TGRIHVLSF,TGRIHVLSFK,RTGRIHVLSF,RIHVLSFKTG,IHVLSFKTGI	CRC
DMPK	c.131G>A	p.R44H	AGVGPGLPGAGAPARPSPGRPPGAG[p.R44H]HLRTGPGQVRGRLLAVGPKSRVFQSV	HLRTGPGQV,HLRTGPGQVR	CESC
DMRT1	c.133T>A	p.S45T	PGVPPQGRAGGFGKASGALVGAASG[p.S45T]TSAGGSSRGGGSGSGASDLGAGSKKS	ALVGAASGT,GTSAGGSSR	ACC
DMRT2	c.317C>G	p.T106S	RGGPQPRPPLAPQASPAGTGPRERC[p.T106S]SPAGGGAEPRKLSRTPKCARCRNHGV	GPRERCSPA,GPRERCSPAG	KIRP
DMXL2	c.7236C>A	p.D2412E	GGGVKLVVKPRRQSENISAPPVLSE[p.D2412E]EIDKHRRRFNMRMLVPGRPVKDATPP	EEIDKHRRRF	MM
DNAH10	c.5558G>T	p.C1853F	GAPAGPAGTGKTETTKDLAKALGLL[p.C1853F]FVVTNCGEGMDYRAVGKIFSGLAQCG	KALGLLFVV,LAKALGLLF,AKALGLLFV,LAKALGLLFV,FVVTNCGEGM,DLAKALGLLF,AKALGLLFVV	THCA
DNAH10	c.5663G>A	p.R1888Q	DYRAVGKIFSGLAQCGAWGCFDEFN[p.R1888Q]QIDASVLSVISSQIQTIRNALIHQLT	QIDASVLSV,EFNQIDASV,DEFNQIDAS,NQIDASVLSV,DEFNQIDASV	UCEC
DNAH14	c.4099C>T	p.R1367C	QDIGPPAVKMLISAEGEGLVLPKKI[p.R1367C]CVRSAVEQWLVNVEKSMFDVLKKERY	KKICVRSAV,CVRSAVEQW,CVRSAVEQWL,LVLPKKICVR,LPKKICVRSA	UCEC
DNAH3	c.10099G>C	p.E3367Q	LNLRIKYIIDHFTLSIYNNVCRSLF[p.E3367Q]QKDKLLFSLLLTIGIMKQKKEITEEV	SLFQKDKLL,NVCRSLFQK,LFQKDKLLF,QKDKLLFSL,FQKDKLLFSL,SLFQKDKLLF	CESC
DNAH5	c.11465G>T	p.R3822L	QKLEISAETEVQINSAREEYRPVAT[p.R3822L]LGSILYFLITEMRLVNEMYQTSLRQF	VATLGSILY,TLGSILYFL,ATLGSILYF,RPVATLGSI,EEYRPVATL,PVATLGSILY,ATLGSILYFL,TLGSILYFLI,RPVATLGSIL,REEYRPVATL,VATLGSILYF	LUAD
DNAH5	c.2225G>A	p.R742Q	LFRETECMAQMGLEVSPLATSLFQK[p.R742Q]QDRYKRNFSNMKMMLAEYQRVKSKIP	LFQKQDRYK,SLFQKQDRY,KQDRYKRNF,SLFQKQDRYK,TSLFQKQDRY,LFQKQDRYKR,QKQDRYKRNF	SKCM
DNAH5	c.2945G>A	p.R982H	ELLSHFNHQNMDALLKVTRNTLEAI[p.R982H]HKRIHSSHTINFRDSNSASNMKQNSL	NTLEAIHKR,AIHKRIHSSH,NTLEAIHKRI,HKRIHSSHTI	CRC
DNAH5	c.5389C>G	p.Q1797E	TIELDKPVMAEGNVEVWLNSLLEES[p.Q1797E]ESSLHLVIRQAAANIQETGFQLTEFL	ESESSLHLV,LLEESESSL,ESSLHLVIR,EESESSLHL,SESSLHLVI,SLLEESESSL,LEESESSLHL,EESESSLHLV	HNSC
DNAH5	c.671G>A	p.R224Q	FLSSLEGFVNVLSGAQESLKEKVNL[p.R224Q]QKCDILELKTLKEPTDYLTLANNPET	LQKCDILEL,NLQKCDILEL,SLKEKVNLQK,LQKCDILELK	CRC

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DNAH5	c.9590G>A	p.R3197Q	HVTPKSYLSFIQGYKFIYGEKHVEV[p.R3197Q]QTLANRMNTGLEKLKEASESVAALSK	EKHVEVQTL,HVEVQTLANR,GEKHVEVQTL,VEVQTLANRM	OV
DNAH5	c.9706G>A	p.D3236N	KEASESVAALSKELEAKEKELQVAN[p.D3236N]NKADMVLKEVTMKAQAAEKVKAEVQK	ANNKADMVLK,QVANNKADMV,LQVANNKADM,KELQVANNKA	SKCM
DNAH7	c.8882G>A	p.R2961Q	LCKGRDIPCSDDCSLMGTLGEAVTI[p.R2961Q]QTWNIAGLPSDSFSIDNGIIIMNARR	IQTWNIAGL,GEAVTIQTW,TIQTWNIAGL,EAVTIQTWNI	UCEC
DNAH9	c.4639G>A	p.D1547N	LESIFTGSEDIRAQLPQDSKRFEGI[p.D1547N]NIDFKELAYDAQKIPNVVQTTNKPGL	NIDFKELAY,RFEGINIDF,SKRFEGINI,RFEGINIDFK,INIDFKELAY,KRFEGINIDF	CRC
DNAH9	c.8979C>G	p.S2993R	KFPAIVNCTAIHWFHEWPQQALESV[p.S2993R]RLRFLQNTEGIEPTVKQSISKFMAFV	SVRLRFLQN,RLRFLQNTE,QALESVRLR,QQALESVRL,ALESVRLRF,LESVRLRFL,SVRLRFLQNT,RLRFLQNTEG,QALESVRLRF	LUAD
DNAI2	c.691G>T	p.V231L	PNKPELALKPSSPLVTLEFNPKDSH[p.V231L]LLLGGCYNGQIACWDTRKGSLVAELS	NPKDSHLLL,SHLLLGGCY,LEFNPKDSHL	LUAD
DNAJC1	c.578delA	p.K193fs	AVVWSIYLEKQLDELLSRKKREKKK[p.K193fs]RLAARVWMYQNSVLQKKMKDC*	RVWMYQNSV,RLAARVWMY,MYQNSVLQK,VWMYQNSVL,REKKKRLAA,KKRLAARVW,KRLAARVWM,WMYQNSVLQ,WMYQNSVLQK,KKRLAARVWM,RVWMYQNSVL,MYQNSVLQKK,KRLAARVWMY,YQNSVLQKKM,KKKRLAARVW,ARVWMYQNSV	STAD
DNAJC10	c.239T>A	p.I80K	FKKLALKLHPDKNPNNPNAHGDFLK[p.I80K]KNRAYEVLKDEDLRKKYDKYGEKGLE	NAHGDFLKK,KNRAYEVLK,LKKNRAYEV,KKNRAYEVL,FLKKNRAYEV,GDFLKKNRAY,LKKNRAYEVL	MM
DNAJC12	c.404G>A	p.R135K	DLMLEESDKTHTTKMENEECNEQRE[p.R135K]KKKEELASTAEKTEQKEPKPLEKSVS	EQREKKKEEL,KKKEELASTA	MM
DNAJC13	c.3742G>A	p.E1248K	TPRLQSNTRALYQYCPIPIINYPQL[p.E1248K]KNELFCNIYYLKQLCDTLRFPDWPIK	PIINYPQLK,KNELFCNIY,YPQLKNELF,LKNELFCNI,QLKNELFCNI,NYPQLKNELF,KNELFCNIYY,INYPQLKNEL,LKNELFCNIY	UCEC
DNAJC24	c.181G>A	p.E61K	LMYHPDKQSTDVPAGTVEECVQKFI[p.E61K]KIDQAWKILGNEETKREYDLQRCEDD	KFIKIDQAW,FIKIDQAWK,IKIDQAWKI,FIKIDQAWKI,KFIKIDQAWK,QKFIKIDQAW,IKIDQAWKIL	CRC
DNASE1L1	c.634G>A	p.D212N	CASLTKKRLDKLELRTEPGFHWVIA[p.D212N]NGEDTTVRASTHCTYDRVVLHGERCR	VIANGEDTTV	CESC
DNM2	c.1134G>C	p.E378D	TLELSGGARINRIFHERFPFELVKM[p.E378D]DFDEKDLRREISYAIKNIHGVRTGLF	LVKMDFDEK,FPFELVKMDF	LIHC
DNM2	c.2371_2372insC	p.P791fs	QRRPVSSIHPPGRPPAVRGPTPGPP[p.P791fs]PDSCSRGGSSLLLGAPNPIPAWTPERVCQQ*	LLLGAPNPI,CSRGGSSLL,SRGGSSLLL,NPIPAWTPE,IPAWTPERV,SLLLGAPNPI,LLGAPNPIPA,CSRGGSSLLL,NPIPAWTPER,LGAPNPIPAW	STAD
DNMBP	c.232A>C	p.T78P	SSFVEIVTIPSLKEGERLFVCICEF[p.T78P]PSQELDNLPLHRGDLVILDGIPTAGW	FPSQELDNL	KIRC
DNMT1	c.1294G>A	p.E432K	LTCFSVYCKHGHLCPIDTGLIEKNI[p.E432K]KLFFSGSAKPIYDDDPSLEGGVNGKN	GLIEKNIKL,KLFFSGSAK,IEKNIKLFF,IKLFFSGSA,NIKLFFSGSA,GLIEKNIKLF	CRC
DNMT1	c.151G>A	p.E51K	RRLKDLERDSLTEKECVKEKLNLLH[p.E51K]KFLQTEIKNQLCDLETKLRKEELSEE	KLNLLHKFL,KEKLNLLHK,EKLNLLHKF,LLHKFLQTEI,KEKLNLLHKF	UCEC
DNMT1	c.2984G>A	p.R995Q	PEHYRKYSDYIKGSNLDAPEPYRIG[p.R995Q]QIKEIFCPKKSNGRPNETDIKIRVNK	QIKEIFCPK,RIGQIKEIF,GQIKEIFCPK,QIKEIFCPKK,APEPYRIGQI,YRIGQIKEIF	TGCT
DNMT1	c.4591G>C	p.E1531Q	RHNHWAGLYGRLEWDGFFSTTVTNP[p.E1531Q]QPMGKQGRVLHPEQHRVVSVRECARS	VTNPQPMGK,TTVTNPQPM,QPMGKQGRV,TVTNPQPMGK,QPMGKQGRVL,STTVTNPQPM	CRC
DNMT3A	c.2207G>A	p.R736H	NDLSIVNPARKGLYEGTGRLFFEFY[p.R736H]HLLHDARPKEGDDRPFFWLFENVVAM	HLLHDARPK,FYHLLHDAR,FEFYHLLHD,EFYHLLHDAR,FEFYHLLHDA	LAML

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DNMT3A	c.2644C>T	p.R882C	DILWCTEMERVFGFPVHYTDVSNMS[p.R882C]CLARQRLLGRSWSVPVIRHLFAPLKE	VSNMSCLAR,NMSCLARQR,DVSNMSCLA,YTDVSNMSCL,NMSCLARQRL,CLARQRLLGR,DVSNMSCLAR,SNMSCLARQR	LAML
DNMT3A	c.2645G>A	p.R882H	DILWCTEMERVFGFPVHYTDVSNMS[p.R882H]HLARQRLLGRSWSVPVIRHLFAPLKE	YTDVSNMSH,VSNMSHLAR,MSHLARQRL,NMSHLARQR,DVSNMSHLA,YTDVSNMSHL,HLARQRLLGR,MSHLARQRLL,DVSNMSHLAR,SNMSHLARQR,NMSHLARQRL	LAML
DNMT3B	c.274C>T	p.R92W	TQDLTGDGDGEDGDGSDTPVMPKLF[p.R92W]WETRTRSESPAVRTRNNNSVSSRERH	VMPKLFWET,KLFWETRTR,MPKLFWETR,TPVMPKLFW,VMPKLFWETR	CRC
DOCK1	c.2590G>A	p.E864K	SKMFTEFILNVPMGLLTIQKLYCLI[p.E864K]KIVHSDLFTQHDCREILLPMMTDQLK	KLYCLIKIV,IQKLYCLIK,IKIVHSDLF,CLIKIVHSDL,TIQKLYCLIK,LIKIVHSDLF,IQKLYCLIKI	CRC
DOCK10	c.5489C>T	p.A1830V	NENILVEQLYMCVEFLWKSERYELI[p.A1830V]VDVNKPIIAVFEKQRDFKKLSDLYYD	LIVDVNKPI,ELIVDVNKPI,WKSERYELIV,SERYELIVDV	CRC
DOCK11	c.505C>G	p.Q169E	FEIDEDCEKDEDSSSLCSQKGGVIK[p.Q169E]EGWLHKANVNSTITVTMKVFKRRYFY	VIKEGWLHKA,GVIKEGWLHK,KEGWLHKANV	TGCT
DOCK3	c.3547C>T	p.R1183C	ELFSLLTQLFGPYPSLLEKVEQETW[p.R1183C]CETGISFVTSVTRLMERLLDYRDCMK	TWCETGISF,QETWCETGI,VEQETWCET,CETGISFVT,ETWCETGISF,CETGISFVTS	CRC
DOCK5	c.529G>A	p.E177K	IDHGNRMLGLDLVVRDDNGNILDPD[p.E177K]KTSTIALFKAHEVASKRIEEKIQEEK	KTSTIALFK,ILDPDKTSTI,KTSTIALFKA,DPDKTSTIAL	CRC
DOCK8	c.3332delT	p.L1111fs	TLISMRLEFLRILCSHEHYLNLNLF[p.L1111fs]L*	HYLNLNLFL	KICH
DOCK8	c.531_532insG	p.A177fs	HKTLPKQTFESETLECSEPAAQAGP[p.A177fs]PPLKRAVRRVWERPRHCL*	AQAGPPPLK,RAVRRVWER,GPPPLKRAV,AAQAGPPPL,LKRAVRRVW,AAQAGPPPLK,AVRRVWERPR,RVWERPRHCL	KIRC
DOK5	c.820C>T	p.R274W	KMSERAASLSTMVPLPRSAYWQHIT[p.R274W]WQHSTGQLYRLQDVSSPLKLHRTETF	SAYWQHITW,YWQHITWQH,WQHSTGQLY,WQHITWQHS,RSAYWQHITW,YWQHITWQHS,TWQHSTGQLY,WQHITWQHST,ITWQHSTGQL	CRC
DOK7	c.1382G>A	p.G461D	GQTSAGCPSGWLGTRRRGLVMEAPQ[p.G461D]DSEATLPGPAPGEPWEAGGPHAGPPP	APQDSEATL,MEAPQDSEA,MEAPQDSEAT	ACC
DOPEY2	c.3586G>A	p.E1196K	KAGAKLSLVRVDSDKTQASESFSSD[p.E1196K]KEADLELQALTTSRLLKQQRERQEAV	ASESFSSDK,KEADLELQA,QASESFSSDK,KEADLELQAL,SESFSSDKEA	BLCA
DOPEY2	c.6143A>C	p.Y2048S	FEQKAMLLKRQAFAVFSGELDQYHL[p.Y2048S]SLPLIQERLTDNLRVGQTSIVAAQMF	SLPLIQERL,QYHLSLPLI,LSLPLIQER,DQYHLSLPL,GELDQYHLS,HLSLPLIQER,GELDQYHLSL,LDQYHLSLPL,DQYHLSLPLI,LSLPLIQERL	KIRC
DPCR1	c.2302_2304delTTG	p.L768del	NRERTANENTTPSPAQPTENGDRTP[p.L768del]ANEKTTPSLAEPTENGKRTPFANEKTTS	TENGDRTPA	KIRC
DPEP1	c.31G>T	p.V11L	MWSGWWLWPL[p.V11L]LAVCTADFFRDEAERIMRDSPVIDGH	WLWPLLAVC,GWWLWPLLA,WWLWPLLAV,LLAVCTADF,SGWWLWPLL,LAVCTADFF,WPLLAVCTA,WLWPLLAVCT,WSGWWLWPLL,GWWLWPLLAV,LAVCTADFFR,LLAVCTADFF	BRCA
DPP10	c.547G>A	p.V183I	TASYVIYNIHTREVWELNPPEVEDS[p.V183I]ILQYAAWGVQGQQLIYIFENNIYYQP	EVEDSILQY,ILQYAAWGV,VEDSILQYA,NPPEVEDSI,SILQYAAWGV,EVEDSILQYA,PEVEDSILQY,VEDSILQYAA	GBM
DPP6	c.2271G>T	p.L757F	TFTCGSALSPITDFKLYASAFSERY[p.L757F]FGLHGLDNRAYEMTKVAHRVSALEEQ	FSERYFGLH,AFSERYFGL,ASAFSERYF,ERYFGLHGL,SAFSERYFGL,YASAFSERYF,SERYFGLHGL	LUAD
DPP8	c.493G>A	p.G165R	QATLDYGMYSREEELLRERKRIGTV[p.G165R]RIASYDYHQGSGTFLFQAGSGIYHVK	RKRIGTVRI,IGTVRIASY,TVRIASYDY,KRIGTVRIA,GTVRIASYDY,RERKRIGTVR,RIGTVRIASY,TVRIASYDYH,RKRIGTVRIA	CRC
DPY19L1	c.1134C>A	p.F378L	ILKYLTSKIFGIADDAHIGNLLTSK[p.F378L]LFSYKDFDTLLYTCAAEFDFMEKETP	LTSKLFSYK,LLTSKLFSY,GNLLTSKLF,SKLFSYKDF,KLFSYKDFDT,LLTSKLFSYK,NLLTSKLFSY,IGNLLTSKLF	CRC
DPY19L1	c.745G>T	p.V249L	MLLVTHILRATKLYRGSLIALCISN[p.V249L]LFFMLPWQFAQFVLLTQIASLFAVYV	LIALCISNL,CISNLFFML,IALCISNLF,LFFMLPWQF,ALCISNLFF,LCISNLFFM,SNLFFMLPW,SLIALCISNL,ALCISNLFFM,IALCISNLFF,NLFFMLPWQF,LIALCISNLF,ISNLFFMLPW	KIRP

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DPY19L2	c.628A>G	p.M210V	INAIKRFHLYPEVIIASWYCTFMGI[p.M210V]VNLFGLETKTCWNVTRIEPLNEVQSC	CTFMGIVNL,CTFMGIVNLF,SWYCTFMGIV	PRAD
DQX1	c.1514G>A	p.R505H	ASCEFDCVDEMLTLAAMLTAAPGFT[p.R505H]HPPLSAEEAALRRALEHTDGDHSSLI	APGFTHPPL,MLTAAPGFTH	GBM
DRD5	c.825C>A	p.S275R	RIAQVQIRRISSLERAAEHAQSCRS[p.S275R]RAACAPDTSLRASIKKETKVLKTLSV	HAQSCRSRA,RSRAACAPD,AQSCRSRAA,RSRAACAPDT,RAACAPDTSL,AQSCRSRAAC	GBM
DSG4	c.383G>T	p.R128L	NPRTGEINITSVVDREITPLFLIYC[p.R128L]LALNSRGEDLERPLELRVKVMDINDN	FLIYCLALN,IYCLALNSR,TPLFLIYCL,FLIYCLALNS,ITPLFLIYCL,LIYCLALNSR,TPLFLIYCLA	LUAD
DSP	c.478C>G	p.R160G	CDAYQKRLLQLQEQMRALYKAISVP[p.R160G]GVRRASSKGGGGYTCQSGSGWDEFTK	AISVPGVRR,KAISVPGVR,GVRRASSKG,YKAISVPGV,KAISVPGVRR,LYKAISVPGV	HNSC
DST	c.13228G>T	p.A4410S	TICGKSVERQNKLEEALLFSGQFTD[p.A4410S]SLQALIDWLYRVEPQLAEDQPVHGDI	FTDSLQALI,SLQALIDWL,FSGQFTDSL,GQFTDSLQA,FTDSLQALID,SLQALIDWLY,GQFTDSLQAL,QFTDSLQALI	LUAD
DST	c.5300C>A	p.S1767Y	ITLTRSLSVQDGLDEMLDWMGNVES[p.S1767Y]YLKEQGQVPLNSTALQDIISKNIMLE	WMGNVESYL,MGNVESYLK,YLKEQGQVPL,WMGNVESYLK,DWMGNVESYL,ESYLKEQGQV,LDWMGNVESY	UCEC
DSTN	c.301_302insT	p.F101fs	KDCRYALYDASFETKESRKEELMFF[p.F101fs]FVGTRTSTSEK*	LMFFFVGTR,GTRTSTSEK,ELMFFFVGT,RKEELMFFF,EELMFFFVG,KEELMFFFV,LMFFFVGTRT,ELMFFFVGTR,SRKEELMFFF,FFFVGTRTST,EELMFFFVGT,KEELMFFFVG	STAD
DUOX2	c.2640C>A	p.F880L	SPEDKSRLMFTMYDLDENGFLSKDE[p.F880L]LFTMMRSFIEISNNCLSKAQLAEVVE	FLSKDELFT,GFLSKDELF,LFTMMRSFI,ELFTMMRSF,LSKDELFTM,SKDELFTMM,DELFTMMRS,FLSKDELFTM,ELFTMMRSFI,NGFLSKDELF,LSKDELFTMM,DELFTMMRSF	CRC
DVL2	c.1801delG	p.A601fs	YGGGSASSQHSEGSRSSGSTRSDGG[p.A601fs]QGARGGPRSGPPSPSPAVAVSLSPPAEGAAFGGVGKQVGLAMGALLHPEAQLGVPLISEPTQGSIPMDRPLAWPSPTTP*	ALLHPEAQL,SLSPPAEGA,GAAFGGVGK,GPPSPSPAV,SPPAEGAAF,EPTQGSIPM,IPMDRPLAW,RPLAWPSPT,VGKQVGLAM,KQVGLAMGA,PEAQLGVPL,AQLGVPLIS,GSIPMDRPL,LAWPSPTTP,AEGAAFGGV,AMGALLHPEA,LLHPEAQLGV,AVAVSLSPPA,SLSPPAEGAA,KQVGLAMGAL,LISEPTQGSI,STRSDGGQGA,RSGPPSPSPA,SPSPAVAVSL,HPEAQLGVPL,RPLAWPSPTT,LSPPAEGAAF,GVGKQVGLAM,SEPTQGSIPM,PEAQLGVPLI,AEGAAFGGVG	CRC
DVL2	c.197T>G	p.V66G	GDFKSVLQRPAGAKYFFKSMDQDFG[p.V66G]GVKEEISDDNARLPCFNGRVVSWLVS	SMDQDFGGV,KSMDQDFGGV,SMDQDFGGVK	GBM
DYNC2H1	c.2649G>T	p.E883D	KEWIVIGQVDMEALVEKHLFTVHDW[p.E883D]DKNFKALKIKGKEVERLPSAVKVDCL	HLFTVHDWDK,TVHDWDKNFK,HDWDKNFKAL	UCEC
DYRK1B	c.1633delC	p.Q545fs	DVPHKTHQAPASASSLPGTGAQLPP[p.Q545fs]SPDTLVVPHHQPHHHPRS*	HHQPHHHPR,LVVPHHQPH,SPDTLVVPH,LPPSPDTLV,QLPPSPDTLV,AQLPPSPDTL,LPPSPDTLVV	STAD
DYRK4	c.1402delA	p.K468fs	TASRRQTFFDSKGFPKNITNNRGKK[p.K468fs]DTQIPRTSRWC*	TQIPRTSRW,DTQIPRTSR,RGKKDTQIPR	STAD
DZIP3	c.964A>C	p.M322L	NLKYPGENDQSFSGKKCLKEGCTGD[p.M322L]LVRMLQCDVPGIVKILFEVVRKDEYI	KEGCTGDLV,CLKEGCTGDL	LUAD
E2F7	c.272T>G	p.I91S	PITPVKFVDRQQAEPWTPTANLKML[p.I91S]SSAASPDIRDREKKKGLFRPIENKDD	NLKMLSSAA,LKMLSSAAS,KMLSSAASP,MLSSAASPDI,LKMLSSAASP	TGCT
EAF2	c.327delA	p.V109fs	CILIINHDTGECRLEKLSSNITVKK[p.V109fs]QELKEAVKFSIVKNNSNNKCGIQPGLPIL*	ITVKKQELK,IVKNNSNNK,KQELKEAVK,KKQELKEAV,QELKEAVKF,KEAVKFSIV,CGIQPGLPI,SIVKNNSNNK,ELKEAVKFSI,KQELKEAVKF,CGIQPGLPIL	STAD
EBAG9	c.559G>A	p.E187K	EEDAAWQAEEVLRQQKLADREKRAA[p.E187K]KQQRKKMEKEAQRLMKKEQNKIGVKL	RAAKQQRKK,KQQRKKMEK,RAAKQQRKKM	CRC
EBF1	c.1058A>G	p.D353G	SYKSKQFCKGTPGRFIYTALNEPTI[p.D353G]GYGFQRLQKVIPRHPGDPERLPKEVI	ALNEPTIGY,PTIGYGFQR,NEPTIGYGF,IGYGFQRLQK,GYGFQRLQKV,TALNEPTIGY,LNEPTIGYGF	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EBPL	c.565C>G	p.L189V	YCWLYLFFFNGVWVLIPGLLLWQSW[p.L189V]VELKKMHQKETSSVKKFQ*	GLLLWQSWV,LLWQSWVEL,WQSWVELKK,LLLWQSWVEL,LLWQSWVELK,WQSWVELKKM	KICH,KIRP,TGCT
EBPL	c.587A>C	p.Q196P	FFNGVWVLIPGLLLWQSWLELKKMH[p.Q196P]PKETSSVKKFQ*	KMHPKETSS,KMHPKETSSV	KICH
ECE2	c.760G>A	p.D254N	DRGVSPCEDFYQFSCGGWIRRNPLP[p.D254N]NGRSRWNTFNSLWDQNQAILKHLLEN	NGRSRWNTF,NPLPNGRSRW	CESC
ECI2	c.164A>G	p.K55R	HMNRTAMRASQKDFENSMNQVKLLK[p.K55R]RDPGNEVKLKLYALYKQATEGPCNMP	LLKRDPGNEV,SMNQVKLLKR	TGCT
ECM1	c.796G>A	p.E266K	EIGYSRCCHCRSHTNRLECAKLVWE[p.E266K]KAMSRFCEAEFSVKTRPHWCCTRQGE	KAMSRFCEA,VWEKAMSRF,LVWEKAMSR,AKLVWEKAM,WEKAMSRFC,KLVWEKAMSR,LVWEKAMSRF,CAKLVWEKAM	BLCA
EDA	c.174G>C	p.L58F	RAGEGNSCLLFLGFFGLSLALHLLT[p.L58F]FCCYLELRSELRRERGAESRLGGSGT	HLLTFCCYL,LTFCCYLEL,SLALHLLTF,TFCCYLELR,LHLLTFCCY,LLTFCCYLEL,SLALHLLTFC,LTFCCYLELR,LSLALHLLTF,ALHLLTFCCY	HNSC
EDNRB	c.1349T>G	p.L450R	SRILKLTLYNQNDPNRCELLSFLLV[p.L450R]WDYIGINMASLNSCINPIALYLVSKR	LSFLLVWDY,LLVWDYIGI,SFLLVWDYI,WDYIGINMA,FLLVWDYIGI,LLSFLLVWDY,CELLSFLLVW,LVWDYIGINM	CRC
EEA1	c.1709delA	p.N570fs	EREDLYAKIQAGEGETAVLNQLQEK[p.N570fs]TIHYRSK*	QLQEKTIHY,QLQEKTIHYR,NQLQEKTIHY	STAD
EEF1A1	c.1294_1295AC>TT	p.T432L	GKPMCVESFSDYPPLGRFAVRDMRQ[p.T432L]LVAVGVIKAVDKKAAGAGKVTKSAQKA	QLVAVGVIK,AVRDMRQLV,FAVRDMRQL,RDMRQLVAV,RQLVAVGVI,QLVAVGVIKA,LVAVGVIKAV,AVRDMRQLVA,RQLVAVGVIK,FAVRDMRQLV	LIHC
EEF1A2	c.1253A>C	p.Y418S	SLKSGDAAIVEMVPGKPMCVESFSQ[p.Y418S]SPPLGRFAVRDMRQTVAVGVIKNVEK	ESFSQSPPL,SPPLGRFAV,SQSPPLGRF,SFSQSPPLGR,VESFSQSPPL,FSQSPPLGRF,SQSPPLGRFA	BLCA,TGCT
EEF1B2	c.127A>G	p.S43G	YLADKSYIEGYVPSQADVAVFEAVS[p.S43G]GPPPADLCHALRWYNHIKSYEKEKAS	EAVSGPPPA,FEAVSGPPP,FEAVSGPPPA	KIRP,PRAD,SKCM
EEF2K	c.2017G>A	p.E673K	TDCDEGGEYDGMQDEPRYMMLAREA[p.E673K]KMLFTGGYGLEKDPQRSGDLYTQAAE	MMLAREAKM,MLAREAKML,YMMLAREAK,AKMLFTGGY,LAREAKMLF,REAKMLFTG,YMMLAREAKM,MMLAREAKML,KMLFTGGYGL,MLAREAKMLF,RYMMLAREAK,EAKMLFTGGY,REAKMLFTGG	BLCA
EFCAB4B	c.793G>C	p.E265Q	MEQQIKSEKEQFLLKDTERFQARSQ[p.E265Q]QLEQKLLCKEQELEQLTQKQKRLEGQ	RFQARSQQL,RSQQLEQKL,SQQLEQKLL,QARSQQLEQK,ERFQARSQQL,FQARSQQLEQ,RSQQLEQKLL	LUAD
EFCAB6	c.1136G>A	p.R379K	NWKQFLTSFHEPQGLQVSSKGPLTK[p.R379K]KNSINSRNESHKENIITKLFRHTEDH	SSKGPLTKK,GPLTKKNSI,VSSKGPLTKK,LTKKNSINSR	BLCA,GBM,PRAD
EFCAB6	c.3004G>A	p.E1002K	DQSKTNYISICKMQEVLEECGCSLT[p.E1002K]KGELTHLLNSWGVSRHDNAINYLDFL	SLTKGELTHL	HNSC
EGFR	c.1786C>T	p.P596S	CTGRGPDNCIQCAHYIDGPHCVKTC[p.P596S]SAGVMGENNTLVWKYADAGHVCHLCH	CVKTCSAGV,VKTCSAGVM,CVKTCSAGVM	GBM
EGFR	c.1787C>T	p.P596L	CTGRGPDNCIQCAHYIDGPHCVKTC[p.P596L]LAGVMGENNTLVWKYADAGHVCHLCH	CVKTCLAGV,GPHCVKTCL,VKTCLAGVM	GBM
EGFR	c.1793G>C	p.G598A	GRGPDNCIQCAHYIDGPHCVKTCPA[p.G598A]AVMGENNTLVWKYADAGHVCHLCHPN	CVKTCPAAV,VKTCPAAVM,AVMGENNTL,AVMGENNTLV,CVKTCPAAVM,AAVMGENNTL	GBM
EGFR	c.1793G>T	p.G598V	GRGPDNCIQCAHYIDGPHCVKTCPA[p.G598V]VVMGENNTLVWKYADAGHVCHLCHPN	CVKTCPAVV,VKTCPAVVM,VVMGENNTLV,CVKTCPAVVM	GBM
EGFR	c.185T>G	p.L62R	KLTQLGTFEDHFLSLQRMFNNCEVV[p.L62R]RGNLEITYVQRNYDLSFLKTIQEVAG	MFNNCEVVR,EVVRGNLEI,VRGNLEITY,RMFNNCEVVR,VVRGNLEITY,CEVVRGNLEI	GBM
EGFR	c.2125G>A	p.E709K	QERELVEPLTPSGEAPNQALLRILK[p.E709K]KTEFKKIKVLGSGAFGTVYKGLWIPE	RILKKTEFK,ILKKTEFKK,QALLRILKK,LRILKKTEF,RILKKTEFKK,NQALLRILKK,LLRILKKTEF	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EGFR	c.2156G>C	p.G719A	PSGEAPNQALLRILKETEFKKIKVL[p.G719A]ASGAFGTVYKGLWIPEGEKVKIPVAI	ASGAFGTVY,VLASGAFGT,LASGAFGTV,KIKVLASGA,KVLASGAFG,IKVLASGAF,KKIKVLASG,VLASGAFGTV,ASGAFGTVYK,KIKVLASGAF,LASGAFGTVY,KKIKVLASGA,TEFKKIKVLA	LUAD
EGFR	c.2235_2249delGGAATTAAGAGAAGC	p.ELREA746del	GAFGTVYKGLWIPEGEKVKIPVAIK[p.ELREA746del]TSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLIT	AIKTSPKANK,KVKIPVAIKT,KTSPKANKEI	LUAD
EGFR	c.2303G>T	p.S768I	AIKELREATSPKANKEILDEAYVMA[p.S768I]IVDNPHVCRLLGICLTSTVQLITQLM	MAIVDNPHV,VMAIVDNPH,DEAYVMAIV,LDEAYVMAI,ILDEAYVMAI,VMAIVDNPHV,AIVDNPHVCR,YVMAIVDNPH,DEAYVMAIVD	LUAD
EGFR	c.2512C>A	p.L838M	YLLNWCVQIAKGMNYLEDRRLVHRD[p.L838M]MAARNVLVKTPQHVKITDFGLAKLLG	RLVHRDMAA,DMAARNVLV,MAARNVLVK,LVHRDMAAR,RDMAARNVL,RLVHRDMAAR,DMAARNVLVK,HRDMAARNVL,RDMAARNVLV	KIRC
EGFR	c.2573T>G	p.L858R	LVHRDLAARNVLVKTPQHVKITDFG[p.L858R]RAKLLGAEEKEYHAEGGKVPIKWMAL	KITDFGRAK,HVKITDFGR,FGRAKLLGA,HVKITDFGRA,RAKLLGAEEK	LUAD
EGFR	c.2582T>A	p.L861Q	RDLAARNVLVKTPQHVKITDFGLAK[p.L861Q]QLGAEEKEYHAEGGKVPIKWMALESI	LAKQLGAEEK,KQLGAEEKEY	LUSC
EGFR	c.323G>A	p.R108K	QEVAGYVLIALNTVERIPLENLQII[p.R108K]KGNMYYENSYALAVLSNYDANKTGLK	QIIKGNMYY,LQIIKGNMY,LQIIKGNMYY,KGNMYYENSY	GBM
EGFR	c.754C>T	p.R252C	SPSDCCHNQCAAGCTGPRESDCLVC[p.R252C]CKFRDEATCKDTCPPLMLYNPTTYQM	RESDCLVCC	GBM
EGFR	c.865G>A	p.A289T	CPPLMLYNPTTYQMDVNPEGKYSFG[p.A289T]TTCVKKCPRNYVVTDHGSCVRACGAD	YSFGTTCVK,TTCVKKCPR,GKYSFGTTC,YSFGTTCVKK,KYSFGTTCVK,GTTCVKKCPR,GKYSFGTTCV	GBM
EGFR	c.866C>A	p.A289D	CPPLMLYNPTTYQMDVNPEGKYSFG[p.A289D]DTCVKKCPRNYVVTDHGSCVRACGAD	YSFGDTCVK,DTCVKKCPR,GKYSFGDTC,YSFGDTCVKK,KYSFGDTCVK,GKYSFGDTCV	GBM
EGFR	c.866C>T	p.A289V	CPPLMLYNPTTYQMDVNPEGKYSFG[p.A289V]VTCVKKCPRNYVVTDHGSCVRACGAD	YSFGVTCVK,KYSFGVTCV,VTCVKKCPR,GKYSFGVTC,YSFGVTCVKK,KYSFGVTCVK,GVTCVKKCPR,GKYSFGVTCV	GBM
EGFR	c.910C>T	p.H304Y	VNPEGKYSFGATCVKKCPRNYVVTD[p.H304Y]YGSCVRACGADSYEMEEDGVRKCKKC	VVTDYGSCV,YVVTDYGSCV,VVTDYGSCVR,CPRNYVVTDY	GBM
EGR1	c.27G>C	p.Q9H	MAAAKAEM[p.Q9H]HLMSPLQISDPFGSFPHSPTMDNYPK	AAKAEMHLM,AEMHLMSPL,MHLMSPLQI,MAAAKAEMHL,AAAKAEMHLM,KAEMHLMSPL,EMHLMSPLQI,AEMHLMSPLQ	MM
EGR1	c.994delC	p.P332fs	TSYQSQLIKPSRMRKYPNRPSKTPP[p.P332fs]TNALTLAQWSPVIAASPAPTSSPATSASTQARSPSSAASACATSAAATTSPPTSAPTQAKSPSPATSVEESLPGAMNARGIPRSTCGRRTRKQTKVLWPLRPPPLSLPTRPRLLPLTRPRLLPLIHPRPPPHTHPLCPPPSPLPAPRPTHPLCTVASPPRRWPPRTPLFPLLSRPRSAASLPQLSPTPSAPPQGFRT*	LTLAQWSPV,TLAQWSPVI,AQWSPVIAA,KQTKVLWPL,VIAASPAPT,AMNARGIPR,RLLPLTRPR,RLLPLIHPR,ATSASTQAR,STCGRRTRK,CTVASPPRR,LWPLRPPPL,STQARSPSS,QARSPSSAA,RSPSSAASA,ASACATSAA,KSPSPATSV,RSTCGRRTR,RTRKQTKVL,QTKVLWPLR,PTRPRLLPL,RPRLLPLTR,LTRPRLLPL,LIHPRPPPH,SLPGAMNAR,ESLPGAMNA,SPVIAASPA,SPAPTSSPA,RPPPLSLPT,LPLTRPRLL,RPRLLPLIH,HPRPPPHTH,RPPPHTHPL,SPLPAPRPT,APRPTHPLC,RPTHPLCTV,SLPTRPRLL,SKTPPTNAL,TQARSPSSA,TQAKSPSPA,VEESLPGAM,LSLPTRPRL,CPPPSPLPA,ALTLAQWSPV,TLAQWSPVIA,VLWPLRPPPL,RLLPLTRPRL,GAMNARGIPR,RSTCGRRTRK,KTPPTNALTL,STQARSPSSA,ASACATSAAA,RGIPRSTCGR,CGRRTRKQTK,RTRKQTKVLW,KQTKVLWPLR,KVLWPLRPPP,LTRPRLLPLI,HTHPLCPPPS,ESLPGAMNAR,WSPVIAASPA,TTSPPTSAPT,RPSKTPPTNA,SPAPTSSPAT,APTSSPATSA,SPATSASTQA,SPATSVEESL,LPGAMNARGI,WPLRPPPLSL,LPTRPRLLPL,HPLCPPPSPL,LPAPRPTHPL,APRPTHPLCT,RPTHPLCTVA,LTLAQWSPVI,AQWSPVIAAS,TQARSPSSAA,TQAKSPSPAT,AKSPSPATSV,RKQTKVLWPL,LSLPTRPRLL,EESLPGAMNA	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EGR2	c.1105G>A	p.E369K	SKTPVHERPYPCPAEGCDRRFSRSD[p.E369K]KLTRHIRIHTGHKPFQCRICMRNFSR	RRFSRSDKL	CLL
EGR2	c.1169G>A	p.R390H	SRSDELTRHIRIHTGHKPFQCRICM[p.R390H]HNFSRSDHLTTHIRTHTGEKPFACDY	RICMHNFSR,HNFSRSDHL,FQCRICMHNF,CMHNFSRSDH,MHNFSRSDHL	CRC
EGR2	c.1189C>A	p.H397N	RHIRIHTGHKPFQCRICMRNFSRSD[p.H397N]NLTTHIRTHTGEKPFACDYCGRKFAR	RNFSRSDNL,RSDNLTTHI,MRNFSRSDNL,FSRSDNLTTH,SRSDNLTTHI	CLL
EHD3	c.130G>A	p.E44K	QTVSEGLKKLYKSKLLPLEEHYRFH[p.E44K]KFHSPALEDADFDNKPMVLLVGQYST	HYRFHKFHS,RFHKFHSPA,FHKFHSPAL,EEHYRFHKF,YRFHKFHSP,RFHKFHSPAL,YRFHKFHSPA,LEEHYRFHKF,EEHYRFHKFH	CRC
EHHADH	c.2112G>T	p.Q704H	LQKYYRQNPDIPQLEPSDYLKKLAS[p.Q704H]HGNPPLKEWQSLAGSPSSKL*	ASHGNPPLK,LASHGNPPL,KLASHGNPPL,LASHGNPPLK	LUAD
EIF1AX	c.26G>A	p.G9D	MPKNKGKG[p.G9D]DKNRRRGKNENESEKRELVFKEDGQE	KGDKNRRRGK	THCA
EIF2C1	c.416G>A	p.R139Q	EVTIPGEGKDRIFKVSIKWLAIVSW[p.R139Q]QMLHEALVSGQIPVPLESVQALDVAM	WLAIVSWQM,WQMLHEALV,AIVSWQMLH,SWQMLHEAL,LAIVSWQML,WLAIVSWQML,IVSWQMLHEA,KWLAIVSWQM,SWQMLHEALV,VSWQMLHEAL,WQMLHEALVS	CRC
EIF3J	c.23C>G	p.A8G	MAAAAAA[p.A8G]GGDSDSWDADAFSVEDPVRKVGGGGT	AAAGGDSDSW	TGCT
EIF4G3	c.23G>A	p.R8H	MNSQPQT[p.R8H]HSPFFQRPQIQPPRATIPNSSPSIRP	QTHSPFFQR,SQPQTHSPF,QPQTHSPFF,SQPQTHSPFF,NSQPQTHSPF	CLL
ELAVL2	c.789G>T	p.L263F	RLDNLLNMAYGVKRFSPMTIDGMTS[p.L263F]FAGINIPGHPGTGWCIFVYNLAPDAD	MTIDGMTSF,TIDGMTSFA,DGMTSFAGI,MTSFAGINI,MTIDGMTSFA,GMTSFAGINI,PMTIDGMTSF	LUAD
ELF3	c.915delC	p.F305fs	DILIHPELNEGLMKWENRHEGVFKF[p.F305fs]CAPRLWPNYGAKRKRTAT*	GVFKFCAPR,RLWPNYGAK,VFKFCAPRL,CAPRLWPNY,YGAKRKRTA,FKFCAPRLW,HEGVFKFCA,RLWPNYGAKR,VFKFCAPRLW,FCAPRLWPNY,EGVFKFCAPR,APRLWPNYGA,GVFKFCAPRL	CRC
ELF4	c.1244C>T	p.S415L	KLTKAVSASSVPSNIHLGVAPVGSG[p.S415L]LALTLQTIPLTTVLTNGPPASTTAPT	GLALTLQTI,GVAPVGSGL,APVGSGLAL,VGSGLALTL,GVAPVGSGLA,LGVAPVGSGL,SGLALTLQTI,LALTLQTIPL	HNSC
ELMOD2	c.422C>T	p.T141M	RKRPYDSDNLQHEELLMKLWNLLMP[p.T141M]MKKLNARISKQWAEIGFQGDDPKTDF	KLWNLLMPM,LWNLLMPMK,MPMKKLNAR,LLMPMKKLNA,KLWNLLMPMK,LWNLLMPMKK,MKKLNARISK,LMPMKKLNAR,MPMKKLNARI,MKLWNLLMPM	CRC
EME1	c.1708G>C	p.D570H	IGPELSRRIYLQMTTLQPHLSLDSA[p.D570H]H*	QPHLSLDSAH	LUSC
EMILIN1	c.79C>G	p.R27G	APRTLWSCYLCCLLTAAAGAASYPP[p.R27G]GGFSLYTGSSGALSPGGPQAQIAPRP	SYPPGGFSL,YPPGGFSLY,AASYPPGGF,SYPPGGFSLY,ASYPPGGFSL,GAASYPPGGF	BLCA
EML6	c.2414A>G	p.K805R	FSADGKCLVSVGLDDFHSIVFWDWK[p.K805R]RGEKIATTRGHKDKIFVVKCNPHHVD	SIVFWDWKR,WDWKRGEKI,HSIVFWDWKR,VFWDWKRGEK	TGCT
EMR1	c.1478G>A	p.R493H	EESESTETTGVAFVSFVGMESVLNE[p.R493H]HFFKDHQAPLTTSEIKLKMNSRVVGG	SVLNEHFFK,MESVLNEHF,ESVLNEHFFK,HFFKDHQAPL,GMESVLNEHF,MESVLNEHFF,NEHFFKDHQA	LUAD
EMR1	c.1892G>A	p.R631Q	SHVGIIISLVCLVLAIATFLLCRSI[p.R631Q]QNHNTYLHLHLCVCLLLAKTLFLAGI	SIQNHNTYL,RSIQNHNTY,IQNHNTYLH,QNHNTYLHL,RSIQNHNTYL,IQNHNTYLHL,CRSIQNHNTY	UCEC
EMR2	c.224C>T	p.S75L	GFSSFSEIITTPMETCDDINECATL[p.S75L]LKVSCGKFSDCWNTEGSYDCVCSPGY	TLLKVSCGK,DINECATLL,LLKVSCGKF,NECATLLKV,ATLLKVSCGK,DINECATLLK,TLLKVSCGKF	CRC
ENAH	c.1541G>T	p.R514L	TPEPTRKPWERTNTMNGSKSPVISR[p.R514L]LDSPRKNQIVFDNRSYDSLHRPKSTP	VISRLDSPR,ISRLDSPRK,SKSPVISRL,VISRLDSPRK,GSKSPVISRL,PVISRLDSPR	LUAD
ENAM	c.1118G>A	p.R373H	PFYRNQQVQRGPRWNFFAWERKQVA[p.R373H]HPGNPVYHKAYPPTSRGNYPNYAGNP	QVAHPGNPV,VAHPGNPVY,KQVAHPGNPV,QVAHPGNPVY,FAWERKQVAH	CRC
ENOX2	c.1066C>T	p.R356W	QFEQIVAVYHSASKQKAWDHFTKAQ[p.R356W]WKNISVWCKQAEEIRNIHNDELMGIR	AQWKNISVW,KAQWKNISV,HFTKAQWKNI,QWKNISVWCK,KAQWKNISVW,AQWKNISVWC	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ENPEP	c.866T>G	p.F289C	EESVDDKWTRTTFEKSVPMSTYLVC[p.F289C]CAVHQFDSVKRISNSGKPLTIYVQPE	STYLVCCAV,MSTYLVCCA,CAVHQFDSV,LVCCAVHQF,YLVCCAVHQF,MSTYLVCCAV,CAVHQFDSVK	KIRC
ENPP1	c.2213G>A	p.G738E	YQDFRIPLSPVHKCSFYKNNTKVSY[p.G738E]EFLSPPQLNKNSSGIYSEALLTTNIV	NTKVSYEFL,YEFLSPPQL,SYEFLSPPQL,EFLSPPQLNK,KNNTKVSYEF,YEFLSPPQLN	LUAD
ENTPD2	c.611delG	p.G204fs	NFIKYGWVGRWFRPRKGTLGAMDLG[p.G204fs]VPLPRSLLRQPVQLRTEPARSSCISTASTTESTPTASSAMAVTRSSRGCWPAPSRPTASTPAGRGAFPPKCCSGMCTSHHAPWPSGPRTSTAVPGSACQGAVTPTSAEIWFLGSSASPPAPSPDALSMGSSSPQWLGTLWPSLPSSTLWTFCGLRWGCPWPPCSSWRQPQ*	TLGAMDLGV,SLLRQPVQL,WLGTLWPSL,TLWPSLPSS,STLWTFCGL,AVTPTSAEI,ASSAMAVTR,TLWTFCGLR,LWTFCGLRW,RSLLRQPVQ,LLRQPVQLR,AMAVTRSSR,RSSRGCWPA,SSRGCWPAP,RGCWPAPSR,AGRGAFPPK,HAPWPSGPR,STTESTPTA,ESTPTASSA,STPTASSAM,EIWFLGSSA,WPAPSRPTA,APSRPTAST,RPTASTPAG,FPPKCCSGM,WPSGPRTST,APSPDALSM,WPSLPSSTL,LPSSTLWTF,GAMDLGVPL,LGVPLPRSL,ARSSCISTA,MCTSHHAPW,SMGSSSPQW,CGLRWGCPW,TPTSAEIWF,SPQWLGTLW,CPWPPCSSW,AEIWFLGSS,GTLGAMDLGV,FLGSSASPPA,SMGSSSPQWL,TLWPSLPSST,AMDLGVPLPR,SAMAVTRSSR,STLWTFCGLR,QWLGTLWPSL,LWPSLPSSTL,SLPSSTLWTF,RSLLRQPVQL,RTEPARSSCI,RSSCISTAST,SSRGCWPAPS,RTSTAVPGSA,SLLRQPVQLR,TASSAMAVTR,HHAPWPSGPR,STPTASSAMA,TSAEIWFLGS,SSTLWTFCGL,WTFCGLRWGC,LPRSLLRQPV,QPVQLRTEPA,TPTASSAMAV,WPAPSRPTAS,WPSGPRTSTA,VPGSACQGAV,SPPAPSPDAL,ASTPAGRGAF,ESTPTASSAM,LSMGSSSPQW,LGAMDLGVPL,GMCTSHHAPW,CQGAVTPTSA,AEIWFLGSSA,SSSPQWLGTL,TPTSAEIWFL,WPSLPSSTLW,TESTPTASSA,LPSSTLWTFC	STAD
ENTPD7	c.979G>A	p.E327K	HTEHVYRVYVTTFLGFGGNFARQRY[p.E327K]KDLVLNETLNKNRLLGQKTGLSPDNP	GNFARQRYK,RQRYKDLVL,FARQRYKDL,KDLVLNETL,GGNFARQRYK,RQRYKDLVLN,FARQRYKDLV,YKDLVLNETL	CRC
EOMES	c.995delG	p.G332fs	LNPTAHYNVFVEVVLADPNHWRFQG[p.G332fs]ANG*	HWRFQGANG	STAD
EP300	c.3491G>A	p.C1164Y	YKYCSKLSEVFEQEIDPVMQSLGYC[p.C1164Y]YGRKLEFSPQTLCCYGKQLCTIPRDA	SLGYCYGRK,YCYGRKLEF,VMQSLGYCY,QSLGYCYGR,LGYCYGRKL,QSLGYCYGRK,GYCYGRKLEF,PVMQSLGYCY,MQSLGYCYGR	HNSC
EP300	c.4195G>A	p.D1399N	FGMHVQEYGSDCPPPNQRRVYISYL[p.D1399N]NSVHFFRPKCLRTAVYHEILIGYLEY	YLNSVHFFR,NSVHFFRPK,VYISYLNSV,ISYLNSVHF,SYLNSVHFF,RVYISYLNS,YISYLNSVH,RVYISYLNSV,SYLNSVHFFR,YISYLNSVHF,ISYLNSVHFF,LNSVHFFRPK	CESC,HNSC,LUSC
EPB41L3	c.2686G>T	p.A896S	SYSAGDSGDAAAQPAFTGIKGKEGS[p.A896S]SLTEGAKEEGGEEVAKAVLEQEETAA	GSSLTEGAK,IKGKEGSSL,KEGSSLTEGA	LUAD
EPG5	c.1105G>A	p.D369N	KVFSYHRYQRVEMNENALVELKKLF[p.D369N]NAKSEHLHQTLALHSYTSVLSRLQVE	KLFNAKSEH,ELKKLFNAK,VELKKLFNA,KLFNAKSEHL	CRC
EPG5	c.6866G>T	p.R2289L	MALSSLFMEVLMMMNNATIPTAEFL[p.R2289L]LGSIRTWIGQKMHGLVVLPLLTAACQ	LLGSIRTWI,TIPTAEFLL,FLLGSIRTW,FLLGSIRTWI,EFLLGSIRTW,ATIPTAEFLL,AEFLLGSIRT	LUAD
EPHA1	c.332G>T	p.G111V	IYRGEEASRVHVELQFTVRDCKSFP[p.G111V]VGAGPLGCKETFNLLYMESDQDVGIQ	FPVGAGPLG,TVRDCKSFPV,KSFPVGAGPL,FPVGAGPLGC	LUAD
EPHA1	c.550G>A	p.A184T	LVSGSVKLNVERCSLGRLTRRGLYL[p.A184T]TFHNPGACVALVSVRVFYQRCPETLN	YLTFHNPGA,LTRRGLYLT,TRRGLYLTF,LTFHNPGACV,LTRRGLYLTF	GBM
EPHA10	c.2604delC	p.P868fs	ERPYWDMSGQDVIKAVEDGFRLPPP[p.P868fs]GTVLTFCTD*	RLPPPGTVL,GFRLPPPGTV,LPPPGTVLTF,FRLPPPGTVL	STAD
EPHA2	c.1379delC	p.P460fs	NQTEPPKVRLEGRSTTSLSVSWSIP[p.P460fs]RRSRAECGSTRSLTARRETPTATMCAAPRVSP*	ATMCAAPRV,LSVSWSIPR,SVSWSIPRR,GSTRSLTAR,RSRAECGST,STRSLTARR,RSLTARRET,TARRETPTA,SWSIPRRSR,TATMCAAPR,ETPTATMCA,IPRRSRAEC,TPTATMCAA,AECGSTRSL,RRETPTATM,RETPTATMC,SLSVSWSIPR,LSVSWSIPRR,SWSIPRRSRA,RSRAECGSTR,VSWSIPRRSR,PTATMCAAPR,ETPTATMCAA,TATMCAAPRV,RAECGSTRSL,ARRETPTATM,RETPTATMCA,AECGSTRSLT	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EPHA3	c.2405C>G	p.T802R	AAYTTRGGKIPIRWTSPEAIAYRKF[p.T802R]RSASDVWSYGIVLWEVMSYGERPYWE	RSASDVWSY,KFRSASDVW,IAYRKFRSA,AYRKFRSAS,EAIAYRKFR,RKFRSASDV,AIAYRKFRSA,KFRSASDVWS,IAYRKFRSAS,RKFRSASDVW,FRSASDVWSY	HNSC
EPHA6	c.2854G>C	p.D952H	TTGGKIPIRWTAPEAIAYRKFSSAS[p.D952H]HAWSYGIVMWEVMSYGERPYWEMSNQ	SSASHAWSY,KFSSASHAW,ASHAWSYGI,HAWSYGIVM,YRKFSSASH,RKFSSASHA,FSSASHAWSY,AYRKFSSASH,ASHAWSYGIV,SASHAWSYGI,RKFSSASHAW,SHAWSYGIVM,HAWSYGIVMW	HNSC
EPHB2	c.1175G>A	p.R392H	SGRGACTRCGDNVQYAPRQLGLTEP[p.R392H]HIYISDLLAHTQYTFEIQAVNGVTDQ	GLTEPHIYI,RQLGLTEPH,LGLTEPHIY,RQLGLTEPHI,QLGLTEPHIY,HIYISDLLAH,TEPHIYISDL	CRC
EPHB6	c.1010G>A	p.R337H	KACQACPRGLYKSSAGNAPCSPCPA[p.R337H]HSHAPNPAAPVCPCLEGFYRASSDPP	HSHAPNPAA	LUAD
EPHB6	c.160delG	p.G54fs	ALEEVLLDTTGETSEIGWLTYPPGG[p.G54fs]GTR*	LTYPPGGGTR	STAD
EPHX1	c.394delC	p.P132fs	ILNRYPHFKTKIEGLDIHFIHVKPP[p.P132fs]SCPQAIPRSPC*	KPPSCPQAI,HVKPPSCPQA,CPQAIPRSPC	STAD
EPHX4	c.845G>A	p.R282Q	TTEDLEAYIYVFSQPGALSGPINHY[p.R282Q]QNIFSCLPLKHHMVTTPTLLLWGEND	HYQNIFSCL,GPINHYQNI,YQNIFSCLP,QNIFSCLPL,YQNIFSCLPL,QNIFSCLPLK,GPINHYQNIF,NHYQNIFSCL	UCEC
EPPK1	c.6044delG	p.G2015fs	FQAMQKQLIEKAEALRLLEVQVATG[p.G2015fs]VSSTHSTTTGSHWKQPTDGAVCTRTSMRSFPTRST*	STTTGSHWK,AVCTRTSMR,TSMRSFPTR,CTRTSMRSF,RTSMRSFPT,SMRSFPTRS,LEVQVATGV,VQVATGVSS,HSTTTGSHW,WKQPTDGAV,GAVCTRTSM,LLEVQVATGV,RTSMRSFPTR,HSTTTGSHWK,STHSTTTGSH,CTRTSMRSFP,SMRSFPTRST,VQVATGVSST,VCTRTSMRSF	STAD
EPPK1	c.7132G>C	p.D2378H	HSHRVPVDVAYRRGYFDEEMNRVLA[p.D2378H]HPSDDTKGFFDPNTHENLTYLQLLQR	EEMNRVLAH,HPSDDTKGF,VLAHPSDDTK,HPSDDTKGFF,DEEMNRVLAH	ACC
EPRS	c.3451G>T	p.V1151L	MYPAYAKWVQSHRDLPIKLNQWCNV[p.V1151L]LRWEFKHPQPFLRTREFLWQEGHSAF	KLNQWCNVL,CNVLRWEFK,NQWCNVLRW,LNQWCNVLR,WCNVLRWEF,KLNQWCNVLR,QWCNVLRWEF,IKLNQWCNVL	LUAD
EPRS	c.4003C>A	p.L1335I	GITNALSEEDKEALIAKCNDYRRRL[p.L1335I]ISVNIRVRADLRDNYSPGWKFNHWEL	RLISVNIRV,RRRLISVNI,DYRRRLISV,RRRLISVNIR,RLISVNIRVR,NDYRRRLISV,YRRRLISVNI	TGCT
ERBB2	c.2264T>C	p.L755S	AFGTVYKGIWIPDGENVKIPVAIKV[p.L755S]SRENTSPKANKEILDEAYVMAGVGSP	VSRENTSPK,IPVAIKVSR,KVSRENTSPK,VSRENTSPKA	BRCA
ERBB2	c.2305G>T	p.D769Y	ENVKIPVAIKVLRENTSPKANKEIL[p.D769Y]YEAYVMAGVGSPYVSRLLGICLTSTV	ILYEAYVMA,YEAYVMAGV,NKEILYEAY,KEILYEAYV,EILYEAYVM,ILYEAYVMAG,ANKEILYEAY,EILYEAYVMA,KEILYEAYVM,SPKANKEILY,YEAYVMAGVG	BRCA
ERBB2	c.2310_2311insGCATACGTGATG	p.774_775insAYVM	AIKVLRENTSPKANKEILDEAYVMA[p.774_775insAYVM]YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLD	VMAYVMAGV,YVMAYVMAG,DEAYVMAYV,EAYVMAYVM,LDEAYVMAY,MAYVMAGVG,ILDEAYVMAY,YVMAYVMAGV,EAYVMAYVMA,DEAYVMAYVM	LUAD
ERBB2	c.2326_2327insTCT	p.776_776G>VC	AIKVLRENTSPKANKEILDEAYVMA[p.776_776G>VC]VCVGSPYVSRLLGICLTSTVQLVTQLMP	AVCVGSPYV,MAVCVGSPY,EAYVMAVCV,YVMAVCVGS,DEAYVMAVC,ILDEAYVMAV,MAVCVGSPYV,VMAVCVGSPY,DEAYVMAVCV	LUAD
ERBB2	c.2524G>A	p.V842I	LGSQDLLNWCMQIAKGMSYLEDVRL[p.V842I]IHRDLAARNVLVKSPNHVKITDFGLA	RLIHRDLAA,SYLEDVRLI,LIHRDLAAR,RLIHRDLAAR,YLEDVRLIHR,MSYLEDVRLI	CRC
ERBB2	c.2748G>A	p.M916I	LESILRRRFTHQSDVWSYGVTVWEL[p.M916I]ITFGAKPYDGIPAREIPDLLEKGERL	YGVTVWELI,VTVWELITF,LITFGAKPY,WELITFGAK,TVWELITFGA,SYGVTVWELI,ELITFGAKPY,GVTVWELITF,WELITFGAKP	HNSC
ERBB2	c.929C>A	p.S310Y	PEGRYTFGASCVTACPYNYLSTDVG[p.S310Y]YCTLVCPLHNQEVTAEDGTQRCEKCS	YLSTDVGYC,STDVGYCTLV,YLSTDVGYCT,YNYLSTDVGY,LSTDVGYCTL,VGYCTLVCPL	LUAD
ERBB2	c.929C>T	p.S310F	PEGRYTFGASCVTACPYNYLSTDVG[p.S310F]FCTLVCPLHNQEVTAEDGTQRCEKCS	STDVGFCTL,YLSTDVGFC,NYLSTDVGF,STDVGFCTLV,YLSTDVGFCT,YNYLSTDVGF,LSTDVGFCTL,VGFCTLVCPL	BLCA,BRCA,CESC,STAD
ERBB3	c.273G>A	p.M91I	VLTGHNADLSFLQWIREVTGYVLVA[p.M91I]INEFSTLPLPNLRVVRGTQVYDGKFA	YVLVAINEF,VAINEFSTL,INEFSTLPL,AINEFSTLPL,GYVLVAINEF,EVTGYVLVAI	BLCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ERBB3	c.310G>A	p.V104M	WIREVTGYVLVAMNEFSTLPLPNLR[p.V104M]MVRGTQVYDGKFAIFVMLNYNTNSSH	RMVRGTQVY,LPLPNLRMV,LRMVRGTQV,TLPLPNLRMV,NLRMVRGTQV,LRMVRGTQVY	CESC,CRC,STAD
ERBB3	c.310G>T	p.V104L	WIREVTGYVLVAMNEFSTLPLPNLR[p.V104L]LVRGTQVYDGKFAIFVMLNYNTNSSH	RLVRGTQVY,LPLPNLRLV,TLPLPNLRLV,NLRLVRGTQV,LRLVRGTQVY	BLCA
ERBB3	c.889G>T	p.D297Y	LEPNPHTKYQYGGVCVASCPHNFVV[p.D297Y]YQTSCVRACPPDKMEVDKNGLKMCEP	FVVYQTSCV,VVYQTSCVR,YQTSCVRAC,ASCPHNFVVY,FVVYQTSCVR	BLCA
ERC1	c.2075A>G	p.K692R	DLSEKEASLLDLKEHASSLASSGLK[p.K692R]RDSRLKTLEIALEQKKEECLKMESQL	GLKRDSRLK,SLASSGLKR,SSLASSGLKR,SGLKRDSRLK,LKRDSRLKTL	TGCT
ERCC2	c.41A>G	p.Y14C	MKLNVDGLLVYFP[p.Y14C]CDYIYPEQFSYMRELKRTLDAKGHGV	LVYFPCDYI,VYFPCDYIY,LLVYFPCDY,CDYIYPEQF,FPCDYIYPE,LLVYFPCDYI,LVYFPCDYIY,GLLVYFPCDY	BLCA
ERCC2	c.713A>G	p.N238S	LDPKIADLVSKELARKAVVVFDEAH[p.N238S]SIDNVCIDSMSVNLTRRTLDRCQGNL	VVFDEAHSI,EAHSIDNVCI	BLCA
ERCC2	c.934G>A	p.D312N	RLVEGLREASAARETDAHLANPVLP[p.D312N]NEVLQEAVPGSIRTAEHFLGFLRRLL	NPVLPNEVL,LPNEVLQEA,VLPNEVLQEA,LANPVLPNEV,LPNEVLQEAV	ACC
ERCC6	c.2338G>A	p.V780I	SLPDKNEQVLFCRLTDEQHKVYQNF[p.V780I]IDSKEVYRILNGEMQIFSGLIALRKI	FIDSKEVYR,NFIDSKEVY,YQNFIDSKEV,FIDSKEVYRI,KVYQNFIDSK,NFIDSKEVYR,QNFIDSKEVY	CRC
ERCC6L	c.1514G>A	p.R505Q	LVFSQSRQILNIIERLLKNRHFKTL[p.R505Q]QIDGTVTHLLEREKRINLFQQNKDYS	KTLQIDGTV,LQIDGTVTH,LQIDGTVTHL,KNRHFKTLQI	CRC
ERCC6L2	c.1333C>A	p.L445I	LGDTSILDDLFKSHGNSPTQLPKKV[p.L445I]ISGPMEKAKQRPKDFWDILNEQNDES	KVISGPMEK,VISGPMEKAK,SPTQLPKKVI,LPKKVISGPM	UCEC
ERN2	c.884C>A	p.T295K	TQDLGVPVMGVYTWHQDGLRQLPHL[p.T295K]KLARDTLHFLALRWGHIRLPASGPRD	GLRQLPHLK,KLARDTLHF,RQLPHLKLA,QLPHLKLAR,HLKLARDTL,KLARDTLHFL,RQLPHLKLAR,LKLARDTLHF	LUAD
ERRFI1	c.1261G>A	p.A421T	LLPERPPYLDKYEKFFREAEETNGG[p.A421T]TQIQPLPADCGISSATEKPDSKTKMD	AEETNGGTQI	CRC
ESCO1	c.899G>A	p.R300Q	TLPKSPQPSVPEQSDNELEQAGKSK[p.R300Q]QGSILQLCEEIAGEIESDNVEVKKES	KSKQGSILQ,GKSKQGSIL,SKQGSILQL,KSKQGSILQL	CRC
ESF1	c.295delA	p.T99fs	LSDSDSNLSGEDSKALSQKKIKKKK[p.T99fs]PRLKKKSIQKI*	RLKKKSIQK,KIKKKKPRL,KKKKPRLKK,KKKPRLKKK,KPRLKKKSI,LKKKSIQKI,RLKKKSIQKI,KIKKKKPRLK,KKKKPRLKKK	STAD
ESPN	c.1286_1348delCACCCCCACCACCCCCACCCAGCTTCCCCCCGCCACCCCCGCCCCCAGGCACCCAACTGCCCC	p.PPPPPPSFPPPPPPPGTQLPP430del	QSYMDMLNPELGLPRGTIGKPTPPP[p.PPPPPPSFPPPPPPPGTQLPP430del]GYPAPKPPVGPQAADIYMQTKNKLRHVETEALKKELSSCDGHDGLRRQDSSRKPRAFSKQPSTGDYYRQLGRCPGETLAARPGMAHSE	IGKPTPPPGY,KPTPPPGYPA	PAAD
ESPNP	c.1880G>A	p.R627Q	EEEQRWKEEEEARLASMPAWRWDLL[p.R627Q]QKKLEEE	AWRWDLLQK,AWRWDLLQKK,WRWDLLQKKL	GBM
ESPNP	c.191_198delACGCGCGC	p.H64fs	PLYLACQEGHLEVTQYLVQECGADP[p.H64fs]RPRRHDPTARRGADGPQPGHRVVGELHRREPVGAGQRRRHRHALRGEPRPQQGAQLAAAARRGDLG*	GQRRRHRHA,RRRHRHALR,RPRRHDPTA,GPQPGHRVV,QRRRHRHAL,RPQQGAQLA,AAAARRGDL,QQGAQLAAA,GELHRREPV,GQRRRHRHAL,LVQECGADPR,QPGHRVVGEL,EPRPQQGAQL,RPQQGAQLAA,LAAAARRGDL,QQGAQLAAAA	PAAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ESPNP	c.888_950delACCCCCACCCAGCTTCCCCCCGCCACCCCCGCCCCCAGGCACCCAACTGCCCCCACC	p.296_317PPPP5FPPPPPPPGTQLPPPPP>P	QSYMDMLNPELGLPWGTIGKPIPPP[p.296_317PPPPSFPPPPPPPPGTQLPPPPP>P]SYPSPKPPVGPQAADIYMQTKNKLRHVETEALKKEPSSCDGHDGLRRQDSSRKPRAFSKQPSTGDYYRQLGRCPGETLVARPGMAHRE	IGKPIPPPSY	PAAD
ESRRA	c.655G>A	p.D219N	VNALVSHLLVVEPEKLYAMPDPAGP[p.D219N]NGHLPAVATLCDLFDREIVVTISWAK	GPNGHLPAV,MPDPAGPNGH	HNSC
ESYT1	c.2446C>T	p.R816W	LQVNSLIQTQKSAELAAALLSIYME[p.R816W]WAEDLPLRKGTKHLSPYATLTVGDSS	LLSIYMEWA,ALLSIYMEW,IYMEWAEDL,EWAEDLPLR,MEWAEDLPL,ALLSIYMEWA,YMEWAEDLPL,AALLSIYMEW	BRCA
ESYT3	c.1721C>T	p.S574F	QILPYADLTLEQRFQLDHSGLDSLI[p.S574F]FMRLVLRFLQVEERELGSPYTGPEAL	SLIFMRLVL,FMRLVLRFL,LIFMRLVLR,IFMRLVLRF,DSLIFMRLV,HSGLDSLIF,SGLDSLIFM,GLDSLIFMRL,SLIFMRLVLR,IFMRLVLRFL,SGLDSLIFMR,LIFMRLVLRF,HSGLDSLIFM	LUSC
ETFDH	c.841A>T	p.I281F	LYKKFDLRANCEPQTYGIGLKELWV[p.I281F]FDEKNWKPGRVDHTVGWPLDRHTYGG	WVFDEKNWK,IGLKELWVF	CLL
ETV6	c.1105C>T	p.R369W	YVYQLLSDSRYENFIRWEDKESKIF[p.R369W]WIVDPNGLARLWGNHKNRTNMTYEKM	WIVDPNGLA,KESKIFWIV,IFWIVDPNGL	CRC
EXOC1	c.1762C>T	p.R588C	QHNCGTPLPVSSEKDMIRQMMIKIF[p.R588C]CCIEPELNNLIALGDKIDSFNSLYML	MMIKIFCCI,RQMMIKIFC,QMMIKIFCCI,KIFCCIEPEL,RQMMIKIFCC	UCEC
EXOSC2	c.32G>C	p.R11P	MAMEMRLPVA[p.R11P]PKPLSERLGRDTKKHLVVPGDTITTD	EMRLPVAPK,APKPLSERL,MEMRLPVAP,MEMRLPVAPK,MRLPVAPKPL	KIRP
EXOSC8	c.480delA	p.L160fs	CDLICLDYDGNILDACTFALLAALK[p.L160fs]MYSCLKLL*	KMYSCLKLL,ALKMYSCLK,ALLAALKMY,FALLAALKM,AALKMYSCL,LKMYSCLKL,LLAALKMYSC,ALKMYSCLKL,AALKMYSCLK,LAALKMYSCL,FALLAALKMY,LKMYSCLKLL	STAD
EZH2	c.1529A>G	p.K510R	VDTPPRKKKRKHRLWAAHCRKIQLK[p.K510R]RDGSSNHVYNYQPCDHPRQPCDSSCP	RDGSSNHVY,LKRDGSSNH,KRDGSSNHVY	TGCT
EZH2	c.1922A>T	p.Y641F	LAPSDVAGWGIFIKDPVQKNEFISE[p.Y641F]FCGEIISQDEADRRGKVYDKYMCSFL	FISEFCGEI,QKNEFISEF,SEFCGEIIS,FISEFCGEII,VQKNEFISEF	DLBCL
F10	c.349G>A	p.E117K	TSPCQNQGKCKDGLGEYTCTCLEGF[p.E117K]KGKNCELFTRKLCSLDNGDCDQFCHE	KGKNCELFT,FKGKNCELF,YTCTCLEGFK,CTCLEGFKGK,GFKGKNCELF,KGKNCELFTR	UCEC
F5	c.1277A>T	p.Q426L	DESFTKHTVNPNMKEDGILGPIIRA[p.Q426L]LVRDTLKIVFKNMASRPYSIYPHGVT	ILGPIIRAL,ALVRDTLKI,LVRDTLKIV,RALVRDTLK,IRALVRDTL,ILGPIIRALV,ALVRDTLKIV,IIRALVRDTL,RALVRDTLKI,LVRDTLKIVF	LIHC
F5	c.3995T>C	p.L1332P	LSQTNLSPALGQMPISPDLSHTTLS[p.L1332P]PDFSQTNLSPELSQTNLSPALGQMPL	TLSPDFSQT,SPDFSQTNL,SHTTLSPDF,LSHTTLSPDF	CLL
F8	c.6806C>A	p.S2269Y	NPKEWLQVDFQKTMKVTGVTTQGVK[p.S2269Y]YLLTSMYVKEFLISSSQDGHQWTLFF	YLLTSMYVK,KYLLTSMYV,GVKYLLTSM,GVTTQGVKY,VKYLLTSMY,TTQGVKYLL,KYLLTSMYVK,GVKYLLTSMY,QGVKYLLTSM,VKYLLTSMYV	CRC
FAM104B	c.223G>C	p.D75H	SSSRINIPERASGPEGNLNQIVTEP[p.D75H]HANFPQFLHEGLSKPVYVINWFMSFG	HANFPQFLH,EPHANFPQF,IVTEPHANF,EPHANFPQFL,QIVTEPHANF,TEPHANFPQF	TGCT
FAM105A	c.376C>A	p.H126N	AREWKGETPRNKLMRKAYEELFWRH[p.H126N]NIKCVRQVRRDNYDALRSVLFQIFSQ	ELFWRHNIK,NIKCVRQVR,EELFWRHNI,FWRHNIKCVR,HNIKCVRQVR,NIKCVRQVRR,YEELFWRHNI	KIRC
FAM109A	c.466_474delGGGGGTGGC	p.GGG156del	LSRASFDYLRLVVRELEQQLAAVRG[p.GGG156del]MALPQPQPQSLPLPPSLPSALAPVPSLPSAPAPV	QLAAVRGMA,LAAVRGMAL,QQLAAVRGM,QLAAVRGMAL,EQQLAAVRGM,QQLAAVRGMA	ACC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FAM111B	c.807delA	p.S269fs	KIYGKQSMVDEVSGKVLEMDISKKK[p.S269fs]HYNRKISIKKLNRMKVPLMKLITRV*	KLNRMKVPL,PLMKLITRV,RMKVPLMKL,ISKKKHYNR,SKKKHYNRK,KHYNRKISI,HYNRKISIK,YNRKISIKK,KISIKKLNR,SIKKLNRMK,LNRMKVPLM,ISIKKLNRM,MKVPLMKLI,KLNRMKVPLM,RMKVPLMKLI,ISIKKLNRMK,ISKKKHYNRK,KHYNRKISIK,HYNRKISIKK,KISIKKLNRM,SIKKLNRMKV,LNRMKVPLMK,KVPLMKLITR,DISKKKHYNR,KKHYNRKISI,KKLNRMKVPL,VPLMKLITRV	PRAD
FAM116A	c.1322delT	p.L441fs	IKQLQKGVQQKRPSEAQSVILRRYF[p.L441fs]WN*	SVILRRYFW	STAD
FAM120B	c.1400C>A	p.P467H	DSEPRQEVPMYTGSEPRQEVPMYTG[p.P467H]HESRQEVPMYTGPESRQEVLIRTDPE	HESRQEVPM,VPMYTGHES,RQEVPMYTGH,HESRQEVPMY	LUAD
FAM126B	c.1145G>A	p.R382H	LSSQPIGTKPSSSSQRGSLRKVATG[p.R382H]HSAKDKETASAIKSSESPRDSVVRKQ	KVATGHSAK,ATGHSAKDK,RKVATGHSA	GBM
FAM127C	c.1S6C>A	p.F52L	IPFPETFDGDTDRLPEFIVQTSSYM[p.F52L]LVDENTFSNDALKVTFLITRLTGPAL	VQTSSYMLV,MLVDENTFS,YMLVDENTF,FIVQTSSYML,IVQTSSYMLV,SYMLVDENTF	LUAD
FAM135B	c.1933A>C	p.S645R	KGIDQEGKMVLLSLKLTPSEPCDPL[p.S645R]RSTLREPLDIRSSLKDSHTEEQEELS	LRSTLREPL,EPCDPLRSTL	STAD
FAM135B	c.1942C>A	p.L648M	DQEGKMVLLSLKLTPSEPCDPLSST[p.L648M]MREPLDIRSSLKDSHTEEQEELSVLS	TMREPLDIR,LSSTMREPL,STMREPLDIR,EPCDPLSSTM	LUSC
FAM135B	c.2651G>A	p.R884H	GHCLPDGRTENTPGVETKGLNLKIP[p.R884H]HVIALENPRTRSLHRALEETPKGMPK	GLNLKIPHV,HVIALENPR,LKIPHVIAL,GLNLKIPHVI,NLKIPHVIAL,KGLNLKIPHV	CRC
FAM135B	c.720G>C	p.W240C	GYCKPTSSEGSFYITSENCMQHAHK[p.W240C]CHRDLCLLLLHAYRGLRLHFLVIMRD	MQHAHKCHR,CMQHAHKCHR	LUAD
FAM135B	c.855G>T	p.Q285H	LVIMRDIPELPHTELEALAVEETLS[p.Q285H]HLCSELQMLNNPEKIAEQISKDLAWL	TLSHLCSEL,HLCSELQML,SHLCSELQM,ETLSHLCSEL,LAVEETLSHL,LSHLCSELQM	LUSC
FAM151A	c.351delC	p.P117fs	LEADVNVEGLGTANETGVPIMAHPP[p.P117fs]LSTVTTHWSSGWTLCWALPKRASNWTSRTSRQWAPPWTSCGS*	IMAHPPLST,MAHPPLSTV,WTLCWALPK,TSRTSRQWA,RTSRQWAPP,TLCWALPKR,SNWTSRTSR,VPIMAHPPL,THWSSGWTL,SGWTLCWAL,TSRQWAPPW,RQWAPPWTS,WSSGWTLCW,IMAHPPLSTV,GWTLCWALPK,WTLCWALPKR,ASNWTSRTSR,HWSSGWTLCW,RTSRQWAPPW,TTHWSSGWTL,WSSGWTLCWA,MAHPPLSTVT,SSGWTLCWAL,WALPKRASNW,RQWAPPWTSC,PPLSTVTTHW	STAD
FAM155A	c.284A>G	p.Q95R	KEHQQQQRQQQQQQQQQRQRQQQQQ[p.Q95R]RRRQQEPSWPALLASMGESSPAAQAH	RQRQQQQQR,RRRQQEPSW,RQRQQQQQRR	TGCT
FAM155B	c.472G>A	p.E158K	VCGGVPEPTGLDAACTKLQSLQRLF[p.E158K]KPTTPAPPLRPPDSLSRAPAEFPSAK	RLFKPTTPA,LQSLQRLFK,KPTTPAPPL,LQRLFKPTT,KLQSLQRLFK,LQRLFKPTTP,RLFKPTTPAP,FKPTTPAPPL	UCEC
FAM169B	c.495G>T	p.K165N	NDRPRQPAPGDGSKERMCGEELEDT[p.K165N]NDDPECGVEEEDAGLAGQPPGKLTRS	DTNDDPECGV	CRC
FAM170A	c.166G>A	p.E56K	DALQPGSTRVAKGWSQGVGEVTSTS[p.E56K]KYCSCVSSSRKLIHSGIQRIHRDSPQ	STSKYCSCV,GEVTSTSKY,SKYCSCVSS,GVGEVTSTSK,VGEVTSTSKY,TSTSKYCSCV,SKYCSCVSSS	CRC
FAM171B	c.1375G>A	p.D459N	SYSPQKKEPSKAETEERVSMVKTRD[p.D459N]NFKIYNEDVSFLSVNQNNYSRNPTQS	MVKTRDNFK,KTRDNFKIY,SMVKTRDNF,SMVKTRDNFK,MVKTRDNFKI,KTRDNFKIYN,VSMVKTRDNF,VKTRDNFKIY	CRC
FAM179A	c.2491G>A	p.A831T	QVFDAFTPRLQDSNKKVNQWALESF[p.A831T]TKMIPLLRESLHPMLLSIITVADNL	FTKMIPLLR,SFTKMIPLL,ESFTKMIPL,WALESFTKM,NQWALESFTK,SFTKMIPLLR,ESFTKMIPLL,WALESFTKMI,LESFTKMIPL	BRCA
FAM181A	c.326G>A	p.R109H	KAALDKSAPCRRSVDHRKYLQKQLK[p.R109H]HFSQKYSRLPRGLPGRAAEPYLKRGS	KQLKHFSQK,YLQKQLKHF,KHFSQKYSR,QLKHFSQKY,KYLQKQLKHF,KQLKHFSQKY,RKYLQKQLKH,KHFSQKYSRL	CRC

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FAM184B	c.2350C>T	p.R784W	RALGRQQASSQCPGDSKDHIIATEE[p.R784W]WGGPGQAGSPPGAAGQGSGEGCGLWE	EEWGGPGQA,EEWGGPGQAG,TEEWGGPGQA	ACC
FAM186A	c.4667_4702delTCCCTCCGCAGGCTCAGGAATTGGAGATCCCTCTCA	p.IPPQAQELEIPL1556del	LIPPQAQELGIPLTPQQVQALGIPL[p.IPPQAQELEIPL1556del]TPQQAQALGIPLTPQQAQELGIPLTPQQAQELGIPLTPQQAQAQGIPLTPQQAQALGISLT	VQALGIPLT,VQALGIPLTP	KIRC
FAM18B2	c.152G>A	p.C51Y	PRKAKIRHPVASFFHLFFRVSAIIV[p.C51Y]YLLCELLSSSFITCMVTIILLLSCDF	IIVYLLCEL,YLLCELLSS,AIIVYLLCEL,IIVYLLCELL,YLLCELLSSS	ACC,KIRP,TGCT
FAM193A	c.1284_1285insC	p.D428fs	NYRRRCACDDCSLSHILTCGIMDPP[p.D428fs]RH*	LTCGIMDPPR	STAD
FAM193A	c.1284delC	p.D428fs	NYRRRCACDDCSLSHILTCGIMDPP[p.D428fs]SLMTSTFTSSHFKWILLLTILLRGARPVCHLQARGPAPALPSQFSSTPGSSSQTVARHQLFVVMMKMLHHCQPNLLIFIH*	SLMTSTFTS,WILLLTILL,ILLRGARPV,VMMKMLHHC,MLHHCQPNL,GIMDPPSLM,FTSSHFKWI,LLTILLRGA,LQARGPAPA,ALPSQFSST,TVARHQLFV,STFTSSHFK,HQLFVVMMK,MTSTFTSSH,GSSSQTVAR,TFTSSHFKW,SHFKWILLL,KWILLLTIL,QTVARHQLF,HCQPNLLIF,CQPNLLIFI,SSHFKWILL,VARHQLFVV,LTILLRGAR,QARGPAPAL,TSTFTSSHF,LMTSTFTSS,FKWILLLTI,RGARPVCHL,SQFSSTPGS,SQTVARHQL,ARHQLFVVM,RHQLFVVMM,QLFVVMMKM,MKMLHHCQP,KMLHHCQPN,TPGSSSQTV,PPSLMTSTF,LLLTILLRGA,TVARHQLFVV,KMLHHCQPNL,MLHHCQPNLL,SLMTSTFTSS,HLQARGPAPA,LQARGPAPAL,QLFVVMMKML,TSTFTSSHFK,TFTSSHFKWI,HFKWILLLTI,KWILLLTILL,SQTVARHQLF,SSHFKWILLL,GARPVCHLQA,VARHQLFVVM,RHQLFVVMMK,MTSTFTSSHF,WILLLTILLR,LLTILLRGAR,FTSSHFKWIL,STPGSSSQTV,QTVARHQLFV,GPAPALPSQF,LMTSTFTSSH,HQLFVVMMKM,CGIMDPPSLM,STFTSSHFKW,FKWILLLTIL,SQFSSTPGSS,ARHQLFVVMM,MKMLHHCQPN,HHCQPNLLIF,LPSQFSSTPG	STAD
FAM194B	c.404_421delAGGAGGAAGAGTATCTGG	p.EEEEYL135del	IEEEEYLGKEGYLEEEEYLGKEEHL[p.EEEEYL135del]GKEGYLEKEDYIEEVDYLGKKAYLEEEEYLGKKSYLEEEKALE	LGKEEHLGK,EEHLGKEGY,HLGKEGYLEK,KEEHLGKEGY,EEHLGKEGYL	KIRC
FAM194B	c.415T>C	p.Y139H	EYLGKEGYLEEEEYLGKEEHLEEEE[p.Y139H]HLGKEGYLEKEDYIEEVDYLGKKAYL	EEHLGKEGY,HLGKEGYLEK,EEEHLGKEGY,EEHLEEEEHL,EEHLGKEGYL	TGCT
FAM210B	c.336G>T	p.L112F	QQLKKIFQEYGTVGVSLHIGISLIS[p.L112F]FGIFYMVVSSGVDMPAILLKLGFKES	GISLISFGI,LISFGIFYM,ISFGIFYMV,SLISFGIFY,ISLISFGIF,SFGIFYMVV,HIGISLISF,ISLISFGIFY,SLISFGIFYM,LISFGIFYMV,ISFGIFYMVV,LHIGISLISF,GISLISFGIF	LUAD
FAM214B	c.124delG	p.A42fs	GPSQPPVRQGALQGGLLMGYSPAGG[p.A42fs]RHPPGSTRYPSFPLRLVPLSLIGP*	RYPSFPLRL,SFPLRLVPL,STRYPSFPL,RHPPGSTRY,MGYSPAGGR,YPSFPLRLV,SPAGGRHPP,RLVPLSLIG,FPLRLVPLS,STRYPSFPLR,RYPSFPLRLV,GGRHPPGSTR,LMGYSPAGGR,SPAGGRHPPG,FPLRLVPLSL,MGYSPAGGRH,GRHPPGSTRY,GSTRYPSFPL,TRYPSFPLRL	STAD
FAM216A	c.106C>T	p.P36S	RGLGAAEMPGQGPGSDWTERSSSAE[p.P36S]SPAVAGTEGGGGGSAGYSCYQN5KGS	RSSSAESPA,AESPAVAGT,RSSSAESPAV	KIRP
FAM21B	c.3691C>T	p.P1231S	DMDDIFSSGIQAKTTKPKSRSAQAA[p.P1231S]SEPRFEHKVSNIFDDPLNAFGGQ*	ASEPRFEHK,KSRSAQAAS,SAQAASEPR,AQAASEPRF,SEPRFEHKV,RSAQAASEPR,AASEPRFEHK,KSRSAQAASE,SAQAASEPRF	TGCT
FAM222F	c.2070_2071delTT	p.P690fs	PGGRGPQGALQSPSAQKRGLSPSPS[p.P690fs]CQQVQEATSLWKPIPC*	VQEATSLWK,EATSLWKPI,SPSPSCQQV,QQVQEATSL,QVQEATSLWK,CQQVQEATSL,QQVQEATSLW,QEATSLWKPI	KIRC
FAM222F	c.2071_2073delTCT	p.S691del	SPGGRGPQGALQSPSAQKRGLSPSP[p.S691del]PASKSKKRPLFGSPSPAEKTPHPGPGLR	LSPSPPASK,RGLSPSPPA,GLSPSPPASK	KIRC,PRAD
FAM32A	c.26A>G	p.K9R	MEAYEQVQ[p.K9R]RGPLKLKGVAELGVTKRKKKKKDKDK	VQRGPLKLK,YEQVQRGPL,QVQRGPLKLK,EQVQRGPLKL	TGCT

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FAM40B	c.2218C>T	p.R740C	LQTKYLGRQWRKSNMKTMSAIYQKV[p.R740C]CHRMNDDWAYGNDIDARPWDFQAEEC	AIYQKVCHR,IYQKVCHRM,AIYQKVCHRM,CHRMNDDWAY,SAIYQKVCHR	STAD
FAM46B	c.1247_1248AC>GT	p.H416R	RPPGTDGVVPATVNYYVTPVQPLLA[p.H416R]RAYPTWLPCN*	LLARAYPTW,LARAYPTWL,RAYPTWLPC,VQPLLARAY,LLARAYPTWL,PVQPLLARAY	TGCT
FAM47A	c.1114G>T	p.G372W	GSSLRSEPSETGVSRLRLAPPKTRR[p.G372W]WSSLHAEPSKTGVSHLSPEPPKTEVS	KTRRWSSLH,WSSLHAEPSK,KTRRWSSLHA,PPKTRRWSSL,RLAPPKTRRW	LUSC
FAM47A	c.2069G>T	p.R690L	EDKFFSQEKYWGRKFHTPSNSYTAQ[p.R690L]LVKMKYGAWYLKPKLWKKLRSDEPLI	NSYTAQLVK,YTAQLVKMK,SYTAQLVKM,YTAQLVKMKY,SNSYTAQLVK,LVKMKYGAWY,TPSNSYTAQL,NSYTAQLVKM,QLVKMKYGAW	LUAD
FAM47B	c.1701G>T	p.L567F	QRGRIRYGPWYFEPKLGKKLRSDEP[p.L567F]FIDPKPVLEKPDEPDILDGLYGPIAF	KLRSDEPFI,KKLRSDEPF,EPFIDPKPV,RSDEPFIDPK,FIDPKPVLEK,EPFIDPKPVL,GKKLRSDEPF,KKLRSDEPFI	LUAD
FAM47B	c.489G>T	p.W163C	GKDMPPDLLLQVLKQLDPERKLEDA[p.W163C]CARCEAREKTTEVPTESGKYPCGESC	CARCEAREK,DACARCEAR,LEDACARCEA	LUAD
FAM47C	c.1162C>T	p.P388S	VSPLRQLPPEAGVSHLCPEPPKTRV[p.P388S]SPLRPETPKNGVSPLFPEPPKTRISN	KTRVSPLRP,RVSPLRPET,PPKTRVSPL,KTRVSPLRPE,EPPKTRVSPL	KIRC
FAM48B1	c.1495A>G	p.I499V	ISSGNSFPPQQAGSPLKRPFSAAAA[p.I499V]VAAAAAAAAAAAAAAAAAAPAPALAA	FSAAAAVAA,SAAAAVAAA,RPFSAAAAV,FSAAAAVAAA,SAAAAVAAAA,RPFSAAAAVA	TGCT
FAM48B1	c.1546G>C	p.A516P	RPFSAAAAIAAAAAAAAAAAAAAA[p.A516P]PAPAPALAAAAAPALAAAAAPALAAA	AAAPAPAPAL,APAPAPALAA	TGCT
FAM50A	c.950A>G	p.H317R	SDATVEKDESHAGKVVLRSWYEKNK[p.H317R]RIFPASRWEPYDPEKKWDKYTIR*	KNKRIFPAS,KRIFPASRW,SWYEKNKRIF,KNKRIFPASR,YEKNKRIFPA,NKRIFPASRW	CLL
FAM58BP	c.208G>A	p.A70T	LGMQSIPIATACTIYPKFFCETILD[p.A70T]TFDPYLIAMSSIYLAGKVEEQPLWAH	ILDTFDPYL,TILDTFDPY,DTFDPYLIA,ETILDTFDPY,TILDTFDPYL,ILDTFDPYLI,FFCETILDTF,DTFDPYLIAM	BRCA
FAM5B	c.1204C>T	p.R402C	AGLKVLFKKTHRILRRLFNLCKRCH[p.R402C]CQPRFRLPKERSLSYWWNRIQSLLYC	CQPRFRLPK,RCHCQPRFR,KRCHCQPRF,RCHCQPRFRL,HCQPRFRLPK,CKRCHCQPRF	CRC
FAM5C	c.1274C>G	p.S425W	WLTRIQSFLYCNENGLLGSFSEETH[p.S425W]WCTCPNDQVVCTAFLPCTVGDASACL	GSFSEETHW	TGCT
FAM5C	c.1369C>G	p.R457G	QVVCTAFLPCTVGDASACLTCAPDN[p.R457G]GTRCGTCNTGYMLSQGLCKPEVAEST	GTRCGTCNT,GTRCGTCNTG,LTCAPDNGTR	LUAD
FAM70B	c.56C>T	p.S19L	MQPPVPGPLGLLDPAEGL[p.S19L]LRRKKTSLWFVGSLLLVSVLIVTVGL	LLDPAEGLL,LLRRKKTSL,GLLDPAEGLL,GLLRRKKTSL,LLRRKKTSLW,LRRKKTSLWF	STAD
FAM70B	c.829C>A	p.P277T	GFRLTPEPVPTCSSYPLPLQPCSRF[p.P277T]TVAPSSALASSEDLQPPSPSSSGSGL	LQPCSRFTV,FTVAPSSAL,TVAPSSALA,CSRFTVAPS,RFTVAPSSA,QPCSRFTVA,FTVAPSSALA,CSRFTVAPSS,LQPCSRFTVA,SRFTVAPSSA,RFTVAPSSAL	LUAD
FAM71B	c.1333C>G	p.H445D	PSAEVWNENKERREKKDRHPSRKSS[p.H445D]DHRKAGESHRRRAGDKNQKASSHRSA	PSRKSSDHRK	CESC
FAM71B	c.1747C>A	p.L583M	VDIVAKMVEKQNIEAKVEKAQGGQE[p.L583M]MEMISGTMTSEKTEMIVFETKSI*	EKAQGGQEM,AQGGQEMEM,QEMEMISGT,EMEMISGTM,MEMISGTMT,QEMEMISGTM,VEKAQGGQEM,KAQGGQEMEM,MEMISGTMTS	LUAD
FAM73A	c.68G>T	p.G23V	MSDCCSAPGISWEAGVGRPAVP[p.G23V]VLELQIRRGAMSEETVSESQFSLKTA	RPAVPVLEL,VGRPAVPVL	CESC
FAM75A6	c.161C>T	p.P54L	FLTLVFALGFFFLLLPYLSYFHCDD[p.P54L]LPSPSPGKRKCPVGRRRRPRGRMKNH	LSYFHCDDL,YLSYFHCDDL	LUAD
FAM75A6	c.910C>A	p.R304S	ASSRWQETARTSCAFNSSVQQDPLS[p.R304S]SHPPETCQMEAGSLFLLSSDGQNVVG	VQQDPLSSH,SSHPPETCQM	LUAD

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FAM75D1	c.3793C>A	p.R1265S	NSQGISSGDMGTSQVVHVHLEDSGI[p.R1265S]SVAQKQEPRVPTCVLQKCQVTNFPPA	HLEDSGISV,SVAQKQEPR,LEDSGISVA,HLEDSGISVA,SVAQKQEPRV	LUAD
FAM75D5	c.665T>C	p.L222P	PPQPVSPLDSKFPIDHSLPQQLPSP[p.L222P]PFPPHHIQRAEPSLQPEASLSLNTVF	PQQLPSPPF,LPSPPFPPH,LPQQLPSPPF,QQLPSPPFPP	THCA
FAM78A	c.575G>T	p.W192L	TWAVPVSESNVAKLTNIYRDQSFTT[p.W192L]LLVATNTSTNDMIILQTLHWRMQLSI	LLVATNTST,YRDQSFTTL,RDQSFTTLL,QSFTTLLVA,IYRDQSFTTL,YRDQSFTTLL,DQSFTTLLVA	KIRC
FAM83B	c.617G>A	p.R206Q	DESNFNHFLNMTEKQGCSVQRLRNI[p.R206Q]QVRTVKGQDYLSKTGAKFHGKMEQKF	VQRLRNIQV,RLRNIQVRT,RNIQVRTVK,RLRNIQVRTV,VQRLRNIQVR,QVRTVKGQDY	UCEC
FAM86A	c.421G>A	p.A141T	SGGSVTLSESTAIISYGTTGLVTWD[p.A141T]TALYLAEWAIENPAVFTNRTVLELGS	LVTWDTALY,GLVTWDTAL,VTWDTALYL,VTWDTALYLA,GLVTWDTALY,LVTWDTALYL,DTALYLAEWA,TALYLAEWAI	TGCT
FAM86C2P	c.359G>A	p.C120Y	RASCSPLSYAGLGSDGKWNLVMTRN[p.C120Y]YFPTKSTWRWQC*	MTRNYFPTK,NYFPTKSTW,YFPTKSTWR,NLVMTRNYF,WNLVMTRNY,VMTRNYFPTK,YFPTKSTWRW,MTRNYFPTKS,KWNLVMTRNY,NYFPTKSTWR,LVMTRNYFPT,WNLVMTRNYF,RNYFPTKSTW	TGCT
FARP1	c.1148C>T	p.S383L	KVQFERKHSKIHSIRSLASQPTELN[p.S383L]LEVLEQSQQSTSLTFGEGAESPGGQS	QPTELNLEV,SQPTELNLEV,LASQPTELNL,QPTELNLEVL	UCEC
FARP1	c.896G>T	p.R299L	KRFLIKLRPDANSAYQDTLEFLMAS[p.R299L]LDFCKSFWKICVEHHAFFRLFEEPKP	FLMASLDFC,TLEFLMASL,LMASLDFCK,EFLMASLDF,ASLDFCKSF,FLMASLDFCK,SLDFCKSFWK,DTLEFLMASL,MASLDFCKSF,LEFLMASLDF,ASLDFCKSFW,LDFCKSFWKI	LUAD
FAS	c.781G>A	p.E261K	IAGVMTLSQVKGFVRKNGVNEAKID[p.E261K]KIKNDNVQDTAEQKVQLLRNWHQLHG	GVNEAKIDK	CESC
FASTKD1	c.9_10insA	p.K3fs	MKK[p.K3fs]NTCFPRVIGYKYASSKSYLSILLESVSISTHQL*	YLSILLESV,IGYKYASSK,KYASSKSYL,SYLSILLES,CFPRVIGYK,ASSKSYLSI,SSKSYLSIL,YKYASSKSY,SVSISTHQL,TCFPRVIGY,FPRVIGYKY,KKNTCFPRV,SKSYLSILL,LESVSISTH,ILLESVSIST,VIGYKYASSK,TCFPRVIGYK,CFPRVIGYKY,SYLSILLESV,SSKSYLSILL,NTCFPRVIGY,GYKYASSKSY,ESVSISTHQL,FPRVIGYKYA,YASSKSYLSI,MKKNTCFPRV,KKNTCFPRVI,YKYASSKSYL,ASSKSYLSIL,LSILLESVSI	STAD
FASTKD3	c.1873C>G	p.Q625E	RFCSNSKHLLGKEAIKQRHLQLLGY[p.Q625E]EVVQIPYHEIGMLKSRRELVEYLQRK	HLQLLGYEV,LQLLGYEVV,LLGYEVVQI,GYEVVQIPY,YEVVQIPYH,HLQLLGYEVV,QLLGYEVVQI,LGYEVVQIPY,EVVQIPYHEI,RHLQLLGYEV	BLCA
FAT1	c.13076G>T	p.R4359L	TKVVDLDPCLSKKPLEEKPSQPYSA[p.R4359L]LESLSEVQSLSSFQSESCDDNGYHWD	SALESLSEV,KPSQPYSAL,QPYSALESL,YSALESLSEV,SQPYSALESL,LESLSEVQSL	LUAD
FAT3	c.10720C>A	p.H3574N	PTAIPLEIFIVTMEDDFPGGVIGKI[p.H3574N]NATDQDMYDVLTFALKSEQKSLFKVN	KINATDQDM,KINATDQDMY,NATDQDMYDV,GKINATDQDM	LUAD
FAT3	c.12475G>A	p.A4159T	GLRPVVVPNIQAGHSYVGKEELIGI[p.A4159T]TVVLFVIFILVVLFIVFRKKVFRKNY	ELIGITVVL,ITVVLFVIF,TVVLFVIFI,KEELIGITV,LIGITVVLF,EELIGITVV,LIGITVVLFV,IGITVVLFVI,ITVVLFVIFI,TVVLFVIFIL,ELIGITVVLF,KEELIGITVV,GITVVLFVIF,EELIGITVVL	UCEC
FAT3	c.3797G>A	p.R1266H	VVQVLDENDNKPQFPEKVYQIKLPE[p.R1266H]HDRKKRGEPIYRAFAFDRDEGPNAEI	KVYQIKLPEH,QIKLPEHDRK	LUAD
FAT3	c.5696G>T	p.G1899V	TDVNDNPPVFTQAVFETILLLPTYV[p.G1899V]VVEVLKVSATDPDSEVPPELTYSLME	ILLLPTYVV,LLLPTYVVV,YVVVEVLKV,LPTYVVVEV,TILLLPTYVV,ILLLPTYVVV,LLPTYVVVEV,PTYVVVEVLK,TYVVVEVLKV,LPTYVVVEVL	LUAD
FBRSL1	c.2507C>T	p.A836V	GRSGAPAEREAEPRVKESRSPAKEE[p.A836V]VAKMPARASPPHSKAAPGDVKVKEER	EVAKMPARA,KEEVAKMPA,RSPAKEEVAK,SPAKEEVAKM,EEVAKMPARA	ACC
FBXL13	c.306T>A	p.S102R	RIQQIIYCHKLTIILTKWRNTARHK[p.S102R]RKKKEDELILKHELQLKKWKNRLILK	RNTARHKRK,TARHKRKKK,KWRNTARHKR,RNTARHKRKK,RKKKEDELIL	CLL

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FBXL14	c.143T>G	p.V48G	RDKGRAAQVCTAWRDAAYHKSVWRG[p.V48G]GEAKLHLRRANPSLFPSLQARGIRRV	SVWRGGEAK,KSVWRGGEA,KSVWRGGEAK,GEAKLHLRRA	TGCT
FBXO18	c.432G>T	p.M144I	KQPCTNDMAKSNSVGQDSCQDSEGD[p.M144I]IIFPAESSCALPQEGSAGPGSPGSAP	CQDSEGDII,SEGDIIFPA,IIFPAESSCA,CQDSEGDIIF	LUAD
FBXO21	c.432delT	p.F144fs	KRFFSEHVPCNGFSDIENLEGPEIF[p.F144fs]LRMNWCVS*	IFLRMNWCV,FLRMNWCVS,PEIFLRMNW,EIFLRMNWCV,LEGPEIFLRM,GPEIFLRMNW	STAD
FBXO24	c.1657A>G	p.M553V	HLPASRVVGTPEPSLGARAPQDPGG[p.M553V]VAQACEEYLSQIHSCQTLQDRTEKMK	GVAQACEEY,APQDPGGVA,GGVAQACEEY	HNSC
FBXO31	c.1329_1330insG	p.G443fs	TPGEDGGEPGDAVAAAEQPAQCGQG[p.G443fs]AAVRAARGRELQE*	AQCGQGAAV,AVRAARGRE,QGAAVRAAR,GQGAAVRAA,VRAARGREL,AVRAARGREL,QPAQCGQGAA	LUAD
FBXW7	c.1268G>T	p.G423V	SDDNTLKVWSAVTGKCLRTLVGHTG[p.G423V]VVWSSQMRDNIIISGSTDRTLKVWNA	TLVGHTGVV,GVVWSSQMR,RTLVGHTGV,LVGHTGVVW,TGVVWSSQM,RTLVGHTGVV,TLVGHTGVVW,HTGVVWSSQM	UCEC
FBXW7	c.1393C>T	p.R465C	DRTLKVWNAETGECIHTLYGHTSTV[p.R465C]CCMHLHEKRVVSGSRDATLRVWDIET	STVCCMHLH,GHTSTVCCM,TLYGHTSTVC,TVCCMHLHEK,HTSTVCCMHL,YGHTSTVCCM	CESC,CRC,STAD,UCEC,UCS
FBXW7	c.1394G>A	p.R465H	DRTLKVWNAETGECIHTLYGHTSTV[p.R465H]HCMHLHEKRVVSGSRDATLRVWDIET	STVHCMHLH,HCMHLHEKR,GHTSTVHCM,TVHCMHLHEK,HTSTVHCMHL,TLYGHTSTVH,YGHTSTVHCM	CLL,CRC,UCEC,UCS
FBXW7	c.1436G>A	p.R479Q	IHTLYGHTSTVRCMHLHEKRVVSGS[p.R479Q]QDATLRVWDIETGQCLHVLMGHVAAV	SQDATLRVW	STAD,UCS
FBXW7	c.1513C>G	p.R505G	DATLRVWDIETGQCLHVLMGHVAAV[p.R505G]GCVQYDGRRVVSGAYDFMVKVWDPET	VAAVGCVQY,HVAAVGCVQY	BLCA,CESC,HNSC,LUSC,UCS
FBXW7	c.1513C>T	p.R505C	DATLRVWDIETGQCLHVLMGHVAAV[p.R505C]CCVQYDGRRVVSGAYDFMVKVWDPET	VAAVCCVQY,VLMGHVAAVC,HVAAVCCVQY,AVCCVQYDGR	CRC,UCEC
FBXW7	c.1637C>T	p.S546L	FMVKVWDPETETCLHTLQGHTNRVY[p.S546L]LLQFDGIHVVSGSLDTSIRVWDVETG	LLQFDGIHV,VYLLQFDGI,TNRVYLLQF,YLLQFDGIH,YLLQFDGIHV,LLQFDGIHVV,RVYLLQFDGI,HTNRVYLLQF,LQGHTNRVYL	BLCA
FBXW7	c.1745C>T	p.S582L	GSLDTSIRVWDVETGNCIHTLTGHQ[p.S582L]LLTSGMELKDNILVSGNADSTVKIWD	QLLTSGMEL,LLTSGMELK,HTLTGHQLL,IHTLTGHQL,GHQLLTSGM,QLLTSGMELK,IHTLTGHQLL,TGHQLLTSGM,HQLLTSGMEL	CRC
FBXW7	c.2065C>T	p.R689W	ESGGSGGVVWRIRASNTKLVCAVGS[p.R689W]WNGTEETKLLVLDFDVDMK*	KLVCAVGSW,GSWNGTEETK,TKLVCAVGSW	CRC,UCEC,UCS
FBXW7	c.41G>A	p.R14Q	MNQELLSVGSKRR[p.R14Q]QTGGSLRGNPSSSQVDEEQMNRVVEE	KRRQTGGSL,RQTGGSLRG,KRRQTGGSLR,SKRRQTGGSL	CRC
FBXW9	c.893_894insG	p.G298fs	YDKKVTIYDPRDRMETRDALMGWGG[p.G298fs]AFEGL*	GWGGAFEGL,ALMGWGGAF,DALMGWGGAF,MGWGGAFEGL	STAD
FCAR	c.697G>A	p.V233M	SNALELVVTDSIHQDYTTQNLIRMA[p.V233M]MAGLVLVALLAILVENWHSHTALNKE	RMAMAGLVL,MAMAGLVLV,AMAGLVLVA,LIRMAMAGL,TQNLIRMAM,IRMAMAGLV,MAGLVLVAL,NLIRMAMAGL,RMAMAGLVLV,MAMAGLVLVA,AMAGLVLVAL,LIRMAMAGLV,IRMAMAGLVL	HNSC
FCGBP	c.12055G>A	p.V4019M	VYYEPEQTVLIDNCRQQCTCHVGKV[p.V4019M]MVCQEHSCKPGQVCQPSGGILSCVTK	VMVCQEHSCK	UCS
FCGBP	c.3064G>T	p.A1022S	EALCGLCGNFNGDPADDLALRGGGQ[p.A1022S]SANALAFGNSWQEETRPGCGATEPGD	ALRGGGQSA,GQSANALAF,LALRGGGQSA,GGQSANALAF	LUAD
FCGBP	c.7478C>T	p.A2493V	RFDFMGTCVYVLAQTCGTRPGLHRF[p.A2493V]VVLQENVAWGNGRVSVTRVITVQVAN	RPGLHRFVV,VVLQENVAW,GTRPGLHRFV,RPGLHRFVVL,FVVLQENVAW	PAAD
FCGR2A	c.665T>G	p.V222G	SSKPVTITVQVPSMGSSSPMGIIVA[p.V222G]GVIATAVAAIVAAVVALIYCRKKRIS	IVAGVIATA,PMGIIVAGV,SPMGIIVAG,IIVAGVIATA,IVAGVIATAV,GVIATAVAAI,SPMGIIVAGV	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FCGRT	c.118C>G	p.P40A	LFLLPGSLGAESHLSLLYHLTAVSS[p.P40A]AAPGTPAFWVSGWLGPQQYLSYNSLR	HLTAVSSAA,SSAAPGTPA,SAAPGTPAF,YHLTAVSSA,SSAAPGTPAF,YHLTAVSSAA,SAAPGTPAFW	THCA
FCRL2	c.1513G>T	p.V505L	MQQPESSANIRTLLENKDSQVIYSS[p.V505L]LKKS*	SQVIYSSLK,QVIYSSLKK,SQVIYSSLKK,DSQVIYSSLK,KDSQVIYSSL	LUAD
FEM1A	c.1858C>A	p.L620M	AIMNALIEAGAHMDATNAFKKTAYE[p.L620M]MLDEKLLARGTMQPFNYVTLQCLAAR	TAYEMLDEK,AFKKTAYEM,FKKTAYEML,YEMLDEKLL,KTAYEMLDEK,EMLDEKLLAR,NAFKKTAYEM,YEMLDEKLLA	PRAD
FER	c.1422delA	p.L474fs	SEKPLAEQDWYHGAIPRIEAQELLK[p.L474fs]NKETFWCERVMGNLVNMSFLYILMDRGDILSYNMLITCIDSRALGFQTFLNL*	CIDSRALGF,RVMGNLVNM,ILMDRGDIL,LVNMSFLYI,NMSFLYILM,LITCIDSRA,SYNMLITCI,RALGFQTFL,NLVNMSFLY,MDRGDILSY,SFLYILMDR,MLITCIDSR,ETFWCERVM,DILSYNMLI,MGNLVNMSF,CERVMGNLV,VNMSFLYIL,RGDILSYNM,SRALGFQTF,LGFQTFLNL,KETFWCERV,GDILSYNML,LMDRGDILSY,NLVNMSFLYI,MLITCIDSRA,ALGFQTFLNL,MSFLYILMDR,VMGNLVNMSF,LYILMDRGDI,KNKETFWCER,GNLVNMSFLY,NMLITCIDSR,DSRALGFQTF,QELLKNKETF,KETFWCERVM,LVNMSFLYIL,VNMSFLYILM,LSYNMLITCI,TCIDSRALGF,SRALGFQTFL,GDILSYNMLI	STAD
FERD3L	c.275C>A	p.P92H	CEVDQGDGEEEEEEERGRGVSLLGR[p.P92H]HKRKRVITYAQRQAANIRERKRMFNL	SLLGRHKRK,GVSLLGRHK,VSLLGRHKR,HKRKRVITY,VSLLGRHKRK,RGVSLLGRHK,SLLGRHKRKR,LGRHKRKRVI,RHKRKRVITY	LUAD
FEZ2	c.149C>T	p.P50L	NCNASPEPGAEAGAEAGGGADGFPA[p.P50L]LACSLEEKLSLCFRPSDPGAEPPRTA	ALACSLEEK,GGADGFPAL,ALACSLEEKL,FPALACSLEE	ACC
FEZF2	c.244G>A	p.E82K	GSQGKKLLNLCSPLPCMIPLQPLGY[p.E82K]KVPSKTLLSYSELWKSSLRAGGGGGG	YKVPSKTLL,MIPLQPLGYK,KVPSKTLLSY,LGYKVPSKTL,IPLQPLGYKV	CESC
FGB	c.1015G>C	p.E339Q	NYCGLPGEYWLGNDKISQLTRMGPT[p.E339Q]QLLIEMEDWKGDKVKAHYGGFTVQNE	RMGPTQLLI,LTRMGPTQL,GPTQLLIEM,TRMGPTQLL,QLTRMGPTQL,LTRMGPTQLL,SQLTRMGPTQ	LUAD
FGF14	c.686C>T	p.T229M	KPLEVAMYREPSLHDVGETVPKPGV[p.T229M]MPSKSTSASAIMNGGKPVNKSKTT*	VMPSKSTSA,MPSKSTSAS,GVMPSKSTSA,VPKPGVMPSK,MPSKSTSASA,GETVPKPGVM	GBM
FGF14	c.707C>T	p.A236V	YREPSLHDVGETVPKPGVTPSKSTS[p.A236V]VSAIMNGGKPVNKSKTT*	VTPSKSTSV,VSAIMNGGK,KSTSVSAIM,SKSTSVSAI,GVTPSKSTSV,SVSAIMNGGK,TPSKSTSVSA,SKSTSVSAIM	CRC
FGFR3	c.1138G>A	p.G380R	VVLPAEEELVEADEAGSVYAGILSY[p.G380R]RVGFFLFILVVAAVTLCRLRSPPKKG	YAGILSYRV,ILSYRVGFF,SYRVGFFLF,VYAGILSYR,GILSYRVGF,LSYRVGFFL,ILSYRVGFFL,RVGFFLFILV,SVYAGILSYR,VYAGILSYRV,LSYRVGFFLF,SYRVGFFLFI,AGILSYRVGF,GILSYRVGFF,YRVGFFLFIL	BLCA
FGFR3	c.1711_1712insG	p.R571fs	QGGPLYVLVEYAAKGNLREFLRARR[p.R571fs]APGPGLLLRHLQAARGAAHLQGPGVLCLPGGPGHGVLGLPEVHPQGPGCPQCAGDRGQRDEDRRLRAGPGRAQPRLLQEDDQRPAAREVDGA*	LLLRHLQAA,RARRAPGPG,LLRHLQAAR,RLRAGPGRA,GPGHGVLGL,FLRARRAPG,LQAARGAAH,REFLRARRA,ARRAPGPGL,RRAPGPGLL,RAPGPGLLL,RHLQAARGA,AHLQGPGVL,LQGPGVLCL,LQEDDQRPA,LPGGPGHGV,CLPGGPGHGV,GLLLRHLQAA,LQAARGAAHL,LLQEDDQRPA,RARRAPGPGL,RLRAGPGRAQ,RAGPGRAQPR,LLLRHLQAAR,LPGGPGHGVL,RPAAREVDGA,FLRARRAPGP,REFLRARRAP,RRAPGPGLLL,RHLQAARGAA,HLQAARGAAH,AAHLQGPGVL,HLQGPGVLCL,LQEDDQRPAA	KIRC
FGFR3	c.2147C>A	p.P716H	GGSPYPGIPVEELFKLLKEGHRMDK[p.P716H]HANCTHDLYMIMRECWHAAPSQRPTF	HANCTHDLY,KHANCTHDLY,RMDKHANCTH,HANCTHDLYM	KIRC
FGFR3	c.2420G>C	p.*807S	SSGDDSVFAHDLLPPAPPSSGGSRT[p.*807S]SRATGPQQCEGSLAAHPAAGAQPLPGMRLSADGETATQSFGLCVCVCVCVCVCVCAHPRVPVCVRILPPGAEVPWVSPLLCNGLLTGAAAPRGLCSGGTQCRM*	RILPPGAEV,RLSADGETA,CVCVCAHPR,GSRTSRATG,GSLAAHPAA,CVRILPPGA,LLTGAAAPR,LAAHPAAGA,ETATQSFGL,QSFGLCVCV,EVPWVSPLL,GPQQCEGSL,HPAAGAQPL,SPLLCNGLL,QQCEGSLAA,AGAQPLPGM,AQPLPGMRL,AEVPWVSPL,LPPGAEVPW,VPWVSPLLC,SLAAHPAAGA,TQSFGLCVCV,GLCVCVCVCV,LLCNGLLTGA,WVSPLLCNGL,ILPPGAEVPW,ETATQSFGLC,CVCAHPRVPV,QPLPGMRLSA,HPRVPVCVRI,QQCEGSLAAH,ADGETATQSF,GETATQSFGL,AEVPWVSPLL,CEGSLAAHPA,LPPGAEVPWV	MM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FGFR3	c.742C>T	p.R248C	RGNYTCVVENKFGSIRQTYTLDVLE[p.R248C]CSPHRPILQAGLPANQTAVLGSDVEF	DVLECSPHR,LECSPHRPI,LECSPHRPIL	BLCA
FGFR3	c.746C>G	p.S249C	GNYTCVVENKFGSIRQTYTLDVLER[p.S249C]CPHRPILQAGLPANQTAVLGSDVEFH	DVLERCPHR,LERCPHRPI,CPHRPILQA,LERCPHRPIL	BLCA,LUSC
FGFRL1	c.1435_1436delCA	p.H479fs	LGPGPVAGPKLYPKLYTDIHTHTHT[p.H479fs]LSHTLTRGGQGPPAHPLSVLDGTVSAVGTGGPARQADWEDGGRSCRRRQGTHGEEEWPAPQAVCV*	SVLDGTVSA,VLDGTVSAV,HTHTHTLSH,HTLSHTLTR,HTHTLSHTL,RSCRRRQGT,DIHTHTHTL,GPPAHPLSV,PPAHPLSVL,WPAPQAVCV,GQGPPAHPL,EEWPAPQAV,EEEWPAPQA,SVLDGTVSAV,HTHTHTLSHT,HTHTLSHTLT,LTRGGQGPPA,RSCRRRQGTH,GPPAHPLSVL,HPLSVLDGTV,TDIHTHTHTL,IHTHTHTLSH,RQGTHGEEEW,EEWPAPQAVC,EEEWPAPQAV,GEEEWPAPQA	BLCA
FGFRL1	c.728G>T	p.R243L	KYTCRVSNRAGAINATYKVDVIQRT[p.R243L]LSKPVLTGTHPVNTTVDFGGTTSFQC	RTLSKPVLT,IQRTLSKPV,VIQRTLSKPV,TLSKPVLTGT,RTLSKPVLTG,IQRTLSKPVL,YKVDVIQRTL	LUAD
FGFRL1	c.820G>T	p.V274L	TGTHPVNTTVDFGGTTSFQCKVRSD[p.V274L]LKPVIQWLKRVEYGAEGRHNSTIDVG	KVRSDLKPV,QCKVRSDLK,FQCKVRSDL,KVRSDLKPVI,DLKPVIQWLK,CKVRSDLKPV	LUAD
FGGY	c.412_413insG	p.G138fs	LDHRAVSQVNRINETKHSVLQYVGG[p.G138fs]GDVCGNAGPETSVAERELERDLLG*	SVAERELER,LQYVGGGDV,AERELERDL,VLQYVGGGDV,LQYVGGGDVC,AERELERDLL	STAD
FHDC1	c.298delT	p.F100fs	PGLPPTTHMNGYSHLGKKKRMRSFF[p.F100fs]GKLFRRSKFEAKPTSGPWQPGRNITTKLIQRPLRSSLGSRKTPPSLPFLGEEEL*	RMRSFFGKL,RSFFGKLFR,KRMRSFFGK,SFFGKLFRR,KTPPSLPFL,KKRMRSFFG,FGKLFRRSK,LFRRSKFEA,RSKFEAKPT,TTKLIQRPL,IQRPLRSSL,PLRSSLGSR,GSRKTPPSL,TSGPWQPGR,NITTKLIQR,GPWQPGRNI,LPFLGEEEL,MRSFFGKLF,GKLFRRSKF,RKTPPSLPF,KLFRRSKFEA,SLPFLGEEEL,RSFFGKLFRR,RMRSFFGKLF,KKRMRSFFGK,LFRRSKFEAK,RSKFEAKPTS,TTKLIQRPLR,IQRPLRSSLG,PLRSSLGSRK,GPWQPGRNIT,LIQRPLRSSL,KRMRSFFGKL,FGKLFRRSKF,SKFEAKPTSG,FEAKPTSGPW,SRKTPPSLPF,RKTPPSLPFL	STAD
FHDC1	c.760C>T	p.R254W	SGDVSKLSLADSFLYGLIQVPNYSL[p.R254W]WIEAMVLKKEFLPSCSSLYTDITVLR	YSLWIEAMV,SLWIEAMVL,LWIEAMVLK,WIEAMVLKK,IQVPNYSLW,NYSLWIEAM,IQVPNYSLWI,SLWIEAMVLK,NYSLWIEAMV,YSLWIEAMVL,VPNYSLWIEA	CRC
FHL1	c.552T>G	p.D184E	AKHCVKCNKAITSGGITYQDQPWHA[p.D184E]ECFVCVTCSKKLAGQRFTAVEDQYYC	AECFVCVTC,QPWHAECFV,AECFVCVTCS	CLL
FIGNL1	c.926delA	p.K309fs	NGPKEDSSLPTFKTAKEQLWVDQQK[p.K309fs]STTNLSVHQGLHMVV*	SVHQGLHMV,LSVHQGLHM,DQQKSTTNL,QKSTTNLSV,SVHQGLHMVV,QQKSTTNLSV,TTNLSVHQGL,QKSTTNLSVH,NLSVHQGLHM	STAD
FILIP1	c.1565T>A	p.I522K	LKDDLTKLKSFTVMLVDERKNMMEK[p.I522K]KKQEERKVDGLNKNFKVEQGKVMDVT	MMEKKKQEER	CLL
FKBPL	c.481G>C	p.E161Q	GPPEGWTELTMGVGPWREETWGELI[p.E161Q]QKCLESMCQGEEAELQLPGHSGPPVR	ETWGELIQK,LIQKCLESM,ELIQKCLESM	CESC
FKBPL	c.959G>T	p.R320L	AQAALGNLEKATADLKKVLAIDPKN[p.R320L]LAAQEELGKVVIQGKNQDAGLAQGLR	VLAIDPKNL,KNLAAQEEL,VLAIDPKNLA	LUAD
FLG	c.477delA	p.K159fs	KGNKGRSKSPRETGGKRHESSSEKK[p.K159fs]KEKDIHLLIEKKNMEKTIITQVKKRKTRLKILD*	KTIITQVKK,LIEKKNMEK,TIITQVKKR,QVKKRKTRL,KKKEKDIHL,KEKDIHLLI,KKNMEKTII,MEKTIITQV,KKRKTRLKI,NMEKTIITQV,LLIEKKNMEK,KTIITQVKKR,TIITQVKKRK,QVKKRKTRLK,ITQVKKRKTR,KKKEKDIHLL,TQVKKRKTRL,KKRKTRLKIL	STAD
FLG	c.8657G>A	p.R2886H	ASTHADISRHSQAVQGQSEGSRRSR[p.R2886H]HQGSSVSQDSDSEGHSEDSERWSGSA	GSRRSRHQG,RSRHQGSSV,RSRHQGSSVS,RRSRHQGSSV	GBM
FLG	c.9761C>A	p.P3254H	ERWSGSASRNHRGSVQEQSRHGSRH[p.P3254H]HRSHHEDRAGHGHSADRSRQSGTRHA	GSRHHRSHH,QSRHGSRHHR	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FLG2	c.1716G>T	p.L572F	GSGSSQSSGYGQYGSRETSGFGQHG[p.L572F]FGSGQSTGFGQYGSGSGQSSGFGQHG	FGSGQSTGF,GFGSGQSTGF	LUAD
FLG2	c.4634G>T	p.G1545V	HTHGQSGSQHGESESIIHDRHRITH[p.G1545V]VQTGDTTRHSYSGHEQTTQTGSRTTG	HVQTGDTTR	LUAD
FLG2	c.5703_5704delCA	p.H1901fs	RRSGHSESSDSEVHSGGSHTHSGHT[p.H1901fs]QPSQVSTWRVRIHSSQETPNYSWTDRRYH*	HSSQETPNY,TWRVRIHSS,RVRIHSSQE,QVSTWRVRI,TQPSQVSTW,SQETPNYSW,HTHSGHTQPS,RVRIHSSQET,IHSSQETPNY,ETPNYSWTDR,HTQPSQVSTW,SQVSTWRVRI,SSQETPNYSW,QPSQVSTWRV	GBM
FLJ43860	c.2549_2550insT	p.L850fs	SHTFQLWRALGAGQPTSHLVLTTLL[p.L850fs]GLSAGATPAHRCQRQQPLPQGEDLPAFAGCHEHAARAAVCPGVQAGRAGGLPQALPGPPHPDALCLGAEPAQRAPQAAGPGGGRAQPPKLQHVTGGTEEPAVHHGALA*	LVLTTLLGL,TLLGLSAGA,GLSAGATPA,ALCLGAEPA,AQPPKLQHV,ATPAHRCQR,AARAAVCPG,GGGRAQPPK,EPAVHHGAL,HRCQRQQPL,LSAGATPAH,PQGEDLPAF,HEHAARAAV,VQAGRAGGL,RAGGLPQAL,AQRAPQAAG,LQHVTGGTE,LPQGEDLPA,HLVLTTLLGL,VLTTLLGLSA,AVCPGVQAGR,AARAAVCPGV,AGRAGGLPQA,RAQPPKLQHV,LSAGATPAHR,FAGCHEHAAR,TTLLGLSAGA,HVTGGTEEPA,LPQGEDLPAF,LPGPPHPDAL,AHRCQRQQPL,GLSAGATPAH,GRAGGLPQAL,LQHVTGGTEE,EEPAVHHGAL,LPAFAGCHEH,LPQALPGPPH,HEHAARAAVC,AEPAQRAPQA,TEEPAVHHGA	PRAD
FLNA	c.3718G>A	p.V1240M	GTHTITYIPLCPGAYTVTIKYGGQP[p.V1240M]MPNFPSKLQVEPAVDTSGVQCYGPGI	TIKYGGQPM,YGGQPMPNF,KYGGQPMPNF,GQPMPNFPSK,QPMPNFPSKL,MPNFPSKLQV,VTIKYGGQPM	GBM
FLNB	c.1586_1587insG	p.W529fs	LDGVYAFEYYPSTPGRYSIAITWGG[p.W529fs]TPHSKEPL*	ITWGGTPHSK,YSIAITWGGT,IAITWGGTPH	STAD
FLNB	c.1586delG	p.W529fs	FLDGVYAFEYYPSTPGRYSIAITWG[p.W529fs]DTTFQRAPLKFKLALKRVCRKSVLGALGSMVGLSGGQRTSW*	VLGALGSMV,TTFQRAPLK,LALKRVCRK,TFQRAPLKF,FQRAPLKFK,RAPLKFKLA,PLKFKLALK,KFKLALKRV,KLALKRVCR,RVCRKSVLG,TWGDTTFQR,MVGLSGGQR,DTTFQRAPL,APLKFKLAL,AITWGDTTF,SVLGALGSM,KRVCRKSVL,LSGGQRTSW,SVLGALGSMV,ALKRVCRKSV,KLALKRVCRK,ITWGDTTFQR,TFQRAPLKFK,IAITWGDTTF,TTFQRAPLKF,RVCRKSVLGA,DTTFQRAPLK,RAPLKFKLAL,LKRVCRKSVL,KSVLGALGSM,FQRAPLKFKL,LKFKLALKRV,GLSGGQRTSW	STAD
FLT3	c.1800_1801insTTCAGAGAATATGAATATGAT	p.600_601insFREYEYD	LQMVQVTGSSDNEYFYVDFREYEYD[p.600_601insFREYEYD]FREYEYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSI	YEYDFREYE,REYEYDFRE,REYEYDFREY,YEYDFREYEY,DFREYEYDFR,VDFREYEYDF,YDFREYEYDL	LAML
FLT3	c.2503G>C	p.D835H	RDLAARNVLVTHGKVVKICDFGLAR[p.D835H]HIMSDSNYVVRGNARLPVKWMAPESL	HIMSDSNYV,RHIMSDSNY,CDFGLARHI,HIMSDSNYVV,CDFGLARHIM,ARHIMSDSNY,RHIMSDSNYV	LAML
FLT3	c.2503G>T	p.D835Y	RDLAARNVLVTHGKVVKICDFGLAR[p.D835Y]YIMSDSNYVVRGNARLPVKWMAPESL	ICDFGLARY,YIMSDSNYV,RYIMSDSNY,CDFGLARYI,YIMSDSNYVV,KICDFGLARY,RYIMSDSNYV,CDFGLARYIM,ARYIMSDSNY	LAML
FLT3	c.2505T>A	p.D835E	RDLAARNVLVTHGKVVKICDFGLAR[p.D835E]EIMSDSNYVVRGNARLPVKWMAPESL	EIMSDSNYV,REIMSDSNY,CDFGLAREI,EIMSDSNYVV,CDFGLAREIM,AREIMSDSNY,REIMSDSNYV	LAML
FMN2	c.2252C>T	p.S751F	CLEALRLEEKEVRHHRILEAKSIQT[p.S751F]FPTEEGGVLTLPPVDGLPGRPPCPPG	FPTEEGGVL,LEAKSIQTF,QTFPTEEGGV,ILEAKSIQTF,FPTEEGGVLT	BRCA
FMN2	c.2974C>A	p.P992T	GIPLPPPLPGAGIPPPPPLPGAGIP[p.P992T]TPPPLPGAGIPPPPPLPGAGIPPPPP	AGIPTPPPL	LUAD
FMNL1	c.2779G>C	p.E927Q	HFLDKAGSVSLDSVLADVRSLQRGL[p.E927Q]QLTQREFVRQDDCMVLKEFLRANSPT	SLQRGLQLT,RSLQRGLQL,QLTQREFVR,LQRGLQLTQ,GLQLTQREF,LQLTQREFV,GLQLTQREFV,RGLQLTQREF	CESC
FMO3	c.1530C>A	p.F510L	AILTQWDRSLKPMQTRVVGRLQKPC[p.F510L]LFFHWLKLFAIPILLIAVFLVLT*	CLFFHWLKL,RLQKPCLFF,LFFHWLKLF,LQKPCLFFH,RLQKPCLFFH,LQKPCLFFHW,CLFFHWLKLF,KPCLFFHWLK,GRLQKPCLFF	CRC
FMOD	c.993C>A	p.S331R	QKIPPVNTNLENLYLQGNRINEFSI[p.S331R]RSFCTVVDVVNFSKLQVLRLDGNEIK	FSIRSFCTV,SIRSFCTVV,RSFCTVVDV,INEFSIRSF,FSIRSFCTVV,RSFCTVVDVV,RINEFSIRSF,NEFSIRSFCT	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FN1	c.868C>T	p.R290C	RGEWKCERHTSVQTTSSGSGPFTDV[p.R290C]CAAVYQPQPHPQPPPYGHCVTDSGVV	FTDVCAAVY,GPFTDVCAAV	UCEC
FNBP4	c.172_177delACCACC	p.TT58del	PEPDTEPDSTAAVPSQPAPSAATTT[p.TT58del]AVTAAAASDDSPSEDEQEAVQEVPRVVQNPP	APSAATTTA,ATTTAVTAAA,APSAATTTAV	PRAD
FNDC1	c.1955G>A	p.R652H	QGTSHRPSLPASLNDNDLVDSDEDE[p.R652H]HAVGSLHPKGAFAQPRPALSPSRQSP	HAVGSLHPK,DEHAVGSLH,DEDEHAVGSL	CRC
FNDC1	c.3535_3537delGAC	p.D1180del	APGKSEPPSKRPLSSKSQQSVSAED[p.D1180del]EEEDAGFFKGGKEDLLSSSVPKWPSSST	AEDEEEDAGF	PAAD
FOLH1	c.1501delA	p.S501fs	NLTKELKSPDEGFEGKSLYESWTKK[p.S501fs]VLPQSSVACPG*	KVLPQSSVA,YESWTKKVL,KKVLPQSSV,SLYESWTKKV,LYESWTKKVL,KKVLPQSSVA	STAD
FOLH1	c.1927G>T	p.A643S	HPQEMKTYSVSFDSLFSAVKNFTEI[p.A643S]SSKFSERLQDFDKSNPIVLRMMNDQL	KNFTEISSK,NFTEISSKF,EISSKFSER,ISSKFSERL,EISSKFSERL,KNFTEISSKF	LUAD
FOXD4L4	c.1215delC	p.C405fs	GQFCSNSSSIRRTAPTAALPPRARC[p.C405fs]GRAPVGLVGAAEVSGSGGGL*	RARCGRAPV,CGRAPVGLV,EVSGSGGGL,APVGLVGAA,RARCGRAPVG,AEVSGSGGGL	KIRC
FOXK1	c.1060C>T	p.R354W	SGIYAHITKHYPYYRTADKGWQNSI[p.R354W]WHNLSLNRYFIKVPRSQEEPGKGSFW	WQNSIWHNL,NSIWHNLSL,WHNLSLNRY,SIWHNLSLNR,GWQNSIWHNL,IWHNLSLNRY,WHNLSLNRYF	CRC
FOXN3	c.287delC	p.P96fs	NLLKSFGESVLRSVSPVQDLDDDTP[p.P96fs]HPLPTLTCPTMPGRTPTANPPTPSAASYLWPSRTLQPSACQ*	TMPGRTPTA,LTCPTMPGR,AASYLWPSR,SYLWPSRTL,DTPHPLPTL,SAASYLWPS,LPTLTCPTM,PPTPSAASY,TPSAASYLW,SAASYLWPSR,ASYLWPSRTL,TLTCPTMPGR,HPLPTLTCPT,CPTMPGRTPT,WPSRTLQPSA,NPPTPSAASY	CRC,STAD
FOXQ1	c.404C>T	p.S135L	RSKPYTRRPKPPYSYIALIAMAIRD[p.S135L]LAGGRLTLAEINEYLMGKFPFFRGSY	AIRDLAGGR,IAMAIRDLA,ALIAMAIRDL,LIAMAIRDLA,AIRDLAGGRL,MAIRDLAGGR,RDLAGGRLTL	BLCA
FOXRED1	c.407G>T	p.R136L	SVGGICQQFSLPENIQLSLFSASFL[p.R136L]LNINEYLAVVDAPPLDLRFNPSGYLL	SLFSASFLL,FSASFLLNI,FLLNINEYL,LLNINEYLA,SFLLNINEY,LNINEYLAV,FLLNINEYLA,LLNINEYLAV,ASFLLNINEY,LFSASFLLNI,SFLLNINEYL,LSLFSASFLL,LNINEYLAVV	LUAD
FPGS	c.64A>G	p.I22V	MSRARSHLRAALFLAAASARG[p.I22V]VTTQVAARRGLSAWPVPQEPSMEYQD	SARGVTTQV,GVTTQVAAR,VTTQVAARR,LAAASARGV,FLAAASARGV,ASARGVTTQV,SARGVTTQVA	ACC
FPGT-TNNI3K	c.1364G>A	p.R455H	NVININHQGRDGHTGLHSACYHGHI[p.R455H]HLVQFLLDNGADMNLVACDPSRSSGE	CYHGHIHLV,HIHLVQFLL,ACYHGHIHL,HGHIHLVQF,GHIHLVQFL,YHGHIHLVQF,HSACYHGHIH,SACYHGHIHL,GHIHLVQFLL	CRC
FPR2	c.161G>A	p.R54Q	PLVVLGVTFVLGVLGNGLVIWVAGF[p.R54Q]QMTRTVTTICYLNLALADFSFTATLP	FQMTRTVTT,QMTRTVTTI,WVAGFQMTR,VIWVAGFQM,AGFQMTRTV,FQMTRTVTTI,IWVAGFQMTR,LVIWVAGFQM	GBM
FRAS1	c.1145G>T	p.C382F	FMSSNASEVKRIPEGEKWEDGPCKV[p.C382F]FECRGAQVTCYEPSCPPCPVGTLALE	WEDGPCKVF,FECRGAQVT,KVFECRGAQV,KWEDGPCKVF	LUAD
FRG1	c.254_256delAAG	p.E86del	AIEMDKGTYIHALDNGLFTLGAPHK[p.E86del]VDEGPSPPEQFTAVKLSDSRIALKSGYG	FTLGAPHKV	PRAD
FRG1B	c.101T>C	p.I34T	RIALKSGYGKYLGINSDELVGHSDA[p.I34T]TGPREQWEPVFQNGKMALLASNSCFI	DELVGHSDAT	PRAD
FRG1B	c.110G>A	p.R37K	LKSGYGKYLGINSDELVGHSDAIGP[p.R37K]KEQWEPVFQNGKMALLASNSCFIRCN	GPKEQWEPV,DAIGPKEQW,VGHSDAIGPK	UCS
FRG1B	c.115C>A	p.Q39K	SGYGKYLGINSDELVGHSDAIGPRE[p.Q39K]KWEPVFQNGKMALLASNSCFIRCNEA	GPREKWEPV,DAIGPREKW,HSDAIGPREK,KWEPVFQNGK,GPREKWEPVF	CLL
FRG1B	c.125C>A	p.P42Q	GKYLGINSDELVGHSDAIGPREQWE[p.P42Q]QVFQNGKMALLASNSCFIRCNEAGDI	GPREQWEQV,EQVFQNGKM,GPREQWEQVF,WEQVFQNGKM,QVFQNGKMAL,REQWEQVFQN	PRAD
FRG1B	c.145A>G	p.M49V	SDELVGHSDAIGPREQWEPVFQNGK[p.M49V]VALLASNSCFIRCNEAGDIEAKSKTA	FQNGKVALL,FQNGKVALLA,VFQNGKVALL,VALLASNSCF,WEPVFQNGKV	TGCT

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FRG1B	c.148G>C	p.A50P	DELVGHSDAIGPREQWEPVFQNGKM[p.A50P]PLLASNSCFIRCNEAGDIEAKSKTAG	FQNGKMPLL,VFQNGKMPL,MPLLASNSC,PLLASNSCF,FQNGKMPLLA,VFQNGKMPLL,MPLLASNSCF	KIRP,PRAD,SKCM
FRG1B	c.155T>C	p.L52S	LVGHSDAIGPREQWEPVFQNGKMAL[p.L52S]SASNSCFIRCNEAGDIEAKSKTAGEE	SASNSCFIR,LSASNSCFI,ALSASNSCF,FQNGKMALSA,ALSASNSCFI,KMALSASNSC,LSASNSCFIR,MALSASNSCF	PRAD,UCS
FRG1B	c.157G>A	p.A53T	VGHSDAIGPREQWEPVFQNGKMALL[p.A53T]TSNSCFIRCNEAGDIEAKSKTAGEEE	LLTSNSCFI,LTSNSCFIR,ALLTSNSCF,ALLTSNSCFI,FQNGKMALLT,KMALLTSNSC,LLTSNSCFIR,MALLTSNSCF	GBM,PRAD
FRG1B	c.163A>G	p.N55D	HSDAIGPREQWEPVFQNGKMALLAS[p.N55D]DSCFIRCNEAGDIEAKSKTAGEEEMI	LLASDSCFI,LASDSCFIR,ALLASDSCF,ALLASDSCFI,LLASDSCFIR,MALLASDSCF	PRAD
FRG1B	c.175A>G	p.I59V	IGPREQWEPVFQNGKMALLASNSCF[p.I59V]VRCNEAGDIEAKSKTAGEEEMIKSLS	LLASNSCFV,LASNSCFVR,ALLASNSCFV,LLASNSCFVR	PRAD,SKCM
FRG1B	c.194G>A	p.G65E	WEPVFQNGKMALLASNSCFIRCNEA[p.G65E]EDIEAKSKTAGEEEMIKSLSHSLPSS	FIRCNEAEDI	UCS
FRG1B	c.29T>C	p.I10T	MAVKLSDSR[p.I10T]TALKSGYGKYLGINSDELVGHSDAIG	LSDSRTALK,KLSDSRTAL,TALKSGYGK,RTALKSGYG,KLSDSRTALK,RTALKSGYGK,AVKLSDSRTA,TALKSGYGKY,VKLSDSRTAL	PRAD,UCS
FRG1B	c.31G>A	p.A11T	MAVKLSDSRI[p.A11T]TLKSGYGKYLGINSDELVGHSDAIGP	KLSDSRITL,ITLKSGYGK,LSDSRITLK,TLKSGYGKY,SRITLKSGY,TLKSGYGKYL,KLSDSRITLK,RITLKSGYGK,ITLKSGYGKY,VKLSDSRITL	PRAD
FRG1B	c.39A>T	p.K13N	MAVKLSDSRIAL[p.K13N]NSGYGKYLGINSDELVGHSDAIGPRE	IALNSGYGK,SRIALNSGY,ALNSGYGKY,ALNSGYGKYL,RIALNSGYGK,IALNSGYGKY,DSRIALNSGY	GBM,PRAD,UCS
FRG1B	c.59T>C	p.L20P	MAVKLSDSRIALKSGYGKY[p.L20P]PGINSDELVGHSDAIGPREQWEPVFQ	YPGINSDEL,KYPGINSDEL,KSGYGKYPGI,YPGINSDELV	KIRP
FRG1B	c.95A>T	p.D32V	DSRIALKSGYGKYLGINSDELVGHS[p.D32V]VAIGPREQWEPVFQNGKMALLASNSC	ELVGHSVAI,VAIGPREQW,DELVGHSVA,NSDELVGHSV,DELVGHSVAI	PRAD,UCS
FRG2B	c.424G>T	p.D142Y	ECSLSLNKKSRSSTPVHNSEIQETC[p.D142Y]YAHHRGRSRACTGRSKRHRSRALGVQ	NSEIQETCY,YAHHRGRSR,TCYAHHRGR,SEIQETCYA,IQETCYAHH,ETCYAHHRGR,CYAHHRGRSR,YAHHRGRSRA,SEIQETCYAH	LUAD
FRMD4A	c.3014delC	p.P1005fs	CKATSAALPQSQRSSTPSSEIGATP[p.P1005fs]QAAPTTS*	SEIGATPQA,SEIGATPQAA	STAD
FRMPD1	c.3277G>C	p.E1093Q	APKYTEPLLSPRDEPRSDECGINPG[p.E1093Q]QKIASIPTKEEPQGQLSLERDREVTN	NPGQKIASI,GQKIASIPT,GQKIASIPTK	LUAD
FRS2	c.140T>C	p.L47S	KVINVDDDGNELGSGIMELTDTELI[p.L47S]SYTRKRDSVKWHYLCLRRYGYDSNLF	LTDTELISY,DTELISYTR,ELISYTRKR,ISYTRKRDSV,SYTRKRDSVK,ELTDTELISY	TGCT
FSHB	c.128C>A	p.T43N	CNSCELTNITIAIEKEECRFCISIN[p.T43N]NTWCAGYCYTRDLVYKDPARPKIQKT	NTWCAGYCY,INNTWCAGY,FCISINNTW,RFCISINNTW,SINNTWCAGY,NTWCAGYCYT	LUAD
FUBP1	c.1288C>T	p.R430C	QSGARIELQRNPPPNADPNMKLFTI[p.R430C]CGTPQQIDYARQLIEEKIGGPVNPLG	CGTPQQIDY,FTICGTPQQI	UCEC

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FUT6	c.418_419insA	p.S140fs	NPSAQLPRSPRRQGQRWIWFSMESP[p.S140fs]KPLLAAESHGRILQSHHVLPQRLRHLHALRLAGAVVRPACPPTAQPLGQDRAGGLGSVQLGAKLRQGALLPEPAGPSQGGRVRTLPQAPAPGNHDGDAVPVQVLSGLRELLAPRLHHREAVEERPGGLGRARGAGPQQKQLREVPATRRLHPRGRLPEPQGPGPVPAGAGQGPRPLPELLSLAGDAAASLLQLGTRFLQGLLETAGGIQVPDTRHSGLVHLRGWCGAWAARNLIFLGPHLSGGLIYLRTRLPEASPA*	VLSGLRELL,FLQGLLETA,GLLETAGGI,NLIFLGPHL,HLSGGLIYL,FSMESPKPL,VLPQRLRHL,ALRLAGAVV,GLGSVQLGA,PLPELLSLA,LLSLAGDAA,LLQLGTRFL,FLGPHLSGG,IWFSMESPK,RLRHLHALR,ASLLQLGTR,LSGGLIYLR,AWAARNLIF,RILQSHHVL,VVRPACPPT,KLRQGALLP,RVRTLPQAP,GLRELLAPR,RARGAGPQQ,ATRRLHPRG,RLHPRGRLP,GTRFLQGLL,AARNLIFLG,QSHHVLPQR,LLAPRLHHR,QLREVPATR,PATRRLHPR,GWCGAWAAR,ESPKPLLAA,DAAASLLQL,WAARNLIFL,RPACPPTAQ,VPVQVLSGL,APRLHHREA,HPRGRLPEP,GPRPLPELL,RPLPELLSL,VPDTRHSGL,GPHLSGGLI,QRLRHLHAL,GAKLRQGAL,SLLQLGTRF,HLRGWCGAW,SMESPKPLL,MESPKPLLA,LQSHHVLPQ,LRHLHALRL,RHLHALRLA,HLHALRLAG,AKLRQGALL,RQGALLPEP,SQGGRVRTL,KQLREVPAT,REVPATRRL,LSLAGDAAA,LAGDAAASL,LETAGGIQV,TRHSGLVHL,RGWCGAWAA,GAWAARNLI,FSMESPKPLL,LLAAESHGRI,RLAGAVVRPA,GLRELLAPRL,SLAGDAAASL,SLLQLGTRFL,FLGPHLSGGL,RLRHLHALRL,HLHALRLAGA,VLSGLRELLA,LLSLAGDAAA,QLGTRFLQGL,LLETAGGIQV,HLRGWCGAWA,WIWFSMESPK,GLGSVQLGAK,HLSGGLIYLR,GAWAARNLIF,AWAARNLIFL,HGRILQSHHV,HVLPQRLRHL,ALRLAGAVVR,VVRPACPPTA,KLRQGALLPE,GGRVRTLPQA,RVRTLPQAPA,RTLPQAPAPG,RARGAGPQQK,ATRRLHPRGR,RLHPRGRLPE,RGWCGAWAAR,ELLAPRLHHR,QLREVPATRR,VPATRRLHPR,EAVEERPGGL,QVPDTRHSGL,LPQRLRHLHA,APGNHDGDAV,APRLHHREAV,GPQQKQLREV,LPEPQGPGPV,PQRLRHLHAL,GPHLSGGLIY,MESPKPLLAA,LAAESHGRIL,GRILQSHHVL,HALRLAGAVV,RAGGLGSVQL,RQGALLPEPA,VQVLSGLREL,RELLAPRLHH,QQKQLREVPA,REVPATRRLH,GQGPRPLPEL,GDAAASLLQL,ASLLQLGTRF,LQLGTRFLQG,RFLQGLLETA,IQVPDTRHSG,VHLRGWCGAW,RNLIFLGPHL,AESHGRILQS,PELLSLAGDA,VPDTRHSGLV	KIRC
FYB	c.972delG	p.G324fs	NQEELASGTPPARFPKAPSKLTVGG[p.G324fs]HGAKVRKRKRETRIQPPRNRSHCLPCLPWVHLHQNPTDHQMLT*	LTVGGHGAK,GGHGAKVRK,HGAKVRKRK,KVRKRKRET,RIQPPRNRS,RNRSHCLPC,TVGGHGAKV,PPRNRSHCL,HQNPTDHQM,IQPPRNRSH,SHCLPCLPW,LPCLPWVHL,LPWVHLHQN,CLPCLPWVHL,KLTVGGHGAK,KVRKRKRETR,RIQPPRNRSH,RNRSHCLPCL,ETRIQPPRNR,LTVGGHGAKV,QPPRNRSHCL,RSHCLPCLPW,LHQNPTDHQM,HQNPTDHQML,LPWVHLHQNP	STAD
FZD3	c.1099G>A	p.D367N	LTIILLAMNKIEGDNISGVCFVGLY[p.D367N]NVDALRYFVLAPLCLYVVVGVSLLLA	NVDALRYFV,GLYNVDALR,LYNVDALRY,YNVDALRYF,GVCFVGLYNV,GLYNVDALRY,LYNVDALRYF,YNVDALRYFV	CRC
FZD6	c.1247G>A	p.R416Q	ISLNHVRQVIQHDGRNQEKLKKFMI[p.R416Q]QIGVFSGLYLVPLVTLLGCYVYEQVN	KLKKFMIQI,IQIGVFSGL,KFMIQIGVF,QIGVFSGLY,KKFMIQIGV,FMIQIGVFSG,MIQIGVFSGL,KLKKFMIQIG,IQIGVFSGLY,KKFMIQIGVF	UCEC
GABRA3	c.218G>A	p.R73H	LSPKHAPDIPDDSTDNITIFTRILD[p.R73H]HLLDGYDNRLRPGLGDAVTEVKTDIY	ILDHLLDGY,IFTRILDHL,HLLDGYDNR,FTRILDHLL,HLLDGYDNRL,TIFTRILDHL,IFTRILDHLL,RILDHLLDGY	UCEC
GABRA4	c.1379G>A	p.R460Q	PFSRANAAETISAARALPSASPTSI[p.R460Q]QTGYMPRKASVGSASTRHVFGSRLQR	SIQTGYMPR,IQTGYMPRK,SPTSIQTGY,SIQTGYMPRK,TSIQTGYMPR,ASPTSIQTGY,SPTSIQTGYM,IQTGYMPRKA	CRC,UCEC
GABRA5	c.377G>A	p.S126N	RQSWKDERLRFKGPMQRLPLNNLLA[p.S126N]NKIWTPDTFFHNGKKSIAHNMTTPNK	NKIWTPDTF,ANKIWTPDTF,NKIWTPDTFF	CRC
GABRA5	c.670C>A	p.Q224K	SEVVYVWTNGSTKSVVVAEDGSRLN[p.Q224K]KYHLMGQTVGTENISTSTGEYTIMTA	KYHLMGQTV,GSRLNKYHL,SRLNKYHLM,GSRLNKYHLM,AEDGSRLNKY,NKYHLMGQTV	LUAD
GABRA6	c.940G>A	p.V314I	SARHSLPKVSYATAMDWFIAVCFAF[p.V314I]IFSALIEFAAVNYFTNLQTQKAKRKA	FIAVCFAFI,FAFIFSALI,FIFSALIEF,IAVCFAFIF,CFAFIFSAL,FIFSALIEFA,WFIAVCFAFI,CFAFIFSALI,AFIFSALIEF,FIAVCFAFIF,VCFAFIFSAL	GBM
GABRB1	c.1246C>T	p.R416C	KATMYSYDSASIQYRKPLSSREAYG[p.R416C]CALDRHGVPSKGRIRRRASQLKVKIP	SSREAYGCA,EAYGCALDR,SREAYGCAL,SSREAYGCAL	PRAD

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GABRB3	c.1498G>A	p.D500N	RSLPHKKTHLRRRSSQLKIKIPDLT[p.D500N]NVNAIDRWSRIVFPFTFSLFNLVYWL	LTNVNAIDR,IKIPDLTNV,KIKIPDLTNV,KIPDLTNVNA,DLTNVNAIDR,NVNAIDRWSR,IPDLTNVNAI	CRC
GABRD	c.1236delG	p.Q412fs	GSYRSVGVETGETKKEGAARSGGQG[p.Q412fs]ASVPGSGPSTQTPLTFTPALCSLRRLRPSMSSTGRHTPCEHRTQATLACPGARRQLPRNFLGERALGLPSPLRVSKWDDSRPRKTRGSLGLPEL*	FLGERALGL,RLRPSMSST,ATLACPGAR,ALGLPSPLR,RVSKWDDSR,TFTPALCSL,AARSGGQGA,RSGGQGASV,SLRRLRPSM,RQLPRNFLG,RALGLPSPL,KWDDSRPRK,KTRGSLGLP,FTPALCSLR,ALCSLRRLR,TLACPGARR,QTPLTFTPA,TPLTFTPAL,RPRKTRGSL,PSTQTPLTF,CEHRTQATL,TQATLACPG,ARRQLPRNF,RRQLPRNFL,RNFLGERAL,GERALGLPS,RKTRGSLGL,RGSLGLPEL,ALGLPSPLRV,ATLACPGARR,RALGLPSPLR,CSLRRLRPSM,SLRRLRPSMS,RLRPSMSSTG,RTQATLACPG,KTRGSLGLPE,TFTPALCSLR,QTPLTFTPAL,LTFTPALCSL,TPALCSLRRL,LPRNFLGERA,RPRKTRGSLG,GSGPSTQTPL,GPSTQTPLTF,TQTPLTFTPA,TQATLACPGA,LACPGARRQL,GARRQLPRNF,RQLPRNFLGE,ERALGLPSPL,TRGSLGLPEL,LPSPLRVSKW,CEHRTQATLA,GERALGLPSP	STAD
GABRG1	c.613G>A	p.E205K	LRLTINAECYLQLHNFPMDEHSCPL[p.E205K]KFSSYGYPKNEIEYKWKKPSVEVADP	KFSSYGYPK,PLKFSSYGY,DEHSCPLKF,HSCPLKFSSY,CPLKFSSYGY,MDEHSCPLKF	SKCM
GABRR2	c.1103C>T	p.A368V	VSYVKAVDIYLWVSFVFVFLSVLEY[p.A368V]VAVNYLTTVQERKERKLREKFPCMCG	VFLSVLEYV,FLSVLEYVA,VAVNYLTTV,VLEYVAVNY,LEYVAVNYL,FVFLSVLEYV,FLSVLEYVAV,VLEYVAVNYL,YVAVNYLTTV,SVLEYVAVNY,LEYVAVNYLT	PRAD
GADL1	c.1054C>A	p.L352I	VAWNPHKMLMAGIQCCALLVKDKSD[p.L352I]ILKKCYSAKASYLFQQDKFYDVSYDT	KSDILKKCY,ILKKCYSAK,ILKKCYSAKA,LVKDKSDILK,DILKKCYSAK	LUAD
GAL3ST3	c.811G>T	p.A271S	ESLVLLRRLLAWDLDDVLYAKLNAR[p.A271S]SASSRLAAIPAALARAARTWNALDAG	SASSRLAAI,KLNARSASS,RSASSRLAA,NARSASSRL,YAKLNARSA,VLYAKLNARS,KLNARSASSR,NARSASSRLA,RSASSRLAAI,LNARSASSRL,ARSASSRLAA	LUAD
GALNT13	c.1072G>T	p.G358C	LEIVTCSHVGHVFRKATPYTFPGGT[p.G358C]CHVINKNNRRLAEVWMDEFKDFFYII	GGTCHVINK,YTFPGGTCH,FPGGTCHVI,YTFPGGTCHV,TFPGGTCHVI	LUSC
GALNT14	c.702T>A	p.D234E	VNRDWLQPLLHRVKEDYTRVVCPVI[p.D234E]EIINLDTFTYIESASELRGGFDWSLH	RVVCPVIEI,IEIINLDTF,CPVIEIINL,EIINLDTFTY,RVVCPVIEII	LUAD
GALNTL1	c.950_951insG	p.W317fs	GIFVIDKSWFNHLGKYDAQMDIWGG[p.W317fs]REF*	AQMDIWGGR,MDIWGGREF,DAQMDIWGGR,QMDIWGGREF	STAD
GALNTL2	c.1183G>A	p.E395K	AMDRHYFQNTGAYDSLMSLRGGENL[p.E395K]KLSFKAWLCGGSVEILPCSRVGHIYQ	SLRGGENLK,GGENLKLSF,NLKLSFKAW,LKLSFKAWL,SLRGGENLKL,MSLRGGENLK,NLKLSFKAWL,RGGENLKLSF,GENLKLSFKA	UCEC
GALNTL5	c.133G>A	p.A45T	TALLFIYLHHNHVSSWQKKSQEPLS[p.A45T]TWSPGKKVHQQIIYGSEQIPKPHVIV	LSTWSPGKK,KSQEPLSTW,KKSQEPLSTW	LIHC
GALNTL5	c.785G>T	p.R262I	LEPLLHAIAKDPKMVVCPLIDVIDD[p.R262I]ITLEYKPSPLVRGTFDWNLQFKWDNV	VIDDITLEY,PLIDVIDDI,VIDDITLEYK,DVIDDITLEY,ITLEYKPSPL,CPLIDVIDDI	CRC
GALNTL6	c.1694_1696delAGA	p.K567del	WGYRKDRTLFHPVSNSCMDCNPAEK[p.K567del]IFMARCDPLSETQQWIFEHINMTVLEKF	NPAEKIFMA,CMDCNPAEKI,NPAEKIFMAR,MDCNPAEKIF	BRCA
GARS	c.124C>G	p.P42A	LLLLPPRLLARPSLLLRRSLSAASC[p.P42A]APISLPAAASRSSMDGAGAEEVLAPL	RSLSAASCA,LSAASCAPI,APISLPAAA,AASCAPISL,SLSAASCAPI,SAASCAPISL	ACC
GART	c.2420delA	p.K807fs	IESMQINGSVLKNGSLTNHFSFEKK[p.K807fs]RPEWLS*	FEKKRPEWL,FSFEKKRPEW	OV
GAS2L2	c.566A>C	p.D189A	AAPTLVQLEEEIEEEVRRELALPPP[p.D189A]APSPPAPPRRQPCHFRNLDQMVQSLV	RELALPPPA,LPPPAPSPPA,RELALPPPAP	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GAS6	c.449delG	p.G150fs	CDRKGTQACQDLMGNFFCLCKAGWG[p.G150fs]AGSATKMSTNAARRTGAASRSATTSRVASTVPATAASSSPLMAGPAKT*	TTSRVASTV,ATAASSSPL,KMSTNAARR,GWGAGSATK,ATKMSTNAA,ARRTGAASR,RTGAASRSA,ASRSATTSR,RSATTSRVA,STVPATAAS,NAARRTGAA,WGAGSATKM,SRVASTVPA,TAASSSPLM,ATTSRVASTV,RVASTVPATA,ATKMSTNAAR,AASRSATTSR,SSPLMAGPAK,AGWGAGSATK,STNAARRTGA,AARRTGAASR,RTGAASRSAT,ASRSATTSRV,TSRVASTVPA,ATAASSSPLM,SRVASTVPAT	STAD
GAS8	c.937C>A	p.R313S	EEMSEMQKQLANYERDKQILLCTKA[p.R313S]SLKVREKELKDLQWEHEVLEQRFTKV	ILLCTKASL,LLCTKASLK,KASLKVREK,CTKASLKVR,SLKVREKEL,LLCTKASLKV,ILLCTKASLK,SLKVREKELK,KQILLCTKAS	LUAD
GATA3	c.1002_1003insG	p.N334fs	ARRAGTSCANCQTTTTTLWRRNANG[p.N334fs]GPCLQCLWALLQASQY*	CLQCLWALL,WALLQASQY,RNANGGPCL,LWALLQASQY,RRNANGGPCL,LQCLWALLQA	BRCA
GATA3	c.1200_1201insA	p.H400fs	CKKVHDSLEDFPKNSSFNPAALSRH[p.H400fs]NVLPEPHLALQPLQPHADHAHADAPAIQPVLWTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	VLPEPHLAL,ALQPLQPHA,AIQPVLWTT,MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,AALSRHNVL,EPHLALQPL,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LALQPLQPH,LQPHADHAH,HAHADAPAI,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,ADAPAIQPV,APAIQPVLW,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,HADAPAIQPV,NPAALSRHNV,QPVLWTTPPL,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,RHNVLPEPHL,HLALQPLQPH,ADAPAIQPVL,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF,PEPHLALQPL	BRCA
GATA3	c.1222_1223insC	p.S408fs	EDFPKNSSFNPAALSRHMSSLSHIS[p.S408fs]ALQPLQPHADHAHADAPAIQPVLWTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	ALQPLQPHA,AIQPVLWTT,MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,MSSLSHISA,SSLSHISAL,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,SHISALQPL,SALQPLQPH,LQPHADHAH,HAHADAPAI,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,ADAPAIQPV,APAIQPVLW,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,HMSSLSHISA,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,MSSLSHISAL,HADAPAIQPV,QPVLWTTPPL,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,LSHISALQPL,ADAPAIQPVL,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GATA3	c.1223_1224insT	p.S408fs	EDFPKNSSFNPAALSRHMSSLSHIS[p.S408fs]ALQPLQPHADHAHADAPAIQPVLWTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	ALQPLQPHA,AIQPVLWTT,MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,MSSLSHISA,SSLSHISAL,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,SHISALQPL,SALQPLQPH,LQPHADHAH,HADAPAI,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,ADAPAIQPV,APAIQPVLW,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,HMSSLSHISA,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,MSSLSHISAL,HADAPAIQPV,QPVLWTTPPL,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,LSHISALQPL,ADAPAIQPVL,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1290_1291insT	p.S430fs	ISPFSHSSHMLTTPTPMHPPSSLSF[p.S430fs]WTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,LSFWTTPPL,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,HPPSSLSFW,SLSFWTTPPL,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,MHPPSSLSFW,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1301_1302insC	p.H434fs	FSHSSHMLTTPTPMHPPSSLSFGPH[p.H434fs]PPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LSFGPHPPL,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,SLSFGPHPPL,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,AVPFDLHFCR,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1304_1305insC	p.H435fs	HSSHMLTTPTPMHPPSSLSFGPHHP[p.H435fs]LQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,LSFGPHHPL,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,HPLQHGHRH,AESKIMFAT,SLSFGPHHPL,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,AVPFDLHFCR,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1329G>T	p.M443I	TTPTPMHPPSSLSFGPHHPSSMVTA[p.M443I]IG*	HPSSMVTAI	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GATA3	c.983_984insCTGGAGG	p.L328fs	RRLSAARRAGTSCANCQTTTTTLWR[p.L328fs]LEEECQWGPCLQCLWALLQASQY*	CLQCLWALL,QWGPCLQCL,TTTTTLWRL,WALLQASQY,EECQWGPCL,QWGPCLQCLW,LWALLQASQY,QTTTTTLWRL,CQWGPCLQCL,LQCLWALLQA	BRCA
GBP7	c.1292_1293insG	p.G431fs	QAELKRLSELLTESISRGTFFVPGG[p.G431fs]AQYLLRSKKED*	FVPGGAQYL,AQYLLRSKK,GAQYLLRSK,FFVPGGAQY,VPGGAQYLL,FVPGGAQYLL,GAQYLLRSKK,FFVPGGAQYL,TFFVPGGAQY	STAD
GCDH	c.1167delG	p.L389fs	VSLLKRNNCGKALDIARQARDMLGG[p.L389fs]MGFLTSIT*	MLGGMGFLT,RDMLGGMGF,GGMGFLTSI,RQARDMLGGM,RDMLGGMGFL	STAD
GCDH	c.244C>T	p.R82C	EEQLTTDEILIRDTFRTYCQERLMP[p.R82C]CILLANRNEVFHREIISEMGELGVLG	RLMPCILLA,MPCILLANR,QERLMPCIL,LMPCILLANR,CQERLMPCIL,QERLMPCILL	LUAD
GDAP1	c.919A>G	p.T307A	RVLKRKTFNKVLGHVNNILISAVLP[p.T307A]AAFRVAKKRAPKVLGTTLVVGLLAGV	ILISAVLPA,LISAVLPAA,AVLPAAFRV,VLPAAFRVA,SAVLPAAFR,LPAAFRVAK,ISAVLPAAF,ILISAVLPAA,VLPAAFRVAK,ISAVLPAAFR,AVLPAAFRVA,SAVLPAAFRV,LISAVLPAAF	BRCA
GDF5	c.315_316insA	p.E105fs	GQTGGLTQPKKDEPKKLPPRPGGPE[p.E105fs]TQARTPSPNKAGYSPDCDPKRTASRRQGTPKSRICPQLLPAEEGQGARAPTRAQGAVSPTPHHTPRVHALAVQDAVRC*	RICPQLLPA,ASRRQGTPK,QARTPSPNK,RTASRRQGT,KSRICPQLL,HTPRVHALA,SPTPHHTPR,HALAVQDAV,APTRAQGAV,TPRVHALAV,RQGTPKSRI,RAQGAVSPT,AQGAVSPTP,HHTPRVHAL,TPSPNKAGY,AEEGQGARA,LLPAEEGQGA,TQARTPSPNK,TASRRQGTPK,QARTPSPNKA,AGYSPDCDPK,ASRRQGTPKS,KSRICPQLLP,RVHALAVQDA,RTPSPNKAGY,HALAVQDAVR,HTPRVHALAV,TPKSRICPQL,SPTPHHTPRV,SRICPQLLPA,AQGAVSPTPH	TGCT
GDPD5	c.1779_1780insC	p.G593fs	SVCSDNSYDTYANSTATPVGPRGGG[p.G593fs]QPHQDPHRAEWALAEDMSVPPVPDTEAGEPRRAGGSVSELGVLWERAPQPPCGLQPLVSRSLS*	GPRGGGQPH,EPRRAGGSV,QPPCGLQPL,HQDPHRAEW,AEWALAEDM,WALAEDMSV,AEDMSVPPV,RAGGSVSEL,WERAPQPPC,LQPLVSRSL,SELGVLWER,DPHRAEWAL,ALAEDMSVPP,GLQPLVSRSL,RAEWALAEDM,RRAGGSVSEL,AEWALAEDMS,SELGVLWERA,QPPCGLQPLV	KIRP
GEM	c.803G>T	p.R268L	RDSKEKNERRLAYQKRKESMPRKAR[p.R268L]LFWGKIVAKNNKNMAFKLKSKSCHDL	RLFWGKIVA,SMPRKARLF,RKARLFWGK,KARLFWGKI,LFWGKIVAK,MPRKARLFW,ESMPRKARL,RLFWGKIVAK,SMPRKARLFW,KARLFWGKIV,MPRKARLFWG,KESMPRKARL,RKARLFWGKI	LUAD
GEN1	c.1526C>T	p.S509L	VMSFQSHMTLKPTCEIFHKQNSKLN[p.S509L]LGISPDPTLPQESISASLNSLLLPKN	HKQNSKLNL,SKLNLGISP,LGISPDPTL,KQNSKLNLGI,FHKQNSKLNL	UCEC
GFM1	c.49_50insC	p.A17fs	MRLLGAAAVAALGRGRAP[p.A17fs]RLPRLAEEAG*	RLPRLAEEA,ALGRGRAPR,RGRAPRLPR,APRLPRLAE,AALGRGRAPR,RGRAPRLPRL	KICH
GFRAL	c.922C>A	p.Q308K	LGTVLQVQCTCRTITQSEESLCKIF[p.Q308K]KHMLHRKSCFNYPTLSNVKGMALYTR	KIFKHMLHR,IFKHMLHRK,SLCKIFKHM,SLCKIFKHML,KIFKHMLHRK,KHMLHRKSCF	LUAD
GGA2	c.188C>T	p.A63V	MSEQDWSAIQNFCEQVNTDPNGPTH[p.A63V]VPWLLAHKIQSPQEKEALYALTVLEM	HVPWLLAHK,THVPWLLAH,VPWLLAHKI,GPTHVPWLL,NTDPNGPTHV,HVPWLLAHKI,DPNGPTHVPW	UCEC
GIGYF2	c.680G>A	p.R227H	PNFEEGGPTSVGRKHEFIRSESENW[p.R227H]HIFREEQNGEDEDGGWRLAGSRRDGE	ESENWHIFR,SESENWHIF,RSESENWHIF	UCEC
GIMAP7	c.827delT	p.V276fs	LLKLKYDEKIKNIREEAERNIFKDV[p.V276fs]LIGFGRCFQKYGIGFCRNVSFILPNLL*	NVSFILPNL,IGFGRCFQK,IFKDVLIGF,CFQKYGIGF,IGFCRNVSF,GFGRCFQKY,VLIGFGRCF,VSFILPNLL,LIGFGRCFQK,KYGIGFCRNV,IGFGRCFQKY,FQKYGIGFCR,NVSFILPNLL,NIFKDVLIGF,AERNIFKDVL,RCFQKYGIGF,GIGFCRNVSF,IGFCRNVSFI,RNVSFILPNL	STAD
GIMAP8	c.1630G>T	p.A544S	SCCEKGDTFFVLVFQLGRFTEEDKT[p.A544S]SVAKLEAIFGADFTKYAIMLFTRKED	KTSVAKLEA,FTEEDKTSV,SVAKLEAIF,KTSVAKLEAI,TSVAKLEAIF,EEDKTSVAKL	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GIPC3	c.679delG	p.G227fs	SRSSKCPVEAKVTSGRETLRLRSGG[p.G227fs]LPQWRKRPVSLRRRHLGRLMTCWKATWAFGTPSWRPPWWRRPRRQRAPRSLHAV*	RLMTCWKAT,RAPRSLHAV,SLRRRHLGR,TCWKATWAF,TWAFGTPSW,RLRSGGLPQ,QWRKRPVSL,RKRPVSLRR,RRRHLGRLM,LGRLMTCWK,CWKATWAFG,SWRPPWWRR,RPRRQRAPR,RQRAPRSLH,WAFGTPSWR,RPPWWRRPR,MTCWKATWA,LPQWRKRPV,TLRLRSGGL,LRSGGLPQW,LMTCWKATW,RRQRAPRSL,TPSWRPPWW,LMTCWKATWA,GLPQWRKRPV,SLRRRHLGRL,HLGRLMTCWK,RSGGLPQWRK,VSLRRRHLGR,RLMTCWKATW,MTCWKATWAF,RLRSGGLPQW,QWRKRPVSLR,RKRPVSLRRR,SWRPPWWRRP,WWRRPRRQRA,RQRAPRSLHA,TWAFGTPSWR,TPSWRPPWWR,RPPWWRRPRR,ETLRLRSGGL,LPQWRKRPVS,RPVSLRRRHL,RPRRQRAPRS,PQWRKRPVSL,LRRRHLGRLM,RHLGRLMTCW,ATWAFGTPSW,FGTPSWRPPW	STAD
GIT2	c.368G>T	p.R123L	KVHPNKAEFIRAKYQMLAFVHRLPC[p.R123L]LDDDSVTAKDLSKQLHSSVRTGNLET	CLDDDSVTA,LPCLDDDSV,RLPCLDDDSV,LAFVHRLPCL	LUAD
GJA1	c.932delC	p.A311fs	YKLVTGDRNNSSCRNYNKQASEQNW[p.A311fs]VITVQNKIEWGRREAPSLTPMHSLLISPMITRILKN*	SLTPMHSLL,LISPMITRI,KQASEQNWV,LLISPMITR,SPMITRILK,QASEQNWVI,WVITVQNKI,REAPSLTPM,SEQNWVITV,WGRREAPSL,MHSLLISPM,IEWGRREAP,KQASEQNWVI,SLTPMHSLLI,LLISPMITRI,LISPMITRIL,SLLISPMITR,ISPMITRILK,NWVITVQNKI,TVQNKIEWGR,APSLTPMHSL,RREAPSLTPM,REAPSLTPMH,PMHSLLISPM,MHSLLISPMI,IEWGRREAPS	KIRC
GJB3	c.479G>A	p.R160H	LIFKLIIEFLFLYLLHTLWHGFNMP[p.R160H]HLVQCANVAPCPNIVDCYIARPTEKK	NMPHLVQCA,HLVQCANVA,MPHLVQCAN,LWHGFNMPHL,MPHLVQCANV	GBM
GJB4	c.64C>A	p.R22S	MNWAFLQGLLSGVNKYSTVLS[p.R22S]SIWLSVVFIFRVLVYVVAAEEVWDDE	VLSSIWLSV,SIWLSVVFI,LSSIWLSVV,KYSTVLSSI,SSIWLSVVF,STVLSSIWL,NKYSTVLSS,YSTVLSSIW,TVLSSIWLSV,VLSSIWLSVV,KYSTVLSSIW,SIWLSVVFIF,SSIWLSVVFI,LSSIWLSVVF,NKYSTVLSSI,YSTVLSSIWL	LUAD
GLB1L2	c.1221C>G	p.I407M	KMPYEPLTPVLYLSLWDALKYLGEP[p.I407M]MKSEKPINMENLPVNGGNGQSFGYIL	ALKYLGEPM,EPMKSEKPI,MKSEKPINM,ALKYLGEPMK,DALKYLGEPM	LUAD
GLI1	c.815delG	p.W272fs	QEQLVHHINSEHIHGERKEFVCHWG[p.W272fs]AAPGS*	KEFVCHWGA,KEFVCHWGAA	STAD
GLI3	c.2993C>T	p.P998L	VHAPRRCSDGGAHGYGRRHLQPHDA[p.P998L]LGHGVRRASDPVRTGSEGLALPRVPR	ALGHGVRRA,DALGHGVRR,RHLQPHDAL,RRHLQPHDAL	ACC
GLI3	c.3098delC	p.P1033fs	PVRTGSEGLALPRVPRFSSLSSCNP[p.P1033fs]RRWPRPRRSAVSCFRITRGPRAASPETSTRPPVLPASPRTSPWSP*	AVSCFRITR,SSLSSCNPR,SLSSCNPRR,SCNPRRWPR,RWPRPRRSA,RRSAVSCFR,RSAVSCFRI,CFRITRGPR,ITRGPRAAS,STRPPVLPA,NPRRWPRPR,WPRPRRSAV,RPRRSAVSC,GPRAASPET,LPASPRTSP,FSSLSSCNPR,SSLSSCNPRR,SSCNPRRWPR,SAVSCFRITR,RWPRPRRSAV,CFRITRGPRA,ITRGPRAASP,RAASPETSTR,STRPPVLPAS,CNPRRWPRPR,SCFRITRGPR,WPRPRRSAVS,RPRRSAVSCF,SPETSTRPPV,LPASPRTSPW,RRWPRPRRSA,RRSAVSCFRI,FRITRGPRAA	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GLIPR1L2	c.276delA	p.G92fs	IPRGSNLRFMTWDVALSRTARAWGK[p.G92fs]NVCLRIIFIYKMYKWSILNFMVLVKICGSALKMNLLQVLLSEVGMQRRKCTILKMAVALETVLIIFSLFGTTLTKLVVLLLHVQKLDILYMQQFSYATMRQEEH*	HVQKLDILY,SILNFMVLV,ALKMNLLQV,KMNLLQVLL,LLQVLLSEV,KMAVALETV,LIIFSLFGT,TLTKLVVLL,KLVVLLLHV,VLLLHVQKL,YMQQFSYAT,VLVKICGSA,CLRIIFIYK,IIFIYKMYK,KMYKWSILN,ILNFMVLVK,SLFGTTLTK,VVLLLHVQK,ILYMQQFSY,QQFSYATMR,IFIYKMYKW,IYKMYKWSI,MYKWSILNF,KWSILNFMV,TVLIIFSLF,IFSLFGTTL,LYMQQFSYA,TARAWGKNV,MQRRKCTIL,QRRKCTILK,RIIFIYKMY,LLSEVGMQR,CTILKMAVA,ETVLIIFSL,LVKICGSAL,YKMYKWSIL,GMQRRKCTI,VQKLDILYM,MQQFSYATM,RAWGKNVCL,KNVCLRIIF,LRIIFIYKM,YKWSILNFM,WSILNFMVL,KICGSALKM,LKMNLLQVL,LQVLLSEVG,RRKCTILKM,LKMAVALET,MAVALETVL,VALETVLII,ALETVLIIF,LHVQKLDIL,LDILYMQQF,FIYKMYKWSI,YKWSILNFMV,WSILNFMVLV,ILNFMVLVKI,NLLQVLLSEV,KMAVALETVL,VLIIFSLFGT,IIFSLFGTTL,SLFGTTLTKL,TLTKLVVLLL,ILYMQQFSYA,YMQQFSYATM,VLVKICGSAL,ALKMNLLQVL,RIIFIYKMYK,KMYKWSILNF,SILNFMVLVK,LVKICGSALK,MQRRKCTILK,FSLFGTTLTK,RAWGKNVCLR,LVVLLLHVQK,MQQFSYATMR,AWGKNVCLRI,IYKMYKWSIL,MYKWSILNFM,KWSILNFMVL,VALETVLIIF,ETVLIIFSLF,LYMQQFSYAT,RTARAWGKNV,CLRIIFIYKM,DILYMQQFSY,CTILKMAVAL,MAVALETVLI,VGMQRRKCTI,GMQRRKCTIL,LQVLLSEVGM,ARAWGKNVCL,GKNVCLRIIF,LRIIFIYKMY,IIFIYKMYKW,VKICGSALKM,LKMNLLQVLL,QRRKCTILKM,LKMAVALETV,LETVLIIFSL,LHVQKLDILY,HVQKLDILYM,KLDILYMQQF,QQFSYATMRQ	STAD
GLOD4	c.667_668insC	p.Q223fs	KLELQGVKGGVDHAAAFGRIAFSCP[p.Q223fs]PERVARLRRLDEKGEPEDSDSPGEPGHPRESNSTGGHSGRP*	IAFSCPPER,NSTGGHSGR,HPRESNSTG,RESNSTGGH,CPPERVARL,RIAFSCPPER,VARLRRLDEK,FSCPPERVAR,IAFSCPPERV	LUAD
GLRA3	c.1360C>A	p.L454I	DTISRACFPLAFLIFNIFYWVIYKI[p.L454I]IRHEDIHQQQD*	FYWVIYKII,IFYWVIYKII,IYKIIRHEDI,FYWVIYKIIR	CRC
GLRA3	c.396C>A	p.F132L	AYSEYPDDSLDLDPSMLDSIWKPDL[p.F132L]LFANEKGANFHEVTTDNKLLRIFKNG	LLFANEKGA,SIWKPDLLF,IWKPDLLFA,DSIWKPDLL,SIWKPDLLFA,LFANEKGANF	CRC
GLT8D2	c.533C>T	p.A178V	IYLDDDVIVQGDIQELYDTTLALGH[p.A178V]VAAFSDDCDLPSAQDINRLVGLQNTY	TLALGHVAA,DTTLALGHV,TTLALGHVA,LALGHVAAF,DTTLALGHVA,TTLALGHVAA,TLALGHVAAF	GBM
GLTSCR2	c.1166A>G	p.Q389R	RHQELFRLRGIKAQVALRLAELARR[p.Q389R]RRRRQARREAEADKPRRLGRLKYQAP	RRRRRQARR,ELARRRRRR,RLAELARRR,LARRRRRRQA,RRRRRRQARR,RLAELARRRR	ACC
GLYR1	c.1139_1140insG	p.G380fs	CYVDMSTVDADTVTELAQVIVSRGG[p.G380fs]ALSGSPRLRESAAV*	SPRLRESAA,GALSGSPRL,RGGALSGSPR,QVIVSRGGAL,SPRLRESAAV	STAD
GNA13	c.598A>G	p.R200G	KYFLDNLDKLGEPDYIPSQQDILLA[p.R200G]GRPTKGIHEYDFEIKNVPFKMVDVGG	ILLAGRPTK,SQQDILLAG,LLAGRPTKGI	BLCA
GNAO1	c.848C>A	p.P283Q	KWFTDTSIILFLNKKDIFEEKIKKS[p.P283Q]QLTICFPEYTGPSAFTEAVAYIQAQY	KIKKSQLTI,QLTICFPEY,KKSQLTICF,KIKKSQLTIC,SQLTICFPEY,IKKSQLTICF,FEEKIKKSQL	LUAD
GNAS	c.2530C>T	p.R844C	QYFLDKIDVIKQADYVPSDQDLLRC[p.R844C]CVLTSGIFETKFQVDKVNFHMFDVGG	CCVLTSGIF,RCCVLTSGIF	LIHC
GNAS	c.2531G>A	p.R844H	QYFLDKIDVIKQADYVPSDQDLLRC[p.R844H]HVLTSGIFETKFQVDKVNFHMFDVGG	LLRCHVLTS,CHVLTSGIF,RCHVLTSGIF	PAAD
GNB1	c.239T>C	p.I80T	LAKIYAMHWGTDSRLLVSASQDGKL[p.I80T]TIWDSYTTNKVHAIPLRSSWVMTCAY	LTIWDSYTT,SQDGKLTIW,GKLTIWDSY,TIWDSYTTNK,ASQDGKLTIW	CLL
GNG12	c.202delA	p.T68fs	CEEHARSDPLLIGIPTSENPFKDKK[p.T68fs]LASSYSGIEKQLLASSQQRKL*	KLASSYSGI,ASSYSGIEK,LLASSQQRK,KDKKLASSY,KKLASSYSG,KQLLASSQQ,IEKQLLASS,LLASSQQRKL,QLLASSQQRK,LASSYSGIEK,SYSGIEKQLL,FKDKKLASSY,KKLASSYSGI,SSYSGIEKQL,SENPFKDKKL	STAD
GNPNAT1	c.162delT	p.F54fs	AISPTHPGEGLVLRPLCTADLNRGF[p.F54fs]LRYWVS*	RGFLRYWVS,DLNRGFLRY,TADLNRGFLR,CTADLNRGFL,ADLNRGFLRY	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GNPTAB	c.3566G>A	p.R1189Q	VKAVLRDFYESMFPIPSQFELPREY[p.R1189Q]QNRFLHMHELQEWRAYRDKLKFWTHC	EYQNRFLHM,LPREYQNRF,REYQNRFLH,YQNRFLHMH,LPREYQNRFL,REYQNRFLHM,SQFELPREYQ	UCEC
GOLGA4	c.4608G>T	p.Q1536H	KKESNLETELKSQTARIMELEDHIT[p.Q1536H]HKTIEIESLNEVLKNYNQQKDIEHKE	MELEDHITH,HKTIEIESL,LEDHITHKTI	CRC
GOLGA5	c.1474C>A	p.L492I	ELEELRHEKEMQREEIQKLMGQIHQ[p.L492I]IRSELQDMEAQQVNEAESAREQLQDL	KLMGQIHQI,KLMGQIHQIR,HQIRSELQDM,QKLMGQIHQI,GQIHQIRSEL	KIRC
GOT2	c.1063C>T	p.R355W	ILNTPDLRKQWLQEVKVMADRIIGM[p.R355W]WTQLVSNLKKEGSTHNWQHITDQIGM	RIIGMWTQL,IIGMWTQLV,WTQLVSNLK,MWTQLVSNL,MADRIIGMW,RIIGMWTQLV,GMWTQLVSNL,MWTQLVSNLK,WTQLVSNLKK,VMADRIIGMW	PRAD
GP2	c.122C>T	p.S41L	LALVSCILTQASAVQRGYGNPIEAS[p.S41L]LYGLDLDCGAPGTPEAHVCFDPCQNY	NPIEASLYG,YGNPIEASLY,NPIEASLYGL,IEASLYGLDL	CRC
GPATCH4	c.629_630insA	p.K210fs	FLARLKGQDPGAPQLQSESKPPKKK[p.K210fs]EKEKEAERGGRSYSI*	EAERGGRSY,KEAERGGRSY,AERGGRSYSI	PRAD
GPATCH4	c.629delA	p.K210fs	AFLARLKGQDPGAPQLQSESKPPKK[p.K210fs]RKRKGGRKRRKKLQHLKGMMQMRSTQNMLSRTSEKARRRKGDIKKERSQMKERVQLKGMRRRTLQEQVGLGN*	MQMRSTQNM,QMRSTQNML,MLSRTSEKA,NMLSRTSEK,QMKERVQLK,RSTQNMLSR,RVQLKGMRR,KRKRKGGRK,KGGRKRRKK,RRKKLQHLK,LSRTSEKAR,RTSEKARRR,KARRRKGDI,RRRKGDIKK,KGMRRRTLQ,GMRRRTLQE,HLKGMMQMR,LKGMRRRTL,KKLQHLKGM,QHLKGMMQM,GMMQMRSTQ,SQMKERVQL,KERVQLKGM,RTLQEQVGL,MQMRSTQNML,MMQMRSTQNM,SQMKERVQLK,RTSEKARRRK,KKRKRKGGRK,KRKGGRKRRK,KRRKKLQHLK,QMRSTQNMLS,QNMLSRTSEK,LSRTSEKARR,KARRRKGDIK,RSQMKERVQL,RVQLKGMRRR,MLSRTSEKAR,QLKGMRRRTL,LQHLKGMMQM,RKRRKKLQHL,RKKLQHLKGM,KKLQHLKGMM,MKERVQLKGM,KERSQMKERV	STAD
GPC5	c.1040G>T	p.R347L	LVNDAVLQAHLNGQKLLEQVNRICG[p.R347L]LPVRTPTQSPRCSFDQSKEKHGMKTT	EQVNRICGL,QVNRICGLPV,VNRICGLPVR,LEQVNRICGL	LUSC
GPC6	c.640G>A	p.A214T	CVSKYTDQLKPFGDVPRKLKIQVTR[p.A214T]TFIAARTFVQGLTVGREVANRVSKVS	VTRTFIAAR,RTFIAARTF,KIQVTRTFI,QVTRTFIAA,TFIAARTFV,LKIQVTRTF,IQVTRTFIA,RTFIAARTFV,KLKIQVTRTF,KIQVTRTFIA,VTRTFIAART,QVTRTFIAAR,LKIQVTRTFI,IQVTRTFIAA,TRTFIAARTF	CRC
GPLD1	c.2150G>A	p.R717Q	TRMYALTSDAQPLLLSTFSGDRRFS[p.R717Q]QFGGVLHLSDLDDDGLDEIIMAAPLR	SQFGGVLHL,SGDRRFSQF,RRFSQFGGV,RFSQFGGVL,FSGDRRFSQF,RRFSQFGGVL,FSQFGGVLHL,SQFGGVLHLS	CRC
GPM6A	c.149C>T	p.A50V	IPYASLIATILLYAGVALFCGCGHE[p.A50V]VLSGTVNILQTYFEMARTAGDTLDVF	VLSGTVNIL,EVLSGTVNI,ALFCGCGHEV,EVLSGTVNIL,HEVLSGTVNI	KIRC
GPNMB	c.522C>G	p.I174M	GQSHHNVFPDGKPFPHHPGWRRWNF[p.I174M]MYVFHTLGQYFQKLGRCSVRVSVNTA	FMYVFHTLG,RRWNFMYVF,NFMYVFHTL,GWRRWNFMY,RWNFMYVFH,MYVFHTLGQY,GWRRWNFMYV,RWNFMYVFHT,HPGWRRWNFM,WNFMYVFHTL,WRRWNFMYVF,FMYVFHTLGQ	LUAD
GPNMB	c.9_10delTC	p.C3fs	MECL[p.C3fs]LFPGISAPGCKIAT*	LLFPGISAP,MECLLFPGI,LLFPGISAPG,MECLLFPGIS	TGCT
GPR110	c.1327A>G	p.R443G	TALPLNFSRKFIDWKGIPVNKSQLK[p.R443G]GGYSYQIKMCPQNTSIPIRGRVLIGS	KGGYSYQIK,SQLKGGYSY,LKGGYSYQI,GGYSYQIKM,QLKGGYSYQI,VNKSQLKGGY,KSQLKGGYSY,SQLKGGYSYQ,KGGYSYQIKM	CLL
GPR112	c.3848C>A	p.S1283Y	KDQMTISLGKTPRTMEVTEMSPSKN[p.S1283Y]YFISYSRGTPSLEMTDTGFPETTKIS	KNYFISYSR,MSPSKNYFI,PSKNYFISY,EMSPSKNYF,TEMSPSKNY,VTEMSPSKNY,EMSPSKNYFI,SPSKNYFISY,TEMSPSKNYF	UCEC
GPR123	c.1889T>C	p.L630P	PRTPHCVGKKVPQPVGAADLAPDTS[p.L630P]PCRKEGSSASRSCRPGPGHLTRREED	DLAPDTSPCR	CLL
GPR125	c.338G>A	p.R113Q	LSNNKISELKNGSFSGLSLLERLDL[p.R113Q]QNNLISSIDPGAFWGLSSLKRLDLTN	LQNNLISSI,LERLDLQNNL	CRC

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GPR137B	c.718G>T	p.G240C	KISKMSLANIYLESKGSSVCQVTAI[p.G240C]CVTVILLYTSRACYNLFILSFSQNKS	QVTAICVTV,ICVTVILLY,TAICVTVIL,CQVTAICVT,CQVTAICVTV,AICVTVILLY,SVCQVTAICV,QVTAICVTVI,TAICVTVILL	LUAD
GPR156	c.2262C>A	p.F754L	PVPSGCASLSSQHSYFDTESSSSDE[p.F754L]LFCRCHRPYCEICFQSSSDSSDSGTS	SSSDELFCR,LFCRCHRPY,TESSSSDEL,SSSSDELFCR,ELFCRCHRPY,TESSSSDELF	CRC
GPR158	c.1696G>A	p.D566N	LIGWTSSVCQNLEKQISLIGQGKTS[p.D566N]NHLIFNMCLIDRWDYMTAVAEFLFLL	KTSNHLIFN,TSNHLIFNM,GQGKTSNHL,GKTSNHLIF,KTSNHLIFNM,GQGKTSNHLI,QGKTSNHLIF	CRC
GPR158	c.2284C>A	p.P762T	NPHLQKKRCSKKGLGRSIMRRITEI[p.P762T]TETVSRQCSKEDKEGADHGTAKGTAL	RITEITETV,RRITEITETV	LUAD
GPR161	c.1550delG	p.G517fs	AEAKINLFGEEALPGVLVTARTVPG[p.G517fs]AASGAAEAAELL*	TARTVPGAA,VTARTVPGA,TVPGAASGA,VPGAASGAA,LVTARTVPGA,RTVPGAASGA,VTARTVPGAA,TVPGAASGAA	STAD
GPR21	c.647G>A	p.R216H	FTLFIVMMLYAPAALIVCFTYFNIF[p.R216H]HICQQHTKDISERQARFSSQSGETGE	FTYFNIFHI,TYFNIFHIC,CFTYFNIFHI,IFHICQQHTK,FTYFNIFHIC	CRC
GPR6	c.106_165delGCGGCGGCGGCGGCCACAGCAGCAGGGGGGCCGGACACGGGCGAATGGGGACCCCCTGCT	p.AAAAATAAGGPDTGEWGPPA36del	AAMNASAASLNDSQVVVVAAEGAAA[p.AAAAATAAGGPDTGEWGPPA36del]LGAGGGANGSLELSSQLSAGPPGLLLPAVNPWDVLLCVSGTVIAGENALVVALIASTPALRTPMFVLVGSLATADLLAGCGLILH	VAAEGAAAL,AEGAAALGA,VVAAEGAAAL,AEGAAALGAG	PAAD
GPR98	c.12424C>T	p.R4142W	RFTIQLISIDEVEISPVKGSASIII[p.R4142W]WGDKRASGEVGIAPSSRHILIGEPSA	ASIIIWGDK,SIIIWGDKR,KGSASIIIW,SASIIIWGDK,VKGSASIIIW	CRC,UCEC
GPR98	c.12919G>T	p.G4307W	QRVNITIIRSSGDFGHVRLWYKTMS[p.G4307W]WTAEAGLDFVPAAGELLFEAGEMRKS	WTAEAGLDF,KTMSWTAEA,RLWYKTMSW,WYKTMSWTA,MSWTAEAGL,TMSWTAEAGL,WTAEAGLDFV,RLWYKTMSWT,SWTAEAGLDF,VRLWYKTMSW,LWYKTMSWTA,YKTMSWTAEA	LUAD
GPR98	c.18455A>T	p.Y6152F	AYRHFWMLVLFVIFNSLQGLYVFMV[p.Y6152F]FFILHNQMCCPMKASYTVEMNGHPGP	YVFMVFFIL,QGLYVFMVF,LYVFMVFFI,VFFILHNQM,GLYVFMVFF,GLYVFMVFFI,LQGLYVFMVF,QGLYVFMVFF,LYVFMVFFIL,MVFFILHNQM	CLL
GPRASP1	c.2117C>T	p.S706L	KEPCMYPAGGGSWKSRPEEEEDIVN[p.S706L]LWFWSRKYTKPEAIIGSWLWATEESN	IVNLWFWSR,VNLWFWSRK,NLWFWSRKY,EEEDIVNLW,EEDIVNLWF,EEEEDIVNL,IVNLWFWSRK,LWFWSRKYTK,VNLWFWSRKY,DIVNLWFWSR,EEEDIVNLWF,EEDIVNLWFW	HNSC
GPRC5A	c.88G>A	p.V30I	VPDGCRNGLKSKYYRLCDKAEAWGI[p.V30I]ILETVATAGVVTSVAFMLTLPILVCK	IILETVATA,AWGIILETV,EAWGIILET,KAEAWGIIL,AEAWGIILE,ILETVATAGV,GIILETVATA,EAWGIILETV,AEAWGIILET	CRC
GPRIN1	c.693_716delGAAGGAGGATCCTGGGTCTTTGAG	p.231_239RKEDPGSLR>R	KEDLGSLGKVDPLCSSKTYTVSPRK[p.231_239RKEDPGSLR>R]VDPVSSDKVDPVFPRKEEPRYSGKEHPVSSEKVAPTSAEKVDLVLSGKR	TVSPRKVDPV,KTYTVSPRKV	KIRC
GPRIN2	c.1337G>A	p.R446H	APASEDSLSVEGRRGPLRAVMQSLR[p.R446H]HPSCCGCSGAAPE*	MQSLRHPSC	ACC
GPRIN2	c.298A>C	p.T100P	ARASGPKARPSAGGHWWSSTVGNVS[p.T100P]PMGGSDLCRLRAPSAAAMQRSHSDLV	STVGNVSPM,SSTVGNVSPM	CESC
GPRIN2	c.721G>A	p.V241M	KAAEQLATTTCHALPPAALLCGMRE[p.V241M]MRAGGCCHALPATGILAFPKLVASVS	ALLCGMREM,LLCGMREMR,REMRAGGCC,AALLCGMREM,REMRAGGCCH,MRAGGCCHAL	ACC
GPRIN3	c.1898delG	p.R633fs	PSDPMGDSSPGSGKKTPSRSVKASP[p.R633fs]PGPAASASSSRSKS*	ASASSSRSK,RSVKASPPG,KASPPGPAA,SPPGPAASA,AASASSSRSK,SVKASPPGPA,VKASPPGPAA	HNSC
GPT2	c.29G>C	p.R10P	MQRAAALVR[p.R10P]PGCGPRTPSSWGRSQSSAAAEASAVL	LVRPGCGPR,RPGCGPRTPS,MQRAAALVRP	TGCT
GRAMD2	c.369C>G	p.I123M	DFLLQGRLYISPNWLCFHASLFGKD[p.I123M]MKVVIPVVSVQMIKKHKMARLLPNGL	SLFGKDMKV,ASLFGKDMK,HASLFGKDM,KDMKVVIPV,SLFGKDMKVV,HASLFGKDMK,FHASLFGKDM,KDMKVVIPVV,MKVVIPVVSV	CESC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GRAP2	c.207G>T	p.E69D	GYVPKNFIDIQFPKWFHEGLSRHQA[p.E69D]DNLLMGKEVGFFIIRASQSSPGDFSI	QADNLLMGK,SRHQADNLL,RHQADNLLM,HQADNLLMG,GLSRHQADNL,HQADNLLMGK,SRHQADNLLM	CRC
GRB14	c.898G>A	p.A300T	RHLQFFSEFGNSDIYVSLAGKKKHG[p.A300T]TPTNYGFCFKPNKAGGPRDLKMLCAE	KKHGTPTNY,HGTPTNYGF,TPTNYGFCF,GTPTNYGFCF,KKKHGTPTNY,KHGTPTNYGF	BRCA
GRB7	c.716G>T	p.R239L	ISHEDLIQNFLNAGSFPEIQGFLQL[p.R239L]LGSGRKLWKRFFCFLRRSGLYYSTKG	LGSGRKLWK,EIQGFLQLL,LLGSGRKLW,LLGSGRKLWK,LQLLGSGRKL,QLLGSGRKLW,PEIQGFLQLL	LUAD
GREB1	c.1031C>A	p.S344Y	ESPSAPDGGCPQGGGNRAKYESAGM[p.S344Y]YCVPQVGLVGPASVTFPVVASGEPVS	AGMYCVPQV,MYCVPQVGL,AKYESAGMY,YESAGMYCV,GMYCVPQVG,GMYCVPQVGL,KYESAGMYCV,MYCVPQVGLV,RAKYESAGMY,YESAGMYCVP	KIRC
GRHL1	c.1822G>T	p.G608W	LVNMDDNIVKHYSNEDTFQLQIEEA[p.G608W]WGSYKLTLTE!*	AWGSYKLTL,QIEEAWGSY,FQLQIEEAW,EEAWGSYKL,QIEEAWGSYK,TFQLQIEEAW,LQIEEAWGSY,IEEAWGSYKL,EEAWGSYKLT	LUAD
GRIA1	c.652C>T	p.R218C	EGYRMLFQDLEKKKERLVVVDCESE[p.R218C]CLNAILGQIIKLEKNGIGYHYILANL	CLNAILGQI,CESECLNAI,CLNAILGQII,CESECLNAIL	CRC
GRIA2	c.2534G>A	p.R845Q	LVGGLGLAMLVALIEFCYKSRAEAK[p.R845Q]QMKVAKNAQNINPSSSQNSQNFATYK	KSRAEAKQM,AEAKQMKVA,KQMKVAKNA,KSRAEAKQMK,YKSRAEAKQM,KQMKVAKNAQ	CRC
GRID1	c.1864G>A	p.E622K	PRPSASATLHSAIWIVYGAFVQQGG[p.E622K]KSSVNSMAMRIVMGSWWLFTLIVCSS	GAFVQQGGK,KSSVNSMAM,VQQGGKSSV,GGKSSVNSM,FVQQGGKSSV,KSSVNSMAMR,GKSSVNSMAM	DLBCL
GRID1	c.2048G>T	p.R683L	VSRMDNPIRTFQDLSKQVEMSYGTV[p.R683L]LDSAVYEYFRAKGTNPLEQDSTFAEL	VLDSAVYEY,VEMSYGTVL,LDSAVYEYF,VLDSAVYEYF,TVLDSAVYEY,MSYGTVLDSA	LUAD
GRID2	c.1947delG	p.T649fs	YTTLATRMMMGAWWLFALIVISSYT[p.T649fs]QTSLLSSLLHALKVPSSLSRTFPSKQKSLMAQS*	SLLSSLLHA,LLSSLLHAL,TQTSLLSSL,LSSLLHALK,SLSRTFPSK,SSYTQTSLL,SSLSRTFPS,KQKSLMAQS,QTSLLSSLL,HALKVPSSL,VPSSLSRTF,FPSKQKSLM,ISSYTQTSL,SLLSSLLHAL,VISSYTQTSL,YTQTSLLSSL,TQTSLLSSLL,LLSSLLHALK,ALKVPSSLSR,SSLSRTFPSK,KVPSSLSRTF,LSRTFPSKQK,RTFPSKQKSL,FPSKQKSLMA,ISSYTQTSLL,LHALKVPSSL	HNSC
GRIK1	c.1103G>A	p.R368Q	VSSLQCHRHKPWRLGPRFMNLIKEA[p.R368Q]QWDGLTGHITFNKTNGLRKDFDLDII	AQWDGLTGH,KEAQWDGLT,AQWDGLTGHI,LIKEAQWDGL,FMNLIKEAQW,KEAQWDGLTG	LUAD
GRIN2B	c.1556G>A	p.R519Q	WNGMIGEVVMKRAYMAVGSLTINEE[p.R519Q]QSEVVDFSVPFIETGISVMVSRSNGT	TINEEQSEV,EEQSEVVDF,LTINEEQSEV,TINEEQSEVV,EQSEVVDFSV,NEEQSEVVDF	OV
GRK4	c.64_65insA	p.K22fs	MELENIVANSLLLKARQGGYGKK[p.K22fs]KWS*	RQGGYGKKKW	STAD
GRM3	c.2046C>A	p.F682L	SALLTKTNCIARIFDGVKNGAQRPK[p.F682L]LISPSSQVFICLGLILVQIVMVSVWL	KLISPSSQV,LISPSSQVF,LISPSSQVFI,KLISPSSQVF,AQRPKLISPS,VKNGAQRPKL	HNSC
GRM3	c.547C>T	p.R183C	ANLLRLFQIPQISYASTSAKLSDKS[p.R183C]CYDYFARTVPPDFYQAKAMAEILRFF	LSDKSCYDY,KSCYDYFAR,AKLSDKSCY,LSDKSCYDYF,KLSDKSCYDY,SAKLSDKSCY	GBM
GRM5	c.2685_2686insC	p.P895fs	SSGETLRYKDRRLAQHKSEIECFTP[p.P895fs]QREYGEWWESNNEQFQWKIRHVGPE*	WWESNNEQF,EIECFTPQR,SEIECFTPQ,REYGEWWES,EQFQWKIRH,FQWKIRHVG,TPQREYGEW,ESNNEQFQW,EWWESNNEQF,EQFQWKIRHV,IECFTPQREY,WESNNEQFQW,FQWKIRHVGP,REYGEWWESN,GEWWESNNEQ,TPQREYGEWW	LUAD
GRM6	c.1089G>T	p.E363D	GFDQYFMTRSLENNRRNIWFAEFWE[p.E363D]DNFNCKLTSSGTQSDDSTRKCTGEER	WEDNFNCKL,EFWEDNFNCK,AEFWEDNFNC	UCEC
GRM6	c.2152_2153insG	p.A718fs	SPTSQLVITFSLTSLQVVGMIAWLG[p.A718fs]GPAPTQRD*	MIAWLGGPA,GMIAWLGGPA	KIRC
GRM7	c.2036G>A	p.R679Q	VCSFRRVFLGLGMCISYAALLTKTN[p.R679Q]QIYRIFEQGKKSVTAPRLISPTSQLA	ALLTKTNQI,LTKTNQIYR,KTNQIYRIF,LLTKTNQIY,QIYRIFEQGK,LTKTNQIYRI,KTNQIYRIFE,ALLTKTNQIY,LLTKTNQIYR,TKTNQIYRIF	CRC

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GRM8	c.2554C>T	p.R852C	SVSLGMLYMPKVYIIIFHPEQNVQK[p.R852C]CKRSFKAVVTAATMQSKLIQKGNDRP	VQKCKRSFK,KCKRSFKAV,CKRSFKAVV,NVQKCKRSFK,VQKCKRSFKA,KCKRSFKAVV	LIHC
GTF2E1	c.575G>T	p.R192L	AMPKKDARTLLARFNEQIEPIYALL[p.R192L]LETEDVNLAYEILEPEPTEIPALKQS	ALLLETEDV,IEPIYALLL,LETEDVNLA,LLLETEDVNL,LETEDVNLAY,EPIYALLLET	LUAD
GTF3A	c.918G>T	p.K306N	HAGCGKTFAMKQSLTRHAVVHDPDK[p.K306N]NKMKLKVKKSREKRSLASHLSGYIPP	VVHDPDKNK,KNKMKLKVK,AVVHDPDKNK,KNKMKLKVKK	CRC
GTF3C1	c.2299delA	p.S767fs	KEGPSGSGDSQLSASSRSESGRMKK[p.S767fs]VIIKWA*	RMKKVIIKW,SGRMKKVII,RMKKVIIKWA,SGRMKKVIIK	STAD
GTF3C4	c.1685delA	p.E562fs	LIDLVRWKILKDKHIPQFLQEALEK[p.E562fs]RLKAVESPIFGVLSFSS*	AVESPIFGV,ALEKRLKAV,RLKAVESPI,SPIFGVLSF,LKAVESPIF,VESPIFGVL,FLQEALEKRL,KAVESPIFGV,RLKAVESPIF,EALEKRLKAV,KRLKAVESPI,VESPIFGVLS,QEALEKRLKA	STAD
GUCY2C	c.1645G>T	p.G549C	NFTEKQKIELNKLLQIDYYNLTKFY[p.G549C]CTVKLDTMIFGVIEYCERGSLREVLN	NLTKFYCTV,LTKFYCTVK,TKFYCTVKL,FYCTVKLDTM,LTKFYCTVKL,YNLTKFYCTV,CTVKLDTMIF	BRCA
GUSB	c.1498T>C	p.C500R	PSRPVTFVSNSNYAADKGAPYVDVI[p.C500R]RLNSYYSWYHDYGHLELIQLQLATQF	RLNSYYSWY,IRLNSYYSW,VIRLNSYYS,DVIRLNSYY,APYVDVIRL,VDVIRLNSY,YVDVIRLNSY,RLNSYYSWYH,DVIRLNSYYS,VDVIRLNSYY,VIRLNSYYSW,IRLNSYYSWY	KIRC
GUSB	c.1501T>G	p.L501V	SRPVTFVSNSNYAADKGAPYVDVIC[p.L501V]VNSYYSWYHDYGHLELIQLQLATQFE	CVNSYYSWY,DVICVNSYY,VDVICVNSY,ICVNSYYSW,APYVDVICV,YVDVICVNSY,CVNSYYSWYH,DVICVNSYYS,VDVICVNSYY,ICVNSYYSWY	KIRC
GXYLT1	c.667_668insT	p.L223fs	SQRLFLPLILKEVDSLLYVDTDILF[p.L223fs]FTTS*	YVDTDILFF,YVDTDILFFT,LYVDTDILFF	STAD
H1FOO	c.642_643insA	p.A214fs	PGAATEKARKQGGAAKDTRAQSGEA[p.A214fs]KEGAPQARQGHAGTFQCWWAQQEGKGQRQQEQPRRC*	APQARQGHA,ARQGHAGTF,GHAGTFQCW,HAGTFQCWW,EAKEGAPQAR,QARQGHAGTF,GEAKEGAPQA,RQGHAGTFQC	BLCA
H2AFV	c.374A>G	p.Q125R	LIKATIAGGGVIPHIHKSLIGKKGQ[p.Q125R]RKTA*	SLIGKKGQR,KSLIGKKGQR	TGCT
H2AFY2	c.432delG	p.K144fs	GKSETILSPPPEKRGRKATSGKKGG[p.K144fs]RNPRLPNHGRPKSPNQRTAIKKELQIPPLKMGQGMDSPFCLLRALFWDRSCP*	GMDSPFCLL,RLPNHGRPK,LLRALFWDR,SPFCLLRAL,MGQGMDSPF,KKELQIPPL,KSPNQRTAIK,GMDSPFCLLR,KMGQGMDSPF,SGKKGGRNPR,GGRNPRLPNH,HGRPKSPNQR,RTAIKKELQI,CLLRALFWDR,RPKSPNQRTA,IPPLKMGQGM,SPFCLLRALF,NQRTAIKKEL,IKKELQIPPL,KELQIPPLKM,GQGMDSPFCL	STAD
H3F3C	c.392G>T	p.R131L	DTNLCAIHAKRVTIMPKDIQLARRI[p.R131L]LGERA*	LARRILGER,QLARRILGER,KDIQLARRIL	LUAD
HAO1	c.514C>T	p.R172C	AEKMGYKAIFVTVDTPYLGNRLDDV[p.R172C]CNRFKLPPQLRMKNFETSTLSFSPEE	RLDDVCNRF,RLDDVCNRFK	CRC
HAO2	c.34C>A	p.H12N	MSLVCLTDFQA[p.H12N]NAREQLSKSTRDFIEGGADDSITRDD	CLTDFQANA,FQANAREQL,QANAREQLSK,CLTDFQANAR	LUAD
HARS2	c.503G>A	p.R168H	NKVKKMKRYHVGKVWRRESPTIVQG[p.R168H]HYREFCQCDFDIAGQFDPMIPDAECL	IVQGHYREF,PTIVQGHYR,SPTIVQGHY,HYREFCQCDF,TIVQGHYREF,RESPTIVQGH	CRC
HAUS6	c.1588delA	p.S530fs	ENSPLSDVAKNTESSAFGGSLPAKK[p.S530fs]VIHFKKSKIIW*	KVIHFKKSK,PAKKVIHFK,AKKVIHFKK,LPAKKVIHF,IHFKKSKII,SLPAKKVIHF,PAKKVIHFKK,KVIHFKKSKI,IHFKKSKIIW	STAD
HBB	c.126C>A	p.F42L	GKVNVDEVGGEALGRLLVVYPWTQR[p.F42L]LFESFGDLSTPDAVMGNPKVKAHGKK	VVYPWTQRL,RLFESFGDL,VYPWTQRLF,WTQRLFESF,RLFESFGDLS,VVYPWTQRLF,PWTQRLFESF,LVVYPWTQRL,YPWTQRLFES	CRC
HBB	c.257T>G	p.F86C	VKAHGKKVLGAFSDGLAHLDNLKGT[p.F86C]CATLSELHCDKLHVDPENFRLLGNVL	NLKGTCATL,KGTCATLSEL	KIRC
HCN1	c.1496G>T	p.G499V	PLFANADPNFVTAMLSKLRFEVFQP[p.G499V]VDYIIREGAVGKKMYFIQHGVAGVIT	VFQPVDYII,EVFQPVDYI,LRFEVFQPV,FEVFQPVDY,KLRFEVFQPV,RFEVFQPVDY,VFQPVDYIIR,EVFQPVDYII,FEVFQPVDYI	LUSC
HCN1	c.1976G>T	p.R659L	QAIAPINYPQMTTLNSTSSTTTPTS[p.R659L]LMRTQSPPVYTATSLSHSNLHSPSPS	LMRTQSPPV,TTTPTSLMR,STTTPTSLM,SSTTTPTSL,SLMRTQSPPV,STTTPTSLMR,LMRTQSPPVY,SSTTTPTSLM	LUSC

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HCN1	c.2140G>T	p.A714S	QPSAILSPCSYTTAVCSPPVQSPLA[p.A714S]SRTFHYASPTASQLSLMQQQPQQQVQ	ASRTFHYAS,PLASRTFHY,LASRTFHYA,VQSPLASRT,PLASRTFHYA,ASRTFHYASP,VQSPLASRTF,SPLASRTFHY	LUSC
HCN1	c.692C>A	p.P231Q	IILDPKVIKMNYLKSWFVVDFISSI[p.P231Q]QVDYIFLIVEKGMDSEVYKTARALRI	FISSIQVDY,QVDYIFLIV,IQVDYIFLI,SSIQVDYIF,VVDFISSIQV,FISSIQVDYI,SIQVDYIFLI,IQVDYIFLIV,SSIQVDYIFL,ISSIQVDYIF	LUAD
HCN1	c.976C>A	p.P326T	LIGMMLLLCHWDGCLQFLVPLLQDF[p.P326T]TPDCWVSLNEMVNDSWGKQYSYALFK	FTPDCWVSL,FLVPLLQDFT	LUSC
HCN4	c.1574G>A	p.R525H	IVGATCYAMFIGHATALIQSLDSSR[p.R525H]HQYQEKYKQVEQYMSFHKLPPDTRQR	SLDSSRHQY,SSRHQYQEK,RHQYQEKYK,IQSLDSSRH,SRHQYQEKY,QSLDSSRHQY,SSRHQYQEKY,HQYQEKYKQV	CRC
HCRTR2	c.26_27insC	p.S9fs	MSGTKLEDSPP[p.S9fs]LSQLVICFGAE*	DSPPLSQLV,SPPLSQLVI,TKLEDSPPL,LEDSPPLSQL	STAD
HCRTR2	c.26delC	p.S9fs	MSGTKLEDSP[p.S9fs]LVATGHLLRS*	LVATGHLLR,SPLVATGHL,LEDSPLVAT,GTKLEDSPLV,SPLVATGHLL	STAD
HCRTR2	c.298G>T	p.D100Y	VCVAVWKNHHMRTVTNYFIVNLSLA[p.D100Y]YVLVTITCLPATLVVDITETWFFGQS	FIVNLSLAY,IVNLSLAYV,NLSLAYVLV,SLAYVLVTI,YVLVTITCL,VNLSLAYVL,FIVNLSLAYV,SLAYVLVTIT,YFIVNLSLAY,AYVLVTITCL,IVNLSLAYVL,LSLAYVLVTI	HNSC
HDAC4	c.2703delC	p.P901fs	PDEVGTGPGVGFNVNMAFTGGLDPP[p.P901fs]WETLSTWRPSERWSCRSPASLPRMWCWCHQASMPWRATPPLLGATTSPPDASGT*	GLDPPWETL,RMWCWCHQA,HQASMPWRA,ASLPRMWCW,RWSCRSPAS,RSPASLPRM,PWRATPPLL,LSTWRPSER,RPSERWSCR,MPWRATPPL,WSCRSPASL,WCWCHQASM,WCHQASMPW,FTGGLDPPW,PPWETLSTW,SPASLPRMW,RMWCWCHQAS,SMPWRATPPL,RWSCRSPASL,MWCWCHQASM,CWCHQASMPW,SCRSPASLPR,TLSTWRPSER,MPWRATPPLL,SERWSCRSPA,CRSPASLPRM,HQASMPWRAT,WETLSTWRPS,DPPWETLSTW	STAD
HDAC5	c.3130G>A	p.A1044T	CVSALLSVELQPLDEAVLQQKPNIN[p.A1044T]TVATLEKVIEIQSKHWSCVQKFAAGL	QQKPNINTV,NTVATLEKV,KPNINTVAT,LQQKPNINTV,NINTVATLEK,NTVATLEKVI,KPNINTVATL,QQKPNINTVA	CRC
HDLBP	c.1507C>T	p.R503C	SNLIRIEGDPQGVQQAKRELLELAS[p.R503C]CMENERTKDLIIEQRFHRTIIGQKGE	LASCMENER,RELLELASC,LELASCMEN,ELASCMENER,RELLELASCM	TGCT
HDLBP	c.2240delG	p.G747fs	EKQTKSFTVDIRAKPEYHKFLIGKG[p.G747fs]AAKFARCATALEHVSSSLRLRTRTRT*	ALEHVSSSL,HVSSSLRLR,SSSLRLRTR,SLRLRTRTR,LIGKGAAKF,AKFARCATA,KFARCATAL,FLIGKGAAKF,KFLIGKGAAK,KGAAKFARCA,AAKFARCATA,SSLRLRTRTR,VSSSLRLRTR,TALEHVSSSL,SLRLRTRTRT,FARCATALEH,HKFLIGKGAA,AKFARCATAL,LEHVSSSLRL	STAD
HEATR7B2	c.3325G>A	p.E1109K	TVVVNLLQKPLPFDRDTKTLWKALA[p.E1109K]KKPASSGKLLQALIDKLETELEDDIA	KTLWKALAK,TLWKALAKK,WKALAKKPA,KTLWKALAKK,LAKKPASSGK,AKKPASSGKL	BLCA
HECA	c.998_999insG	p.R333fs	MAGGHVFRNAHFDYSPAGLAVHRGG[p.R333fs]TLRHPRAVPSAAGPLRTPHSHPQA*	AVHRGGTLR,RGGTLRHPR,GTLRHPRAV,RTPHSHPQA,HPRAVPSAA,LAVHRGGTL,GLAVHRGGTL,RGGTLRHPRA,LAVHRGGTLR,HPRAVPSAAG,RAVPSAAGPL,LRHPRAVPSA,SAAGPLRTPH	STAD
HECTD2	c.55C>G	p.P19A	MSEAVRVPSPATPLVVAA[p.P19A]AAPEERKGKESEREKLPPIVSAGAGA	ATPLVVAAA,AAAAPEERK,TPLVVAAAA,VAAAAPEERK,ATPLVVAAAA	ACC
HECW1	c.547G>T	p.A183S	ICFKYYHGVSGALRATTPSVTVKNS[p.A183S]SAPIFKSIGADETVQGQGSRRLISFS	KNSSAPIFK,TVKNSSAPI,SSAPIFKSI,VKNSSAPIF,VTVKNSSAPI,NSSAPIFKSI,TVKNSSAPIF	LUAD
HERC1	c.6989G>A	p.R2330H	PVLAVIGGVDAGLRVGGRCVHKQTG[p.R2330H]HHATLLGVVKEGSTSAKVQWDEAEIT	HKQTGHHAT,KQTGHHATL,HKQTGHHATL,KQTGHHATLL	GBM
HERC2	c.986C>T	p.S329F	SQMLSAILLLLQLWDSGAQETDNER[p.S329F]FAQGTSAPLLPLLQRFQSIICRKDAP	FAQGTSAPL,AQETDNERF,ERFAQGTSA,RFAQGTSAPL,GAQETDNERF,NERFAQGTSA,FAQGTSAPLL	CESC
HES3	c.286C>A	p.P96T	SCLPGVSQLLRRGDEVGSGLRCPLV[p.P96T]TESAAGSTMDSAGLGQEAPALFRPCT	TESAAGSTM,CPLVTESAA,VTESAAGSTM	ACC

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HEXDC	c.1444A>C	p.T482P	CRSWRLPCSWLSTRMPWRSGWRKTC[p.T482P]PPACSGCKLCCRTSARCLPPRCHPPA	GWRKTCPPA	KIRC,LUSC
HGF	c.1400C>A	p.S467Y	NPDDDAHGPWCYTGNPLIPWDYCPI[p.S467Y]YRCEGDTTPTIVNLDHPVISCAKTKQ	IPWDYCPIY,LIPWDYCPIY,IPWDYCPIYR	CRC
HGF	c.2057T>C	p.M686T	AEKIGSGPCEGDYGGPLVCEQHKMR[p.M686T]TVLGVIVPGRGCAIPNRPGIFVRVAY	KMRTVLGVI,EQHKMRTVL,HKMRTVLGV,CEQHKMRTV,KMRTVLGVIV,TVLGVIVPGR,CEQHKMRTVL,HKMRTVLGVI	LUAD
HGF	c.686G>C	p.G229A	PQCSEVECMTCNGESYRGLMDHTES[p.G229A]AKICQRWDHQTPHRHKFLPERYPDKG	GLMDHTESA,LMDHTESAK,LMDHTESAKI,GLMDHTESAK,HTESAKICQR,TESAKICQRW	CESC
HHIPL1	c.2075T>C	p.V692A	AFRDGEVRLVRPAGLSSGSGRVEVF[p.V692A]AGGRWGTVCDDSWNISGAAVVCRQLG	VEVFAGGRW,EVFAGGRWGT	ACC
HIF3A	c.214G>A	p.A72T	VSAHLDKASIMRLTISYLRMHRLCA[p.A72T]TGEWNQVGAGGEPLDACYLKALEGFV	RMHRLCATG,LRMHRLCAT,HRLCATGEW,YLRMHRLCAT,MHRLCATGEW	CESC
HIP1	c.2819G>T	p.R940L	AQLVAASKVKADKDSPNLAQLQQAS[p.R940L]LGVNQATAGVVASTISGKSQIEETDN	QLQQASLGV,LAQLQQASL,LQQASLGVN,AQLQQASLGV,NLAQLQQASL,QQASLGVNQA	LUAD
HIPK4	c.839G>A	p.R280H	PDAANPWQLKSSADYLAETKVRPLE[p.R280H]HRKYMLKSLDQIETVNGGSVASRLTF	KVRPLEHRK,LEHRKYMLK,RPLEHRKYM,HRKYMLKSL,KVRPLEHRKY,ETKVRPLEHR,RPLEHRKYML,EHRKYMLKSL	CRC
HIST1H1B	c.564G>C	p.K188N	AAAGVKKVAKSPKKAKAAAKPKKAT[p.K188N]NSPAKPKAVKPKAAKPKAAKPKAAKP	ATNSPAKPK,KKATNSPAK,KATNSPAKPK,ATNSPAKPKA,KPKKATNSPA	CESC
HIST1H1C	c.194C>T	p.A65V	VSELITKAVAASKERSGVSLAALKK[p.A65V]VLAAAGYDVEKNNSRIKLGLKSLVSK	ALKKVLAAA,VLAAAGYDV,AALKKVLAA,KKVLAAAGY,KVLAAAGYDV,SLAALKKVLA,LAALKKVLAA,LKKVLAAAGY	DLBCL
HIST1H1D	c.243C>G	p.I81M	SGVSLAALKKALAAAGYDVEKNNSR[p.I81M]MKLGLKSLVSKGTLVQTKGTGASGSF	RMKLGLKSL,NSRMKLGLK,MKLGLKSLV,RMKLGLKSLV,YDVEKNNSRM,SRMKLGLKSL	BLCA
HIST1H1E	c.398G>C	p.G133A	NKKAASGEAKPKAKKAGAAKAKKPA[p.G133A]AAAKKPKKATGAATPKKSAKKTPKKA	AAAAKKPKK,AAKAKKPAA,AKKPAAAAK,KAKKPAAAAK,AAKAKKPAAA,AKAKKPAAAA	DLBCL
HIST1H1E	c.74G>C	p.R25P	MSETAPAAPAAPAPAEKTPVKKKA[p.R25P]PKSAGAAKRKASGPPVSELITKAVAA	KTPVKKKAPK,KAPKSAGAAK,KKAPKSAGAA	LUAD
HIST1H2AL	c.89G>C	p.R30P	GKQGGKARAKAKTRSSRAGLQFPVG[p.R30P]PVHRLLRKGNYAERVGAGAPVYLAAV	GLQFPVGPV,FPVGPVHRL,LQFPVGPVH,QFPVGPVHRL,FPVGPVHRLL	CESC
HIST1H2BF	c.229G>A	p.E77K	DTGISSKAMGIMNSFVNDIFERIAG[p.E77K]KASRLAHYNKRSTITSREIQTAVRLL	RIAGKASRL,GKASRLAHY,DIFERIAGK,RIAGKASRLA,KASRLAHYNK,AGKASRLAHY,DIFERIAGKA	HNSC
HIST1H2BJ	c.38A>G	p.K13R	MPEPAKSAPAPK[p.K13R]RGSKKAVTKAQKKDGKKRKRSRKESY	RGSKKAVTK,APAPKRGSK,SAPAPKRGSK,APKRGSKKAV	TGCT
HIST1H3B	c.142G>T	p.A48S	TKAARKSAPATGGVKKPHRYRPGTV[p.A48S]SLREIRRYQKSTELLIRKLPFQRLVR	RYRPGTVSL,SLREIRRYQ,VSLREIRRY,TVSLREIRR,HRYRPGTVS,SLREIRRYQK,GTVSLREIRR,RYRPGTVSLR,TVSLREIRRY,RPGTVSLREI,HRYRPGTVSL	DLBCL
HIST1H3B	c.220G>A	p.E74K	LREIRRYQKSTELLIRKLPFQRLVR[p.E74K]KIAQDFKTDLRFQSSAVMALQEACEA	LVRKIAQDF,FQRLVRKIA,KLPFQRLVRK,LVRKIAQDFK,LPFQRLVRKI,RLVRKIAQDF	LUSC
HIST1H3C	c.110A>T	p.K37M	TGGKAPRKQLATKAARKSAPATGGV[p.K37M]MKPHRYRPGTVALREIRRYQKSTELL	GVMKPHRYR,VMKPHRYRP,KSAPATGGVM,VMKPHRYRPG	HNSC
HIST1H4C	c.203G>C	p.R68P	GVKRISGLIYEETRGVLKVFLENVI[p.R68P]PDAVTYTEHAKRKTVTAMDVVYALKR	FLENVIPDA,VIPDAVTYT,NVIPDAVTY,LENVIPDAV,FLENVIPDAV,NVIPDAVTYT,IPDAVTYTEH,LENVIPDAVT	HNSC
HIST2H2AC	c.89G>C	p.R30P	GKQGGKARAKAKSRSSRAGLQFPVG[p.R30P]PVHRLLRKGNYAERVGAGAPVYMAAV	GLQFPVGPV,FPVGPVHRL,LQFPVGPVH,QFPVGPVHRL,FPVGPVHRLL	CESC

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HIST2H2BE	c.161G>A	p.G54D	KRKRSRKESYSIYVYKVLKQVHPDT[p.G54D]DISSKAMGIMNSFVNDIFERIAGEAS	KQVHPDTDI	LUSC
HIVEP3	c.1601delC	p.P534fs	LSSHSEKTKPEQSLLSLQHPPSTAP[p.P534fs]LCLS*	LQHPPSTAPL,HPPSTAPLCL	STAD
HIVEP3	c.1660delC	p.H554fs	PSTAPPVPLLRSHSMPSAACTISTP[p.H554fs]TTPSEVATPSMTISPTPKP*	SMTISPTPK,STPTTPSEV,EVATPSMTI,TPSMTISPT,TPSEVATPS,SEVATPSMT,PSMTISPTPK,TPSEVATPSM,SEVATPSMTI	STAD
HLA-A	c.233A>G	p.Q78R	DDTQFVRFDSDAASQRMEPRAPWIE[p.Q78R]REGPEYWDQETRNVKAQSQTDRVDLG	WIEREGPEY,IEREGPEYW,PWIEREGPEY	BLCA,PRAD
HLA-C	c.312C>A	p.N104K	EGPEYWDRNTQIYKAQAQTDRESLR[p.N104K]KLRGYYNQSEAGSHTLQSMYGCDVGP	QTDRESLRK,SLRKLRGYY,KLRGYYNQS,SLRKLRGYYN,KLRGYYNQSE,RESLRKLRGY,ESLRKLRGYY	CESC
HLA-DMA	c.250G>A	p.E84K	LSEAYDEDQLFFFDFSQNTRVPRLP[p.E84K]KFADWAQEQGDAPAILFDKEFCEWMI	RLPKFADWA,NTRVPRLPK,RVPRLPKFA,TRVPRLPKF	CRC
HLA-DMA	c.706_707insG	p.A236fs	YTAIAYWVPRNALPSDLLENVLCGV[p.A236fs]GLWPGCAGHHRGHCSHHLLPEALLR*	HLLPEALLR,RGHCSHHLL,SHHLLPEAL,LENVLCGVGL,HHRGHCSHHL,CSHHLLPEAL	LUAD
HLA-DPB1	c.340_341insA	p.G114fs	NSQKDILEEKRAVPDRMCRHNYELG[p.G114fs]EAHDPAAPSPA*	ELGEAHDPA,HNYELGEAH,RHNYELGEAH,YELGEAHDPA	CESC
HLA-DQB2	c.740G>A	p.R247H	AQSKMLSGIGGFVLGLIFLGLGLII[p.R247H]HHRGQKGPRGPPPAGNISAMIQSGER	LIIHHRGQK,GLIIHHRGQK	PRAD
HLA-DQB2	c.748G>A	p.G250S	KMLSGIGGFVLGLIFLGLGLIIRHR[p.G250S]SQKGPRGPPPAGNISAMIQSGERAQA	LIIRHRSQK,RHRSQKGPR,GLIIRHRSQK	PRAD
HLCS	c.1084G>A	p.E362K	LPPSSNIVQTPEDFNLLKSSNFRRY[p.E362K]KVLREILTTLGLSCDMKQVPALTPLY	KSSNFRRYK,RYKVLREIL,SSNFRRYKV,NFRRYKVLR,SNFRRYKVL,RRYKVLREI,KVLREILTTL,KSSNFRRYKV,SSNFRRYKVL,SNFRRYKVLR,RYKVLREILT,FRRYKVLREI,RRYKVLREIL	CRC
HLX	c.34T>A	p.S12T	MFAAGLAPFYA[p.S12T]TNFSLWSAAYCSSAGPGGCSFPLDPA	ATNFSLWSA,PFYATNFSL,FYATNFSLW,LAPFYATNF,TNFSLWSAA,GLAPFYATNF,PFYATNFSLW,ATNFSLWSAA,TNFSLWSAAY,YATNFSLWSA,APFYATNFSL	HNSC
HLX	c.693C>G	p.N231K	GRPAGVHLSGLQPSAGQFFASLDPI[p.N231K]KEASAILSPLNSNPRNSVQHQFQDTF	KEASAILSP,DPIKEASAI,QFFASLDPIK,KEASAILSPL,DPIKEASAIL	TGCT
HMCN1	c.398C>A	p.S133Y	RELYVQGGGDCPEMSIGAIKIALEI[p.S133Y]YLPGSFIYVFTDARSKDYRLTHEVLQ	YLPGSFIYV,IYLPGSFIY,AIKIALEIY,EIYLPGSFI,LEIYLPGSF,IKIALEIYL,YLPGSFIYVF,IYLPGSFIYV,AIKIALEIYL,GAIKIALEIY,EIYLPGSFIY,ALEIYLPGSF,LEIYLPGSFI	UCEC
HMG20A	c.744G>C	p.E248D	EEFLNHSKAREAELRQLRKSNMEFE[p.E248D]DRNAALQKHVESMRTAVEKLEVDVIQ	MEFEDRNAA,MEFEDRNAAL	CRC
HNF1B	c.1250C>T	p.T417M	GHNLLSPDGKMISVSGGGLPPVSTL[p.T417M]MNIHSLSHHNPQQSQNLIMTPLSGVM	GLPPVSTLM,STLMNIHSL,LMNIHSLSH,MNIHSLSHH,PPVSTLMNI,TLMNIHSLSH,LMNIHSLSHH,GGLPPVSTLM,LPPVSTLMNI	GBM
HNF1B	c.906C>G	p.N302K	GVSPSKAHGLGSNLVTEVRVYNWFA[p.N302K]KRRKEEAFRQKLAMDAYSSNQTHSLN	RVYNWFAKR,VYNWFAKRR,FAKRRKEEA,AKRRKEEAF,RVYNWFAKRR,EVRVYNWFAK,WFAKRRKEEA,FAKRRKEEAF	KIRC
HOOK1	c.1083delA	p.L361fs	QVKTLQETNMMYMHNTVSLEEELKK[p.L361fs]QMQHVHN*	LEEELKKQM,LKKQMQHVH,EELKKQMQHV	STAD
HOXA5	c.31G>T	p.G11C	MSSYFVNSFC[p.G11C]CRYPNGPDYQLHNYGDHSSVSEQFRD	FVNSFCCRY,CRYPNGPDY,YFVNSFCCR,YFVNSFCCRY,CCRYPNGPDY,SYFVNSFCCR	LUAD
HOXD10	c.452A>G	p.Y151C	AEVPSYQRLVPESCPVENPEVPVPG[p.Y151C]CFRLSQTYATGKTQEYNNSPEGSSTV	CFRLSQTYA,EVPVPGCFR,VPVPGCFRL,GCFRLSQTY,EVPVPGCFRL,NPEVPVPGCF	HNSC
HOXD8	c.201G>C	p.Q67H	GRHAAAAAALQLYGNSAAGFPHAPP[p.Q67H]HAHAHPHPSPPPSGTGCGGREGRGQE	FPHAPPHAH,AGFPHAPPH,AGFPHAPPHA,FPHAPPHAHA	KIRP

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HOXD8	c.364delC	p.P122fs	GSPAAAYQAAPPPPPHPPPPPPPPP[p.P122fs]AAGLPVTGSPRSFTDTITYRDSRFLRPSKRPSWYNILTVNRPVVILARTQTT*	FTDTITYRD,RSFTDTITY,KRPSWYNIL,ITYRDSRFL,TYRDSRFLR,DSRFLRPSK,SFTDTITYR,DTITYRDSR,WYNILTVNR,NILTVNRPV,TVNRPVVIL,SPRSFTDTI,RPSKRPSWY,SKRPSWYNI,RSFTDTITYR,ITYRDSRFLR,RDSRFLRPSK,RFLRPSKRPS,VNRPVVILAR,DSRFLRPSKR,SWYNILTVNR,TVNRPVVILA,LPVTGSPRSF,SPRSFTDTIT,RPSWYNILTV,FLRPSKRPSW,SKRPSWYNIL,YNILTVNRPV	STAD
HPD	c.852_853delAG	p.R284fs	GGAGVQHIALKTEDITAIRHLRER[p.R284fs]PGVLICSLHVLQTTAGEAEDGQDQGEGEH*	GVLICSLHV,VLICSLHVL,SLHVLQTTA,VLQTTAGEA,HLRERPGVL,RPGVLICSL,RERPGVLIC,HLRERPGVLI,RHLRERPGVL,RERPGVLICS	UCEC
HPS3	c.1403C>T	p.S468L	NHIILLTKAEPEAIPERRQSPKRLL[p.S468L]LRKDTSVKIKIPPVAEAGWNLYIVNT	LLLRKDTSV,LLRKDTSVK,RQSPKRLLL,RLLLRKDTSV,LLRKDTSVKI,LLLRKDTSVK,RQSPKRLLLR,QSPKRLLLRK,RRQSPKRLLL	CRC
HPS3	c.2436G>C	p.K812N	VACLPDVVLQELFFKLTSQYIWRLS[p.K812N]NRQPPDTTPLRTSEDLINACSHYGLI	QYIWRLSNR,SQYIWRLSN,SQYIWRLSNR,NRQPPDTTPL	HNSC
HPSE2	c.174G>T	p.K58N	LHLSLSSQAGDRRPLPVDRAAGLKE[p.K58N]NTLILLDVSTKNPVRTVNENFLSLQL	GLKENTLIL,LKENTLILL,GLKENTLILL,RAAGLKENTL,KENTLILLDV	CRC
HRAS	c.181C>A	p.Q61K	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61K]KEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGKEEY,AGKEEYSAM,ILDTAGKEEY,DTAGKEEYSA	THCA
HRAS	c.182A>G	p.Q61R	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61R]REEYSAMRDQYMRTGEGFLCVFAINN	LDTAGREEY,AGREEYSAM,ILDTAGREEY,AGREEYSAMR,DTAGREEYSA	THCA
HRAS	c.34G>A	p.G12S	MTEYKLVVVGA[p.G12S]SGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGASGV,KLVVVGASGV,YKLVVVGASG	HNSC
HRAS	c.35G>A	p.G12D	MTEYKLVVVGA[p.G12D]DGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGADGV,VVGADGVGK,KLVVVGADGV,VVVGADGVGK	BLCA,HNSC
HRAS	c.35G>C	p.G12A	MTEYKLVVVGA[p.G12A]AGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGAAGV,VVGAAGVGK,YKLVVVGAA,KLVVVGAAGV,VVVGAAGVGK,YKLVVVGAAG,GAAGVGKSAL	HNSC
HRAS	c.38G>T	p.G13V	MTEYKLVVVGAG[p.G13V]VVGKSALTIQLIQNHFVDEYDPTIED	KLVVVGAGV,VVGAGVVGK,KLVVVGAGVV,VVVGAGVVGK,YKLVVVGAGV	HNSC
HRC	c.1317_1318insC	p.P439fs	PHHHHHRVPREEDEEVSAELGHQAP[p.P439fs]QPQAKPPR*	HQAPQPQAK,AELGHQAPQ	KIRC
HRCT1	c.275A>C	p.H92P	LGIFHHHRHPGHVSHVPNVGLHHHH[p.H92P]PPRHTPHHLHHHHHPHRHHPRHAR*	GLHHHHPPR,PPRHTPHHL,VGLHHHHPPR,HPPRHTPHHL,HHHPPRHTPH	BLCA
HRNR	c.1delA	p.M1fs	[p.M1fs]CLNSYKASSLSSMFSTNMPPSMGSMIR*	NMPPSMGSM,SYKASSLSS,KASSLSSMF,MPPSMGSMI,LNSYKASSL,YKASSLSSM,LSSMFSTNM,FSTNMPPSM,SMFSTNMPP,SLSSMFSTNM,CLNSYKASSL,SMFSTNMPPS,NMPPSMGSMI,SYKASSLSSM,KASSLSSMFS,YKASSLSSMF,MFSTNMPPSM,TNMPPSMGSM	OV
HRNR	c.7615G>A	p.G2539S	QHGSGSSQSSGYGRQGSGSGQSPGH[p.G2539S]SQRGSGSRQSPSYGRHGSGSGRSSSS	HSQRGSGSR	CESC
HRSP12	c.359G>A	p.R120Q	IYKQYFKSNFPARAAYQVAALPKGS[p.R120Q]QIEIEAVAIQGPLTTASL*	SQIEIEAVA,LPKGSQIEI,AALPKGSQI,SQIEIEAVAI,ALPKGSQIEI	CRC
HS3ST1	c.859G>A	p.E287K	RDRCLHESKGRAHPQVDPKLLNKLH[p.E287K]KYFHEPNKKFFELVGRTFDWH*	KLLNKLHKY,HKYFHEPNK,LLNKLHKYF,KLLNKLHKYF,KYFHEPNKKF,LHKYFHEPNK	CRC
HS3ST3A1	c.1195G>T	p.G399W	EIDREVVRRLREFYRPFNLKFYQMT[p.G399W]WHDFGWDG*	FYQMTWHDF,NLKFYQMTW,LKFYQMTWH,YQMTWHDFG,QMTWHDFGW,FNLKFYQMTW,KFYQMTWHDF,YQMTWHDFGW	LUAD
HSD17B1	c.937G>A	p.G313S	VPAKAEAGAEAGGGAGPGAEDEAGR[p.G313S]SAVGDPELGDPPAAPQ*	AEDEAGRSA,RSAVGDPEL,AEDEAGRSAV,GRSAVGDPEL	ACC
HSD17B6	c.627C>G	p.F209L	EAFSDILRREIQHFGVKISIVEPGY[p.F209L]LRTGMTNMTQSLERMKQSWKEAPKHI	YLRTGMTNM,SIVEPGYLR,YLRTGMTNMT,ISIVEPGYLR,GYLRTGMTNM,VEPGYLRTGM	LUAD
HSF4	c.505C>T	p.R169W	QALRGVQESTEARLRELRQQNEILW[p.R169W]WEVVTLRQSHGQQHRVIGKLIQCLFG	ILWWEVVTL,RQQNEILWW,LWWEVVTLR,NEILWWEVV,WEVVTLRQS,QQNEILWWEV,ILWWEVVTLR,EILWWEVVTL,WEVVTLRQSH,NEILWWEVVT	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
HSPA13	c.253G>T	p.V85L	DENGHISIPSMVSFTDNDVYVGYES[p.V85L]LELADSNPQNTIYDAKRFIGKIFTAE	DVYVGYESL,YVGYESLELA,VYVGYESLEL	LUAD
HSPA4L	c.1447C>T	p.R483C	RIGSFTIQNVFPQSDGDSSKVKVKV[p.R483C]CVNIHGIFSVASASVIEKQNLEGDHS	KVKVKVCVN,KVKVCVNIH,VCVNIHGIF,CVNIHGIFSV,SSKVKVKVCV,KVKVKVCVNI,KVKVCVNIHG,VKVCVNIHGI,KVCVNIHGIF	UCEC
HSPBAP1	c.845G>T	p.R282L	HYVESIDPVTVSINSWIELEEDHLA[p.R282L]LVEEAITRMLVCALKTAENPQNTRAW	HLALVEEAI,LEEDHLALV,ALVEEAITRM,IELEEDHLAL	LUAD
HTR2A	c.656C>T	p.S219L	LKIIAVWTISVGISMPIPVFGLQDD[p.S219L]LKVFKEGSCLLADDNFVLIGSFVSFF	LQDDLKVFK,GLQDDLKVF,PVFGLQDDLK,GLQDDLKVFK,IPVFGLQDDL,FGLQDDLKVF,LKVFKEGSCL	UCEC
HTR3B	c.706C>T	p.R236C	SVSSTYSILQSSAGGFAQIQFNVVM[p.R236C]CRHPLVYVVSLLIPSIFLMLVDLGSF	VVMCRHPLV,IQFNVVMCR,VMCRHPLVY,MCRHPLVYV,NVVMCRHPL,VMCRHPLVYV,VVMCRHPLVY,QIQFNVVMCR,NVVMCRHPLV,AQIQFNVVMC,IQFNVVMCRH,FNVVMCRHPL	CRC
HTR5A	c.454C>T	p.R152C	ASIWNVTAIALDRYWSITRHMEYTL[p.R152C]CTRKCVSNVMIALTWALSAVISLAPL	CTRKCVSNV,HMEYTLCTR,YTLCTRKCV,RHMEYTLCT,HMEYTLCTRK,CTRKCVSNVM,MEYTLCTRKC	CRC
HTR5A	c.894G>T	p.W298C	DTWREQKEQRAALMVGILIGVFVLC[p.W298C]CIPFFLTELISPLCSCDIPAIWKSIF	VLCCIPFFL,CIPFFLTEL,VFVLCCIPF,FVLCCIPFF,FVLCCIPFFL,CIPFFLTELI,VFVLCCIPFF,GVFVLCCIPF	LUAD
HTRA3	c.1208A>G	p.Q403R	DFPEVSSGIYVQEVAPNSPSQRGGI[p.Q403R]RDGDIIVKVNGRPLVDSSELQEAVLT	GIRDGDIIVK	GBM
HYAL4	c.664G>A	p.D222N	AFMKETIKLGIKSRPKGLWGYYLYP[p.D222N]NCHNYNVYAPNYSGSCPEDEVLRNNE	YLYPNCHNY,YPNCHNYNV,GLWGYYLYPN,YLYPNCHNYN,YYLYPNCHNY,LYPNCHNYNV,YPNCHNYNVY	TGCT
HYDIN	c.1352G>A	p.R451Q	NPLEAKLYQQTIYCDILGREIRLPL[p.R451Q]QIKGEGMGPKIHFNFELLDIGKVFTG	EIRLPLQIK,REIRLPLQI,QIKGEGMGPK,LPLQIKGEGM	CRC
HYDIN	c.2816G>A	p.R939Q	PELNLGAHFSLDTHYYHFKLINKGR[p.R939Q]QIQQLFWMNDSFRPQAKLSKKGRVKK	RQIQQLFWM,KLINKGRQI,KGRQIQQLF,KGRQIQQLFW,FKLINKGRQI,NKGRQIQQLF,RQIQQLFWMN	CRC
HYDIN	c.3559C>T	p.R1187C	VHYPNLSFETKELDFGCILNDTELI[p.R1187C]CYVTITNCSPLVVKFRWFFLVNDEEN	LNDTELICY,TELICYVTI,ILNDTELICY,DTELICYVTI,TELICYVTIT	CRC
HYOU1	c.472C>T	p.R158C	TVHFQISSQLQFSPEEVLGMVLNYS[p.R158C]CSLAEDFAEQPIKDAVITVPVFFNQA	MVLNYSCSL,VLNYSCSLA,YSCSLAEDF,GMVLNYSCSL,MVLNYSCSLA,NYSCSLAEDF	CRC
IARS2	c.2494C>T	p.R832C	YCEKENDPKRRSCQTALVEILDVIV[p.R832C]CSFAPILPHLAEEVFQHIPYIKEPKS	VIVCSFAPI,CSFAPILPH,ILDVIVCSF,ILDVIVCSFA,VIVCSFAPIL,DVIVCSFAPI,EILDVIVCSF,CSFAPILPHL	SKCM
IBA57	c.390C>A	p.S130R	RTLYDVILYGLQEHSEVSGFLLECD[p.S130R]RSVQGALQKHLALYRIRRKVTVEPHP	FLLECDRSV,RSVQGALQK,LECDRSVQGA	ACC
IBTK	c.3638delA	p.K1213fs	PVNAWASSLHSVSSKSFRDFLLEEK[p.K1213fs]SLLLAIVQAIMSKKFLLKELKILRHQKLSDALPMVPQDQKATIFQIYHF*	FLLEEKSLL,LLEEKSLLL,SLLLAIVQA,LLLAIVQAI,AIMSKKFLL,FLLKELKIL,KLSDALPMV,LLAIVQAIM,AIVQAIMSK,IVQAIMSKK,IMSKKFLLK,KFLLKELKI,ATIFQIYHF,ELKILRHQK,LLKELKILR,VPQDQKATI,VQAIMSKKF,SKKFLLKEL,LKILRHQKL,RHQKLSDAL,QKLSDALPM,QKATIFQIY,EEKSLLLAI,LEEKSLLLA,FLLEEKSLLL,SLLLAIVQAI,LLLAIVQAIM,LLEEKSLLLA,AIVQAIMSKK,AIMSKKFLLK,LAIVQAIMSK,IVQAIMSKKF,KATIFQIYHF,KSLLLAIVQA,MSKKFLLKEL,DQKATIFQIY,VPQDQKATIF,ELKILRHQKL,HQKLSDALPM,RDFLLEEKSL,LEEKSLLLAI,VQAIMSKKFL,KKFLLKELKI,LRHQKLSDAL,EEKSLLLAIV,LPMVPQDQKA	STAD
IDE	c.110delA	p.K37fs	ALPSTFRSVLGARLPPPERLCGFQK[p.K37fs]RLTAK*	GFQKRLTAK,CGFQKRLTAK	STAD
IDH1	c.394C>G	p.R132G	VFREAIICKNIPRLVSGWVKPIIIG[p.R132G]GHAYGDQYRATDFVVPGPGKVEITYT	PIIIGGHAY,GGHAYGDQY,KPIIIGGHAY,IGGHAYGDQY	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
IDH1	c.394C>T	p.R132C	VFREAIICKNIPRLVSGWVKPIIIG[p.R132C]CHAYGDQYRATDFVVPGPGKVEITYT	PIIIGCHAY,GCHAYGDQY,KPIIIGCHAY,IGCHAYGDQY	LAML,LIHC,MM,SKCM
IDH1	c.395G>A	p.R132H	VFREAIICKNIPRLVSGWVKPIIIG[p.R132H]HHAYGDQYRATDFVVPGPGKVEITYT	PIIIGHHAY,GHHAYGDQY,KPIIIGHHAY,IGHHAYGDQY	GBM,LAML,PRAD
IDH2	c.419G>A	p.R140Q	TITPDEARVEEFKLKKMWKSPNGTI[p.R140Q]QNILGGTVFREPIICKNIPRLVPGWT	IQNILGGTV,QNILGGTVF,SPNGTIQNI,TIQNILGGTV,SPNGTIQNIL,IQNILGGTVF	LAML
IDH2	c.515G>A	p.R172K	VFREPIICKNIPRLVPGWTKPITIG[p.R172K]KHAHGDQYKATDFVADRAGTFKMVFT	WTKPITIGK,KHAHGDQYK,GKHAHGDQY,IGKHAHGDQY	LAML
IDUA	c.1120A>C	p.T374P	DNAFLSYHPHPFAQRTLTARFQVNN[p.T374P]PRPPHVQLLRKPVLTAMGLLALLDEE	NPRPPHVQL,FQVNNPRPP,TARFQVNNPR,QVNNPRPPHV,NPRPPHVQLL,FQVNNPRPPH	ACC
IDUA	c.99T>G	p.H33Q	AALLALLASLLAAPPVAPAEAPHLV[p.H33Q]QVDAARALWPLRRFWRSTGFCPPLPH	HLVQVDAAR,VQVDAARAL,AEAPHLVQV,HLVQVDAARA,APHLVQVDAA,VQVDAARALW	KIRP
IER5	c.580C>G	p.R194G	SRAARRPCGCPLGGEDPPGTPAATP[p.R194G]GAACCCAPQPAEDEPPAPPAVCPRKR	TPAATPGAA,TPAATPGAAC	KIRP
IFNA10	c.236T>C	p.V79A	KDRHDFRIPQEEFDGNQFQKAQAIS[p.V79A]ALHEMIQQTFNLFSTEDSSAAWEQSL	ALHEMIQQT,AISALHEMI,KAQAISALH,QAISALHEM,QKAQAISAL,FQKAQAISAL,QAISALHEMI,AQAISALHEM,ALHEMIQQTF	GBM,LUSC
IFNA10	c.238C>T	p.L80F	DRHDFRIPQEEFDGNQFQKAQAISV[p.L80F]FHEMIQQTFNLFSTEDSSAAWEQSLL	KAQAISVFH,QAISVFHEM,QKAQAISVF,AQAISVFHEM,VFHEMIQQTF,QAISVFHEMI,FQKAQAISVF	GBM
IFT140	c.1990G>A	p.E664K	VDEGLKNYVPVNHFWDQSEPRLFVC[p.E664K]KAVQETPRSQPQSANGQPQDGRAGPA	QSEPRLFVCK,EPRLFVCKAV,SEPRLFVCKA	HNSC
IFT172	c.2509G>A	p.A837T	YERAGDLFEKIHNPQKALECYRKGN[p.A837T]TFMKAVELARLAFPVEVVKLEEAWGD	CYRKGNTFM,KGNTFMKAV,NTFMKAVEL,CYRKGNTFMK,TFMKAVELAR,NTFMKAVELA,LECYRKGNTF,RKGNTFMKAV	STAD
IFT172	c.2831C>T	p.A944V	AQHYASLQEYEIAEELYTKGDRTKD[p.A944V]VIDMYTQAGRWEQAHKLAMKCMRPED	RTKDVIDMY,DVIDMYTQA,RTKDVIDMYT	CRC
IGF2BP2	c.556A>T	p.T186S	SSPSPPQRAQRGDHSSREQGHAPGG[p.T186S]SSQARQIDFPLRILVPTQFVGAIIGK	SSQARQIDF,GSSQARQIDF	CLL
IGF2R	c.3942_3943insG	p.T1314fs	HKVAGLLTQKLTYENGLLKMNFTGG[p.T1314fs]GHLP*	KMNFTGGGH,MNFTGGGHL,KMNFTGGGHL,LKMNFTGGGH	STAD
IGHMBP2	c.1843C>A	p.R615S	FLAEDRRINVAVTRARRHVAVICDS[p.R615S]STVNNHAFLKTLVEYFTQHGEVRTAF	AVICDSSTV,STVNNHAFL,SSTVNNHAF,STVNNHAFLK,DSSTVNNHAF	LUAD
IGJ	c.230G>A	p.R77Q	KCARITSRIIRSSEDPNEDIVERNI[p.R77Q]QIIVPLNNRENISDPTSPLRTRFVYH	QIIVPLNNR,DIVERNIQI,VERNIQIIV,RNIQIIVPL	CRC
IK	c.268_269delGA	p.E90fs	DPAARRRKKKSYYAKLRQQEIERER[p.E90fs]ASREVPGSCQGTERWSEQRL*	EIERERASR,REVPGSCQG,TERWSEQRL,RQQEIERERA,IERERASREV,REVPGSCQGT	UCEC
IKZF3	c.485T>G	p.L162R	KRSHTGERPFQCNQCGASFTQKGNL[p.L162R]RRHIKLHTGEKPFKCHLCNYACQRRD	KGNLRRHIK,SFTQKGNLR,FTQKGNLRR,ASFTQKGNLR,KGNLRRHIKL,SFTQKGNLRR,NLRRHIKLHT,TQKGNLRRHI	CLL
IL17B	c.100C>T	p.R34W	FLLTISIFLGLGQPRSPKSKRKGQG[p.R34W]WPGPLAPGPHQVPLDLVSRMKPYARM	GQGWPGPLA,RKGQGWPGPL,WPGPLAPGPH	BRCA
IL17RA	c.2409_2410insC	p.Q803fs	PYEEEQRQSVQSDQGYISRSSPQPP[p.Q803fs]RGTHGNGGRGGRGAGPREAGPATLSRGPGEPEEPPAAAAFPPAAEELGLGHDGVRVRGAQCMRAAPQGPPRSQL*	GLGHDGVRV,RAAPQGPPR,RGGRGAGPR,RVRGAQCMR,GPREAGPAT,VRVRGAQCM,EEPPAAAAF,REAGPATLS,ISRSSPQPPR,GVRVRGAQCM,RVRGAQCMRA,GPREAGPATL,APQGPPRSQL,AAFPPAAEEL,EELGLGHDGV	CRC

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IL1R2	c.1091_1092insG	p.L364fs	KEASSTFSWGIVLAPLSLAFLVLGG[p.L364fs]NMDAQTVQTQNWKSRWSDCAMASSSRLSILSQVK*	RLSILSQVK,QTVQTQNWK,KSRWSDCAM,MASSSRLSI,AQTVQTQNW,CAMASSSRL,ASSSRLSIL,SRLSILSQV,FLVLGGNMDA,AMASSSRLSI,KSRWSDCAMA,SSRLSILSQV,TVQTQNWKSR,MASSSRLSIL,LAFLVLGGNM,VQTQNWKSRW,WKSRWSDCAM,DAQTVQTQNW	CLL
IL1RAP	c.149T>G	p.F50C	DDWGLDTMRQIQVFEDEPARIKCPL[p.F50C]CEHFLKFNYSTAHSAGLTLIWYWTRQ	RIKCPLCEH,IKCPLCEHF,CEHFLKFNY,RIKCPLCEHF,CPLCEHFLKF,CEHFLKFNYS	KIRC
IL1RAPL2	c.1940C>T	p.T647M	KHEIPATTLPVPSLGNHHTYCNLPL[p.T647M]MLLNGQLPLNNTLKDTQEFHRNSSLL	MLLNGQLPL,TYCNLPLML,HTYCNLPLM,LMLLNGQLPL,HTYCNLPLML,TYCNLPLMLL,LPLMLLNGQL,HHTYCNLPLM	CRC
IL2	c.308G>T	p.R103M	CLEEELKPLEEVLNLAQSKNFHLRP[p.R103M]MDLISNINVIVLELKGSETTFMCEYA	RPMDLISNI,NFHLRPMDL,SKNFHLRPM,QSKNFHLRPM,KNFHLRPMDL,MDLISNINVI	LUAD
IL25	c.502_503delTG	p.C168fs	HGEKGTHKGYCLERRLYRVSLACVC[p.C168fs]AAPCDGLAGPAGGWSLFGKPGARCTTTCHEGPGCPDAWPL*	AGGWSLFGK,SLFGKPGAR,GPAGGWSLF,HEGPGCPDA,SLACVCAAPC,RVSLACVCAA,WSLFGKPGAR,GPGCPDAWPL,LAGPAGGWSL,HEGPGCPDAW	KIRP
IL3	c.268G>A	p.A90T	DILMENNLRRPNLEAFNRAVKSLQN[p.A90T]TSAIESILKNLLPCLPLATAAPTRHP	TSAIESILK,KSLQNTSAI,NTSAIESIL,LQNTSAIESI,NTSAIESILK,AVKSLQNTSA,VKSLQNTSAI	CRC
IL32	c.643C>A	p.P215T	LWKQFQSFCCSLSELFMSSFQSYGA[p.P215T]TRGDKEELTPQKCSEPQSSK*	SYGATRGDK,SFQSYGATR,SSFQSYGAT,FQSYGATRG,SSFQSYGATR,QSYGATRGDK	LUAD
IL32	c.653_654insG	p.D218fs	QFQSFCCSLSELFMSSFQSYGAPRG[p.D218fs]EQGGADTPEVL*	APRGEQGGA	SKCM
IL5RA	c.139C>A	p.L47I	LLPDEKISLLPPVNFTIKVTGLAQV[p.L47I]ILQWKPNPDQEQRNVNLEYQVKINAP	GLAQVILQW,GLAQVILQWK,IKVTGLAQVI,TGLAQVILQW	CRC
IL6ST	c.647C>A	p.P216H	FVNIEVWVEAENALGKVTSDHINFD[p.P216H]HVYKVKPNPPHNLSVINSEELSSILK	TSDHINFDH,HINFDHVYK,DHINFDHVY,TSDHINFDHV,HINFDHVYKV,SDHINFDHVY	MM
IL7R	c.161C>T	p.S54L	DLEDAELDDYSFSCYSQLEVNGSQH[p.S54L]LLTCAFEDPDVNITNLEFEICGALVE	EVNGSQHLL,SQHLLTCAF,LEVNGSQHL,GSQHLLTCAF,LEVNGSQHLL	LUSC
ILF3	c.1450G>A	p.E484K	VKVLQDMGLPTGAEGRDSSKGEDSA[p.E484K]KETEAKPAVVAPAPVVEAVSTPSAAF	SSKGEDSAK,KETEAKPAV,KETEAKPAVV,GEDSAKETEA	BLCA
INADL	c.4018C>G	p.P1340A	KLVFIRNEDAVNQMAVTPFPVPSSS[p.P1340A]ASSIEDQSGTEPISSEEDGSVEVGIK	FPVPSSSAS,VPSSSASSI,TPFPVPSSSA,FPVPSSSASS	LUSC
INF2	c.1581delC	p.S527fs	PLLPGMGWGPPPPPPPLLPCTCSPP[p.S527fs]WREAWRRSSWPRWTMAWAQHGSPAIGG*	SWPRWTMAW,AWRRSSWPR,RSSWPRWTM,SSWPRWTMA,WPRWTMAWA,WAQHGSPAI,REAWRRSSW,WRRSSWPRW,AWAQHGSPA,AQHGSPAIG,LPCTCSPPW,AWRRSSWPRW,SSWPRWTMAW,RSSWPRWTMA,MAWAQHGSPA,CSPPWREAWR,EAWRRSSWPR,WTMAWAQHGS,WPRWTMAWAQ,LLPCTCSPPW,WREAWRRSSW,RRSSWPRWTM,AWAQHGSPAI	STAD
ING1	c.658G>T	p.A220S	DECYERFSRETDGAQKRRMLHCVQR[p.A220S]SLIRSQELGDEKIQIVSQMVELVENR	MLHCVQRSL,RSLIRSQEL,RMLHCVQRS,RMLHCVQRSL,MLHCVQRSLI,RSLIRSQELG	LUAD
INMT	c.167G>T	p.G56V	PSPEAEMLKFNLECLHKTFGPGGLQ[p.G56V]VDTLIDIGSGPTIYQVLAACDSFQDI	LQVDTLIDI,GLQVDTLIDI,KTFGPGGLQV	LUAD
INMT	c.635C>T	p.S212F	LKPGGHLVTTVTLRLPSYMVGKREF[p.S212F]FCVALEKEEVEQAVLDAGFDIEQLLH	EFFCVALEK,YMVGKREFF,GKREFFCVA,KREFFCVAL,REFFCVALE,MVGKREFFCV,YMVGKREFFC,SYMVGKREFF,GKREFFCVAL,REFFCVALEK	SKCM
INPP5D	c.1568G>A	p.R523Q	SFMFNGTSLGFVNSHLTSGSEKKLR[p.R523Q]QNQNYMNILRFLALGDKKLSPFNITH	RQNQNYMNI,KLRQNQNYM,KKLRQNQNY,KLRQNQNYMN,RQNQNYMNIL,KKLRQNQNYM	CRC
INPP5K	c.787C>T	p.R263C	EGRLLFPPTYKFDRNSNDYDTSEKK[p.R263C]CKPAWTDRILWRLKRQPCAGPDTPIP	KCKPAWTDR,SEKKCKPAW	CRC

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INPPL1	c.1478C>T	p.T493M	VFGTQENSVGDREWLDLLRGGLKEL[p.T493M]MDLDYRPIAMQSLWNIKVAVLVKPEH	LMDLDYRPI,LKELMDLDY,ELMDLDYRPI,GLKELMDLDY,LLRGGLKELM,MDLDYRPIAM	HNSC
INPPL1	c.2921delC	p.A974fs	APREEPLTPRLKPEGAPEPEGVAAP[p.A974fs]HPRTASITLPTTSLKGSRTSCCPRSHPRLPGPLSHLPPRTKWPLQCLLHSLGTTGTLVWERGVLQMRSLEAHCPLQTFHLHHCRTQPSSCPPAWILYQGQWSGAVVGLRPVAHHLPRPIQGLHCPQAPHQPALSWGKWPVGMTGPARCCRWPRR*	RLPGPLSHL,SLGTTGTLV,YQGQWSGAV,ALSWGKWPV,VLQMRSLEA,GLRPVAHHL,HLPRPIQGL,ITLPTTSLK,LSHLPPRTK,TTGTLVWER,QTFHLHHCR,HQPALSWGK,MTGPARCCR,AWILYQGQW,SWGKWPVGM,RTASITLPT,GSRTSCCPR,RTSCCPRSH,RSHPRLPGP,RTKWPLQCL,RSLEAHCPL,RPVAHHLPR,PARCCRWPR,SCPPAWILY,EGVAAPHPR,SCCPRSHPR,WSGAVVGLR,APHPRTASI,HPRTASITL,HPRLPGPLS,LPPRTKWPL,CPQAPHQPA,APHQPALSW,WPVGMTGPA,LQMRSLEAH,EAHCPLQTF,SHLPPRTKW,TKWPLQCLL,LLHSLGTTG,HSLGTTGTL,LGTTGTLVW,RGVLQMRSL,TQPSSCPPA,SSCPPAWIL,ILYQGQWSG,GQWSGAVVG,VAHHLPRPI,GLHCPQAPH,PQAPHQPAL,EPEGVAAPH,CPLQTFHLH,QPSSCPPAW,QPALSWGKW,LEAHCPLQT,SSCPPAWILY,HLPPRTKWPL,ILYQGQWSGA,YQGQWSGAVV,GQWSGAVVGL,LLHSLGTTGT,SITLPTTSLK,TSCCPRSHPR,GTTGTLVWER,RTASITLPTT,KGSRTSCCPR,RSHPRLPGPL,RTKWPLQCLL,RTQPSSCPPA,PARCCRWPRR,LQTFHLHHCR,QWSGAVVGLR,HSLGTTGTLV,APHPRTASIT,CPRSHPRLPG,HPRLPGPLSH,WPLQCLLHSL,CPQAPHQPAL,LEAHCPLQTF,LVWERGVLQM,ASITLPTTSL,LSHLPPRTKW,LHSLGTTGTL,SLGTTGTLVW,LQMRSLEAHC,MRSLEAHCPL,TQPSSCPPAW,HQPALSWGKW,LSWGKWPVGM,WERGVLQMRS,QPSSCPPAWI	STAD
INPPL1	c.3460delC	p.P1154fs	SEVDYAPAGPARSALLPGPLELQPP[p.P1154fs]GDCPRTMAGPSASLHPASGRASRKTWQRRLRACRAGGPAGWARQA*	TMAGPSASL,SLHPASGRA,ASLHPASGR,RASRKTWQR,RTMAGPSAS,ASRKTWQRR,KTWQRRLRA,WQRRLRACR,RLRACRAGG,RACRAGGPA,HPASGRASR,CPRTMAGPS,GPSASLHPA,SGRASRKTW,RTMAGPSASL,RASRKTWQRR,ASRKTWQRRL,KTWQRRLRAC,RLRACRAGGP,ELQPPGDCPR,SASLHPASGR,TWQRRLRACR,CPRTMAGPSA,WQRRLRACRA,TMAGPSASLH,ASGRASRKTW	STAD
INTS12	c.1A>G	p.M1V	[p.M1V]VAATVNLELDPIFLKALGFLHSKSKD	VAATVNLEL	MM
INTS4	c.1378T>G	p.S460A	MRKISNNITLREDQLDTVLAVLEDS[p.S460A]ARDIREALHELLCCTNVSTKEGIHLA	VLAVLEDSA,SARDIREAL,SARDIREALH,DSARDIREAL	TGCT
INTS7	c.2818C>T	p.R940C	GIVWKTGPRTTIFVKSLEDPYSQQI[p.R940C]CLQQQQAQQPLQQQQQRNAYTRF*	DPYSQQICL,QQICLQQQQA	UCEC
INTS7	c.317G>T	p.R106I	LCVLKVTQQSEKHLEKILNVDEFVK[p.R106I]IIFSVIHSNDPVARAITLRMLGSLAS	FVKIIFSVI,EFVKIIFSV,DEFVKIIFS,ILNVDEFVKI,EFVKIIFSVI,DEFVKIIFSV	UCEC
INVS	c.2396G>A	p.R799K	WKPSRRHDTEPKAKCAPQKRRTQEL[p.R799K]KGGRCSPAGSSRPGSARGEAVHAGQN	PQKRRTQELK,ELKGGRCSPA	CESC
INVS	c.2444delG	p.R815fs	KRRTQELRGGRCSPAGSSRPGSARG[p.R815fs]RRSMLGRILPTIVHQETK*	SMLGRILPT,MLGRILPTI,SARGRRSML,RGRRSMLGR,RSMLGRILP,GSARGRRSM,RRSMLGRIL,SMLGRILPTI,MLGRILPTIV,ILPTIVHQET,SSRPGSARGR,SARGRRSMLG,RGRRSMLGRI,RSMLGRILPT	STAD
IPO11	c.2532delT	p.S844fs	ERYPVVMSTYLGVMGRVLLQNTSFF[p.S844fs]LHYLMRWPINLIRRWTSFWEI*	LLQNTSFFL,YLMRWPINL,LMRWPINLI,TSFFLHYLM,SFFLHYLMR,FFLHYLMRW,RRWTSFWEI,LQNTSFFLH,QNTSFFLHY,NTSFFLHYL,LHYLMRWPI,NLIRRWTSF,LIRRWTSFW,WPINLIRRW,NTSFFLHYLM,VLLQNTSFFL,FLHYLMRWPI,YLMRWPINLI,TSFFLHYLMR,SFFLHYLMRW,HYLMRWPINL,RWPINLIRRW,LMRWPINLIR,LQNTSFFLHY,INLIRRWTSF,NLIRRWTSFW,IRRWTSFWEI	STAD
IRAK3	c.800G>A	p.R267Q	PYMRNGTLFDRLQCVGDTAPLPWHI[p.R267Q]QIGILIGISKAIHYLHNVQPCSVICG	IQIGILIGI,APLPWHIQI,WHIQIGILI,LPWHIQIGI,QIGILIGIS K,TAPLPWHIQI,LPWHIQIGIL	CRC

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IREB2	c.1256G>A	p.R419Q	HLEHTGFSKAKLESMETYLKAVKLF[p.R419Q]QNDQNSSGEPEYSQVIQINLNSIVPS	FQNDQNSSG	CRC
IRF4	c.368A>G	p.K123R	RCALNKSNDFEELVERSQLDISDPY[p.K123R]RVYRIVPEGAKKGAKQLTLEDPQMSM	ISDPYRVYR,RVYRIVPEG,DISDPYRVY,DPYRVYRIV,QLDISDPYRV,RVYRIVPEGA,SQLDISDPYR,DISDPYRVYR,LDISDPYRVY	MM
IRS4	c.1771_1772insG	p.G591fs	GHGSGGGQGPGDGHGSGGGKNSGGG[p.G591fs]QRLRKWERIRW*	GQRLRKWER,RLRKWERIR,RLRKWERIRW,GKNSGGGQRL	STAD
IRS4	c.63_65delGGC	p.21_22AA>A	MASCSFTRDQATRRLRGAAAAAAA[p.21_22AA>A]LAAVVTTPLLSSGTPTALIGTGSSCPGA	RGAAAAAAAL	PAAD
IRX3	c.1265T>C	p.L422P	LVSAPLGKFPAWTNRPFPGPPPGPR[p.L422P]PHPLSLLGSAPPHLLGLPGAAGHPAA	PPGPRPHPL,GPRPHPLSL,GPRPHPLSLL	ACC
IRX6	c.1274C>T	p.A425V	CDESSCIPKAFGNPKFALQGLPLNC[p.A425V]VPCPRRSEPVVQCQYPSGAEAG*	PLNCVPCPR,ALQGLPLNCV,VPCPRRSEPV	STAD
ISX	c.256C>T	p.R86C	AASGSGLEKPPKDQPQEGRKSKRRV[p.R86C]CTTFTTEQLHELEKIFHFTHYPDVHI	KSKRRVCTT,CTTFTTEQL,SKRRVCTTF,RRVCTTFTT,KSKRRVCTTF	SKCM
ISX	c.5G>T	p.C2F	M[p.C2F]FAEVGPALCRGMERNSLGCCEAPKKL	MFAEVGPAL	LUSC
ITGA10	c.2006G>A	p.R669Q	PIVHLTPSLEVTPQAISVVQRDCRR[p.R669Q]QGQEAVCLTAALCFQVTSRTPGRWDH	CRRQGQEAV,RQGQEAVCL,RRQGQEAVCL,RQGQEAVCLT	HNSC
ITGA4	c.2018C>T	p.T673M	YLAVGSMKTLMLNVSLFNAGDDAYE[p.T673M]MTLHVKLPVGLYFIKILELEEKQINC	MTLHVKLPV,DAYEMTLHV,YEMTLHVKL,NAGDDAYEM,AYEMTLHVKL,DAYEMTLHVK,EMTLHVKLPV,FNAGDDAYEM,YEMTLHVKLP	CRC
ITGA4	c.2700C>A	p.F900L	GIVRFLSKTDKRLLYCIKADPHCLN[p.F900L]LLCNFGKMESGKEASVHIQLEGRPSI	HCLNLLCNF,CLNLLCNFGK,IKADPHCLNL	CRC
ITGA5	c.143C>A	p.A48D	PPLLPLLLLLLPPPPRVGGFNLDAE[p.A48D]DPAVLSGPPGSFFGFSVEFYRPGTDG	NLDAEDPAV	KICH
ITGA8	c.1846G>T	p.G616C	TEFRDKLSPINISLNYSLDESTFKE[p.G616C]CLEVKPILNYYRENIVSEQAHILVDC	STFKECLEV,TFKECLEVK,KECLEVKPI,DESTFKECL,CLEVKPILNY,STFKECLEVK,ESTFKECLEV,KECLEVKPIL	LUAD
ITGAX	c.2054G>A	p.R685H	KRSKNLLGSRDLQSSVTLDLALDPG[p.R685H]HLSPRATFQETKNRSLSRVRVLGLKA	GHLSPRATF	LUSC
ITGAX	c.848G>A	p.R283H	TDGKKEGDSLDYKDVIPMADAAGII[p.R283H]HYAIGVGLAFQNRNSWKELNDIASKP	GIIHYAIGV,DAAGIIHYA,ADAAGIIHY,IHYAIGVGL,MADAAGIIHY,IIHYAIGVGL,HYAIGVGLAF,DAAGIIHYAI,IHYAIGVGLA	LUAD
ITGB1	c.1132C>A	p.L378I	PKSAVGTLSANSSNVIQLIIDAYNS[p.L378I]ISSEVILENGKLSEGVTISYKSYCKN	LIIDAYNSI,QLIIDAYNSI,AYNSISSEVI,DAYNSISSEV	STAD
ITGB1	c.472G>A	p.D158N	LKFKRAEDYPIDLYYLMDLSYSMKD[p.D158N]NLENVKSLGTDLMNEMRRITSDFRIG	SMKDNLENV,LSYSMKDNL,YSMKDNLENV,SMKDNLENVK	HNSC
ITGB8	c.21_22insT	p.A7fs	MCGSALAFF[p.A7fs]YRCICLPAKRPARSRLVPLGSLGVFTCSWTGPR*	CGSALAFFY,ALAFFYRCI,LVPLGSLGV,GSALAFFYR,FTCSWTGPR,FYRCICLPA,RSRLVPLGS,CLPAKRPAR,RPARSRLVP,VPLGSLGVF,PARSRLVPL,AKRPARSRL,SRLVPLGSL,SLGVFTCSW,RLVPLGSLGV,FFYRCICLPA,CGSALAFFYR,FYRCICLPAK,RSRLVPLGSL,MCGSALAFFY,VFTCSWTGPR,RPARSRLVPL,LAFFYRCICL,GSLGVFTCSW,SALAFFYRCI	STAD
ITIH1	c.760G>T	p.G254W	KGHVLFRPTVSQQQSCPTCSTSLLN[p.G254W]WHFKVTYDVSRDKICDLLVANNHFAH	SLLNWHFKV,TSLLNWHFK,STSLLNWHF,LNWHFKVTY,STSLLNWHFK,CSTSLLNWHF,LLNWHFKVTY,TSLLNWHFKV	LUAD
ITIH2	c.2524C>G	p.L842V	TLDKEMSFSVLLHRVWKKHPVNVDF[p.L842V]VGIYIPPTNKFSPKAHGLIGQFMQEP	VNVDFVGIY,NVDFVGIYI,HPVNVDFVG,VGIYIPPTNK,PVNVDFVGIY,HPVNVDFVGI	LUAD
ITK	c.586G>A	p.E196K	PEETVVIALYDYQTNDPQELALRRN[p.E196K]KEYCLLDSSEIHWWRVQDRNGHEGYV	LALRRNKEY,RRNKEYCLL,KEYCLLDSS,ALRRNKEYCL,ELALRRNKEY	CRC

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ITK	c.86G>T	p.R29L	FILLEEQLIKKSQQKRRTSPSNFKV[p.R29L]LFFVLTKASLAYFEDRHGKKRTLKGS	SNFKVLFFV,VLFFVLTKA,KVLFFVLTK,NFKVLFFVL,SPSNFKVLF,KVLFFVLTKA,TSPSNFKVLF,RTSPSNFKVL,SPSNFKVLFF,SNFKVLFFVL,LFFVLTKASL	LUAD
ITM2C	c.499G>A	p.E167K	ADIIHDFQRGLTAYHDISLDKCYVI[p.E167K]KLNTTIVLPPRNFWELLMNVKRGTYL	YVIKLNTTI,VIKLNTTIV,SLDKCYVIK,IKLNTTIVL,SLDKCYVIKL,YVIKLNTTIV,ISLDKCYVIK,CYVIKLNTTI	UCEC
ITPR1	c.4707G>T	p.M1569I	CGLERDKFDNKTVTFEEHIKEEHNM[p.M1569I]CHYLCFIVLVKVKDSTEYTGPESYVA	NMCHYLCFI,HNMCHYLCF,KEEHNMCHY,CHYLCFIVL,EEHNMCHYL,NMCHYLCFIV,HNMCHYLCFI,IKEEHNMCHY,KEEHNMCHYL,MCHYLCFIVL	TGCT
ITPR2	c.1073C>A	p.P358Q	RDGVPPTSKKKRQAGEKIMYTLVSV[p.P358Q]QHGNDIASLFELDATTLQRADCLVPR	IMYTLVSVQ,VQHGNDIAS,IMYTLVSVQH,VQHGNDIASL,QHGNDIASLF	LUAD
IWS1	c.2404delA	p.S802fs	FQATSKKGISRLDKQMRKFTDIRKK[p.S802fs]ADLHTQ*	RKFTDIRKKA	STAD
JAG1	c.1384G>A	p.A462T	DCLPGWMGQNCDININDCLGQCQND[p.A462T]TSCRDLVNGYRCICPPGYAGDHCERD	TSCRDLVNGY,CQNDTSCRDL	CRC
JAK1	c.928G>A	p.V310I	IFETSMLLISSENEMNWFHSNDGGN[p.V310I]ILYYEVMVTGNLGIQWRHKPNVVSVE	SNDGGNILY,NILYYEVMV,ILYYEVMVT,HSNDGGNIL,GNILYYEVM,HSNDGGNILY,SNDGGNILYY,FHSNDGGNIL	CRC
JAKMIP2	c.848G>T	p.R283I	MSSPKREIPGRAGDGSEHCSSPDLR[p.R283I]INQKRIAELNATIRKLEDRNTLLGDE	INQKRIAEL,RINQKRIAEL,SSPDLRINQK	UCEC
JARID2	c.1180_1181insG	p.G394fs	VNHTISGKTESSNAKTRKQVLSLGG[p.G394fs]GVQVHWARRQWPQGQWQVEPKVMH*	GQWQVEPKV,QWPQGQWQV,GVQVHWARR,RQWPQGQWQ,WQVEPKVMH,VLSLGGGVQV,RQWPQGQWQV,KQVLSLGGGV,LSLGGGVQVH,SLGGGVQVHW,VQVHWARRQW,ARRQWPQGQW,GQWQVEPKVM	STAD
JARID2	c.1266delG	p.V422fs	TGPAVNGLKVSGRLNPKSCTKEVGG[p.V422fs]GSCGRACSCGRGCGTPRGDWKRHTRRRSRSRPPRR*	CGRACSCGR,KRHTRRRSR,HTRRRSRSR,RRSRSRPPR,RSRSRPPRR,EVGGGSCGR,HTRRRSRSRP,RRRSRSRPPR	STAD
JHDM1D	c.289delA	p.R97fs	HHAVDIDLYHCPNCAVLHGSSLMKK[p.R97fs]GGTGTDMTTQKLMMVPNQCKLELELSLRNYALESSQVPMK*	MMVPNQCKL,MTTQKLMMV,LMMVPNQCK,VPNQCKLEL,ELSLRNYAL,KKGGTGTDM,TDMTTQKLM,NQCKLELEL,CKLELELSL,ALESSQVPM,LELSLRNYA,GTDMTTQKLM,LMMVPNQCKL,SLMKKGGTGT,KLMMVPNQCK,ALESSQVPMK,GTGTDMTTQK,YALESSQVPM,MKKGGTGTDM,TDMTTQKLMM,LELELSLRNY,LELSLRNYAL,RNYALESSQV	STAD
JHDM1D	c.938G>A	p.R313H	TSVWYHVLWGEKIFYLIKPTDENLA[p.R313H]HYESWSSSVTQSEVFFGDKVDKCYKC	PTDENLAHY,AHYESWSSS,DENLAHYES,KPTDENLAHY,AHYESWSSSV,DENLAHYESW	GBM
JMJD1C	c.3592C>A	p.R1198S	SHSVTTFRNDCRSPTHLTVSSTNTL[p.R1198S]SSMPALHRAPVFHPPIHHSLERKEGS	LSSMPALHR,SSMPALHRA,NTLSSMPAL,SSTNTLSSM,TLSSMPALHR,STNTLSSMPA,VSSTNTLSSM	LUAD
JMJD4	c.32C>T	p.A11V	MRAGPEPQAL[p.A11V]VGQKRGALRLLVPRLVLTVSAPAEVR	LVGQKRGAL,LVGQKRGALR	ACC
JMY	c.2429_2464delCACCACCACCTCCCCCACCTCCTCCCCCTCCCCCAC	p.PPPPPPPPPPPPP811del	LNNNLEPCSVTINPLPSPLPPTPPP[p.PPPPPPPPPPPP811del]LPVAKDSGPETLEKDLPRKEGNEKRIPKSASAPSAHLFDSSQLVSARKKLRKTAEGLQRRR	SPLPPTPPPL,LPPTPPPLPV	PAAD
JPH1	c.1183G>A	p.A395T	ARTKVEIANSRTAHARAKADAADQA[p.A395T]TLAARQECDIARAVARELSPDFYQPG	DAADQATLA,TLAARQECDI,DAADQATLAA,KADAADQATL	GBM
JPH3	c.1299G>C	p.Q433H	EARIARITAKEFSPSFQHRENGLEY[p.Q433H]HRPKRQTSCDDIEVLSTGTPLQQESP	NGLEYHRPKR,YHRPKRQTSC	CESC
JSRP1	c.275T>C	p.V92A	EKEPAARGTPGTGKERLKAGASPRS[p.V92A]APARKKAQTAPPLQPPPPPPALSEEL	KAGASPRSA,SPRSAPARK,RSAPARKKA,ASPRSAPARK,GASPRSAPAR,APARKKAQTA,LKAGASPRSA	KIRP

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JUP	c.1880C>T	p.S627L	RVAAGVLCELAQDKEAADAIDAEGA[p.S627L]LAPLMELLHSRNEGTATYAAAVLFRI	ALAPLMELL,AEGALAPLM,GALAPLMEL,DAIDAEGAL,DAIDAEGALA,IDAEGALAPL	CESC
KAL1	c.907G>A	p.V303I	SKHFRSSKDPSAPPAPANLRLANST[p.V303I]INSDGSVTVTIVWDLPEEPDIPVHHY	STINSDGSV,NLRLANSTI,TINSDGSVTV,NSTINSDGSV,ANLRLANSTI	CRC
KANK3	c.1076G>A	p.R359H	VEADAWVTEALLGLPAAAERELELL[p.R359H]HASLEHQRGVSELLRGRLRELEEARE	AERELELLH,RELELLHAS,LLHASLEHQR,AERELELLHA,RELELLHASL,LELLHASLEH	ACC
KANK4	c.757T>C	p.S253P	VQEGAEPPEGVVKVPNHLPLPGPPF[p.S253P]PFQNVLVVLEDKEDEHNAREAEVLFT	PLPGPPFPF,PFQNVLVVL,FPFQNVLVV,GPPFPFQNV,LPLPGPPFPF,GPPFPFQNVL,FPFQNVLVVL,PPFPFQNVLV	KIRC
KANSL3	c.1127G>A	p.G376E	IGWNTGALVACHVSVMEYVTAVVCL[p.G376E]EFPLLTVDGPRGDVDDPLLDMKTPVL	AVVCLEFPL,CLEFPLLTV,VTAVVCLEF,LEFPLLTVD,YVTAVVCLEF,TAVVCLEFPL	TGCT
KBTBD13	c.242C>T	p.A81V	GGFRATLQVLRGDRPALAAEDELLQ[p.A81V]VVECAAFLQAPALARFLEHNLTSDNC	QVVECAAFL,LQVVECAAF,AEDELLQVV,LLQVVECAAF,LQVVECAAFL,DELLQVVECA	ACC
KBTBD6	c.1325_1326insG	p.G442fs	LADRLLCREGMDVAYLNGYIYILGG[p.G442fs]ARPYYWS*	YILGGARPY,ILGGARPYY,YIYILGGAR,ILGGARPYYW,IYILGGARPY,YILGGARPYY,GYIYILGGAR	STAD
KBTBD8	c.1645G>A	p.V549I	YLKLVLFQNKLHLFVRATQVTVEEH[p.V549I]IFRTSRKNSLYQYDDIADQWMKVYET	VTVEEHIFR,TQVTVEEHI,IFRTSRKNSL,QVTVEEHIFR,TQVTVEEHIF	CRC
KCNA1	c.1126G>T	p.G376C	EAESHFSSIPDAFWWAVVSMTTVGY[p.G376C]CDMYPVTIGGKIVGSLCAIAGVLTIA	TTVGYCDMY,VGYCDMYPV,MTTVGYCDMY,TVGYCDMYPV,GYCDMYPVTI,SMTTVGYCDM	LUAD
KCNA3	c.1244C>T	p.A415V	TLKASMRELGLLIFFLFIGVILFSS[p.A415V]VVYFAEADDPTSGFSSIPDAFWWAVV	ILFSSVVYF,GVILFSSVV,VILFSSVVY,SSVVYFAEA,FIGVILFSSV,ILFSSVVYFA,FSSVVYFAEA,VILFSSVVYF,GVILFSSVVY	CRC
KCNB2	c.692G>A	p.R231H	STIALSLNTLPELQETDEFGQLNDN[p.R231H]HQLAHVEAVCIAWFTMEYLLRFLSSP	HQLAHVEAV,QLNDNHQLA,GQLNDNHQL,GQLNDNHQLA,HQLAHVEAVC,DEFGQLNDNH	BRCA
KCNC1	c.1363delA	p.K455fs	VPVIVNNFGMYYSLAMAKQKLPKKK[p.K455fs]RSIFRGHRSWDLPIIVNLS*	KQKLPKKKR,RSWDLPIIV,LPKKKRSIF,SIFRGHRSW,GHRSWDLPI,WDLPIIVNL,IFRGHRSWDL,KKRSIFRGHR,RGHRSWDLPI,LPKKKRSIFR,RSIFRGHRSW,GHRSWDLPII	STAD
KCND3	c.1313C>T	p.S438L	NQRADKRRAQKKARLARIRVAKTGS[p.S438L]LNAYLHSKRNGLLNEALELTGTPEEE	SLNAYLHSK,KTGSLNAYL,LNAYLHSKR,IRVAKTGSL,AKTGSLNAY,GSLNAYLHSK,KTGSLNAYLH,SLNAYLHSKR,RIRVAKTGSL,RVAKTGSLNA,VAKTGSLNAY,AKTGSLNAYL	CRC,UCEC
KCNH2	c.446G>C	p.G149A	MFILNFEVVMEKDMVGSPAHDTNHR[p.G149A]APPTSWLAPGRAKTFRLKLPALLALT	RAPPTSWLA,NHRAPPTSW,HRAPPTSWL	STAD
KCNH8	c.1365G>A	p.M455I	SSLTSVGFGNVSANTDAEKIFSICT[p.M455I]ILIGALMHALVFGNVTAIIQRMYSRW	KIFSICTIL,ILIGALMHA,SICTILIGA,IFSICTILI,CTILIGALM,EKIFSICTI,KIFSICTILI,FSICTILIGA,ILIGALMHAL,SICTILIGAL,AEKIFSICTI,EKIFSICTIL	LUAD
KCNJ10	c.305delC	p.P102fs	GTWFLFGVVWYLVAVAHGDLLELDP[p.P102fs]RPTTPPVWYRCTHSLEPSSSPLNPKPPLAMASATSVRNVHWPLCFLLPSWCSPPSWKSSSQVPSWRRLPGPRSGLRPFVSASMQLWPPTMASPAS*	LAMASATSV,SMQLWPPTM,MQLWPPTMA,SLEPSSSPL,NVHWPLCFL,RLPGPRSGL,AMASATSVR,SSSQVPSWR,SSQVPSWRR,VWYRCTHSL,RNVHWPLCF,VHWPLCFLL,SVRNVHWPL,SWCSPPSWK,SWRRLPGPR,SGLRPFVSA,PTTPPVWYR,DPRPTTPPV,SPLNPKPPL,KPPLAMASA,VPSWRRLPG,GPRSGLRPF,WPPTMASPA,FLLPSWCSP,KSSSQVPSW,SQVPSWRRL,LRPFVSASM,FVSASMQLW,ASMQLWPPT,WPLCFLLPS,LPSWCSPPS,LELDPRPTT,FLLPSWCSPP,SMQLWPPTMA,PLAMASATSV,LLPSWCSPPS,GLRPFVSASM,LAMASATSVR,PSWCSPPSWK,KSSSQVPSWR,SSSQVPSWRR,PFVSASMQLW,HSLEPSSSPL,SVRNVHWPLC,SWKSSSQVPS,SWRRLPGPRS,RSGLRPFVSA,ASMQLWPPTM,RPTTPPVWYR,MASATSVRNV,TSVRNVHWPL,NVHWPLCFLL,GPRSGLRPFV,RPFVSASMQL,SATSVRNVHW,VRNVHWPLCF,RNVHWPLCFL,WKSSSQVPSW,SQVPSWRRLP,RRLPGPRSGL,MQLWPPTMAS,WPLCFLLPSW,LPSWCSPPSW,DPRPTTPPVW	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KCNJ3	c.1290G>T	p.L430F	KITGREDFPKKLLRMSSTTSEKAYS[p.L430F]FGDLPMKLQRISSVPGNSEEKLVSKT	YSFGDLPMK,AYSFGDLPM,SFGDLPMKL,TTSEKAYSF,KAYSFGDLPM,AYSFGDLPMK,YSFGDLPMKL,STTSEKAYSF,SEKAYSFGDL	LUAD
KCNK17	c.61A>G	p.S21G	MYRPRARAAPEGRVRGCAVP[p.S21G]GTVLLLLAYLAYLALGTGVFWTLEGR	GTVLLLLAY,RVRGCAVPG,CAVPGTVLL,VPGTVLLLL,RVRGCAVPGT,PGTVLLLLAY,RGCAVPGTVL,CAVPGTVLL,VPGTVLLLLA	ACC
KCNK18	c.68G>T	p.G23V	MEVSGHPQARRCCPEALGKLFP[p.G23V]VLCFLCFLVTYALVGAVVFSAIEDGQ	ALGKLFPVL,KLFPVLCFL,VLCFLCFLV,EALGKLFPV,GKLFPVLCF,FPVLCFLCF,KLFPVLCFLC,LFPVLCFLCF,FPVLCFLCFL,LGKLFPVLCF,GKLFPVLCFL,PEALGKLFPV	LUAD
KCNK2	c.17C>G	p.S6W	MLPSA[p.S6W]WRERPGYRAGVAAPDLLDPKSAAQNS	AWRERPGYR,SAWRERPGY,MLPSAWRER,SAWRERPGYR,AWRERPGYRA,PSAWRERPGY	BLCA
KCNK2	c.497G>T	p.R166L	HWDLGSSFFFAGTVITTIGFGNISP[p.R166L]LTEGGKIFCIIYALLGIPLFGFLLAG	IGFGNISPL,SPLTEGGKIF	LUAD
KCNMB2	c.453T>G	p.N151K	KLLLYHTEETIKINQKCSYIPKCGK[p.N151K]KFEESMSLVNVVMENFRKYQHFSCYS	CGKKFEESM,KKFEESMSL,CSYIPKCGKK,SYIPKCGKKF,KKFEESMSLV	STAD
KCNS2	c.631G>A	p.D211N	SRVFSILSILVVMGSIITMCLNSLP[p.D211N]NFQIPDSQGNPGEDPRFEIVEHFGIA	MCLNSLPNF,CLNSLPNFQI,TMCLNSLPNF	UCEC
KCTD20	c.942delA	p.L314fs	KLYRFFKYIENRDVAKTVLKERGLK[p.L314fs]TFALELKVTLPVKKKLREGLAAGLKSSIIMYNAPSSRCHGKRKKGRVAMWISSVFEANPSRIW*	KTFALELKV,RVAMWISSV,GLKTFALEL,KLREGLAAG,KVTLPVKKK,IMYNAPSSR,SVFEANPSR,VAMWISSVF,ELKVTLPVK,KSSIIMYNA,SSRCHGKRK,KRKKGRVAM,KGRVAMWIS,GLKSSIIMY,LKERGLKTF,FALELKVTL,LELKVTLPV,KKLREGLAA,LAAGLKSSI,AGLKSSIIM,RKKGRVAMW,MWISSVFEA,FEANPSRIW,KERGLKTFA,ALELKVTLPV,KLREGLAAGL,GLAAGLKSSI,AMWISSVFEA,IMYNAPSSRC,SVFEANPSRI,GLKTFALELK,IIMYNAPSSR,TFALELKVTL,RVAMWISSVF,VFEANPSRIW,RGLKTFALEL,SSRCHGKRKK,KGRVAMWISS,AGLKSSIIMY,VTLPVKKKLR,VLKERGLKTF,KERGLKTFAL,LAAGLKSSII,AAGLKSSIIM,GKRKKGRVAM,RKKGRVAMWI,GRVAMWISSV,REGLAAGLKS	CRC
KCTD21	c.17C>T	p.T6M	MSDPI[p.T6M]MLNVGGKLYTTSLATLTSFPDSMLGA	MSDPIMLNV,MLNVGGKLY,IMLNVGGKL,IMLNVGGKLY	STAD
KDELC1	c.1339C>A	p.L447I	LKWAKDHDEEAKKIAKAGQEFARNN[p.L447I]IMGDDIFCYYFKLFQEYANLQVSEPQ	IMGDDIFCY,GQEFARNNI,QEFARNNIM,IMGDDIFCYY,NIMGDDIFCY,GQEFARNNIM,RNNIMGDDIF	CRC
KDM1B	c.1083C>A	p.F361L	HLSNLEYACGSNLHQVSARSWDHNE[p.F361L]LFAQFAGDHTLLTPGYSVIIEKLAEG	RSWDHNELF,ARSWDHNEL,DHNELFAQF,NELFAQFAG,SARSWDHNEL,RSWDHNELFA,ARSWDHNELF,WDHNELFAQF	UCEC
KDM3B	c.3946delC	p.P1316fs	SLRDLLHSGPGKLPQTPLDTGIPFP[p.P1316fs]RSSLHPQQE*	FPRSSLHPQ,IPFPRSSLH,TGIPFPRSSL	STAD
KDM5A	c.1267C>T	p.P423S	VSSIEEDVIVEYGADISSKDFGSGF[p.P423S]SVKDGRRKILPEEEEYALSGWNLNNM	SVKDGRRKI,DFGSGFSVK,KDFGSGFSV,SSKDFGSGFS,KDFGSGFSVK,SVKDGRRKIL	TGCT
KEAP1	c.1408C>T	p.R470C	PERDEWHLVAPMLTRRIGVGVAVLN[p.R470C]CLLYAVGGFDGTNRLNSAECYYPERN	VAVLNCLLY,AVLNCLLYA,VLNCLLYAV,CLLYAVGGF,GVAVLNCLLY,AVLNCLLYAV	LUSC
KEAP1	c.1438G>T	p.G480W	PMLTRRIGVGVAVLNRLLYAVGGFD[p.G480W]WTNRLNSAECYYPERNEWRMITAMNT	LYAVGGFDW,AVGGFDWTNR,LLYAVGGFDW,FDWTNRLNSA	LUSC
KEAP1	c.1807G>T	p.G603W	LDSVECYDPDTDTWSEVTRMTSGRS[p.G603W]WVGVAVTMEPCRKQIDQQNCTC*	RMTSGRSWV,SWVGVAVTM,SGRSWVGVA,TRMTSGRSW,GRSWVGVAV,RSWVGVAVT,MTSGRSWVGV,SGRSWVGVAV,RSWVGVAVTM,VTRMTSGRSW,RMTSGRSWVG	LUAD
KEAP1	c.431C>T	p.S144F	GMEVVSIEGIHPKVMERLIEFAYTA[p.S144F]FISMGEKCVLHVMNGAVMYQIDSVVR	FISMGEKCV,TAFISMGEK,FAYTAFISM,YTAFISMGE,LIEFAYTAF,IEFAYTAFI,RLIEFAYTAF,LIEFAYTAFI,FISMGEKCVL,YTAFISMGEK,IEFAYTAFIS,EFAYTAFISM	LUAD
KEAP1	c.463G>T	p.V155F	PKVMERLIEFAYTASISMGEKCVLH[p.V155F]FMNGAVMYQIDSVVRACSDFLVQQLD	VLHFMNGAV,FMNGAVMYQ,HFMNGAVMY,CVLHFMNGA,MGEKCVLHF,GEKCVLHFM,LHFMNGAVM,CVLHFMNGAV,FMNGAVMYQI,SMGEKCVLHF,LHFMNGAVMY,VLHFMNGAVM	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KEAP1	c.779G>T	p.R260L	DDLNVRCESEVFHACINWVKYDCEQ[p.R260L]LRFYVQALLRAVRCHSLTPNFLQMQL	QLRFYVQAL,KYDCEQLRF,LRFYVQALL,QLRFYVQALL,KYDCEQLRFY,WVKYDCEQLR,EQLRFYVQAL,VKYDCEQLRF,CEQLRFYVQA	LUAD
KEL	c.1231G>A	p.V411M	RKLSQKLRELTEQPPMPARPRWMKC[p.V411M]MEETGTFFEPTLAALFVREAFGPSTR	CMEETGTFF,KCMEETGTF,MKCMEETGTF,KCMEETGTFF	GBM
KHDRBS2	c.608C>T	p.S203L	LNGSEDSGRGRGIRGRGIRIAPTAP[p.S203L]LRGRGGAIPPPPPPGRGVLTPRGSTV	RIAPTAPLR,APLRGRGGA,PLRGRGGAI,IRIAPTAPL,GIRIAPTAPL,APLRGRGGAI	LUAD
KIAA0020	c.188A>G	p.K63R	RKVAKEGGPKVTSRNFEKSITKLGK[p.K63R]RGVKQFKNKQQGDKSPKNKFQPANKF	KSITKLGKR,ITKLGKRGV,RGVKQFKNK,LGKRGVKQF,ITKLGKRGVK,LGKRGVKQFK,KLGKRGVKQF	TGCT
KIAA0182	c.359_360insC	p.T120Ifs	STPKRVPMGPIIVPPGGHSVPSTPP[p.T120fs]RGDHRSNQNREWCLEE*	HSVPSTPPR,RSNQNREWCL	STAD
KIAA0195	c.2706delC	p.I902Ifs	GLETGWNCHISLTPNGDMPGSEIPP[p.I902fs]PAPATQAPCMMT*	APATQAPCM,SEIPPPAPA,APATQAPCMM,SEIPPPAPAT,MPGSEIPPPA	STAD
KIAA0240	c.2683delA	p.K895Ifs	PMNHDQFHLVPNHIVVSAEGNISKK[p.K895fs]QNALAEH*	ISKKQNALA,NISKKQNAL,KKQNALAEH	STAD
KIAA0528	c.542G>A	p.R181Q	YRAVIIHGFVEELVVNEDPEYQWID[p.R181Q]QIRTPRASNEARQRLISLMSGELQRK	EYQWIDQIR,WIDQIRTPR,PEYQWIDQI,QWIDQIRTPR,YQWIDQIRTP,DPEYQWIDQI	CRC
KIAA0556	c.3244C>T	p.R1082W	SHSITIDFTHPCHVALIRIWNYNKS[p.R1082W]WIHSFRGVKDITMLLDTQCIFEGEIA	WIHSFRGVK,YNKSWIHSF,KSWIHSFRG,NKSWIHSFR,RIWNYNKSW,WNYNKSWIH,NYNKSWIHSF,RIWNYNKSWI,KSWIHSFRGV,SWIHSFRGVK,YNKSWIHSFR,IRIWNYNKSW	CRC
KIAA0556	c.988C>A	p.L330I	FPDQERMCSRPGSRRERPLSATRKT[p.L330I]ICEAEYPEEDASAVLQAIQVENAALQ	ATRKTICEA,RKTICEAEY,RPLSATRKTI,TRKTICEAEY	UCEC
KIAA0586	c.4775delC	p.A1592fs	PRWESSATLRFTDAPCQDVSDAAVS[p.A1592fs]DLEDCSQSLSLSTMQEDMESSGADTF*	DVSDAAVSDL,SDLEDCSQSL	STAD
KIAA0907	c.1337A>C	p.Q446P	GQSPMGGPFIPAAPVKTALPAGPQP[p.Q446P]PPQPQPPLPSQPQAQKRRFTEELPDE	QPPPQPQPPL	BLCA
KIAA0907	c.1546_1547delAG	p.R516fs	TGFSSQNEIEGAGSKPASSSGKERE[p.R516fs]GQAVDASTSLSSDWNKNRVR*	TSLSSDWNK,LSSDWNKNR,QAVDASTSL,STSLSSDWNK,SLSSDWNKNR,KEREGQAVDA,REGQAVDAST,GQAVDASTSL,DASTSLSSDW	GBM
KIAA1109	c.14039T>C	p.L4680P	SMSLHGNHMTLACFHGPNFRSKSWA[p.L4680P]PFHLEEPNIAFWTEAQKIWEDGSSDH	RSKSWAPFH,KSWAPFHLE,FRSKSWAPF,SKSWAPFHL,NFRSKSWAPF,RSKSWAPFHL,APFHLEEPNI	CLL
KIAA1109	c.14810C>A	p.S4937Y	ITYTTVDWRDFMCNTWHLEPTLRLI[p.S4937Y]YWTGRKIDPVGVDYILQKLGFHHART	RLIYWTGRK,LEPTLRLIY,LIYWTGRKI,EPTLRLIYW,HLEPTLRLIY,RLIYWTGRKI,TLRLIYWTGR	CRC
KIAA1109	c.4763delA	p.E1588fs	ANSLLDRGMQLSGSTSNTPYTPLEK[p.E1588fs]NSLITQMMKH*	NSLITQMMK,EKNSLITQM,KNSLITQMM,TPLEKNSLI,KNSLITQMMK,LEKNSLITQM,EKNSLITQMM	STAD
KIAA1147	c.446C>T	p.A149V	YFRKGPFFGLACFANMPVESELERG[p.A149V]VRMKSVGILSPSYTLLYRYMHFLENQ	GVRMKSVGI,SELERGVRM,VRMKSVGIL,VESELERGV,GVRMKSVGIL,LERGVRMKSV	UCEC
KIAA1211	c.3608C>A	p.P1203Q	SVTVEISDSAPPAPLVKEVTKRFST[p.P1203Q]QDAAPVSTEPAWLALAKRKAKAWSDC	FSTQDAAPV,KRFSTQDAA,VTKRFSTQDA	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KIAA1211	c.924delT	p.R308fs	ERAPREEQQRSLEAPGWEDAERRER[p.R308fs]RSASAWRRRRSEGVCRPRPKRRRGGGWRRTPGWRSGGGRRRRKEDARRSSKGRRRRRLRDGKSWNSRRRRCRGRPRRWRRLGRAGGARRRRIWGKRRRRARRTWRTGGGSSVSF*	RSASAWRRR,SASAWRRRR,KRRRGGGWR,GWRRTPGWR,GWRSGGGRR,RSGGGRRRR,SGGGRRRRK,RSSKGRRRR,SSKGRRRRR,KGRRRRRLR,RRRRLRDGK,KSWNSRRRR,RRRCRGRPR,RGRPRRWRR,RWRRLGRAG,LGRAGGARR,RAGGARRRR,GARRRRIWG,ARRRRIWGK,RRRRIWGKR,RIWGKRRRR,RRRARRTWR,RARRTWRTG,DGKSWNSRR,RPRRWRRLG,RERRSASAW,RRLRDGKSW,RRRRARRTW,WRTGGGSSV,TGGGSSVSF,AERRERRSA,RTGGGSSVSF,RERRSASAWR,RSASAWRRRR,AWRRRRSEGV,KRRRGGGWRR,RSGGGRRRRK,RSSKGRRRRR,SSKGRRRRRL,KGRRRRRLRD,RRRRRLRDGK,RLRDGKSWNS,KSWNSRRRRC,NSRRRRCRGR,RRRRCRGRPR,RRRCRGRPRR,RCRGRPRRWR,RGRPRRWRRL,RPRRWRRLGR,RWRRLGRAGG,LGRAGGARRR,RAGGARRRRI,GARRRRIWGK,RIWGKRRRRA,RRRRARRTWR,RARRTWRTGG,TWRTGGGSSV,DARRSSKGRR,DGKSWNSRRR,SWNSRRRRCR,RPRPKRRRGG,RPKRRRGGGW,ERRERRSASA,RRERRSASAW,RRRLRDGKSW	CESC
KIAA1211	c.926_927insG	p.E309fs	RAPREEQQRSLEAPGWEDAERRERE[p.E309fs]GARAPGGGGGAKASAGPGSGGEAAAGGGRQAGGAEAAGGGGRKMRGGAQKAGGGGG*	RKMRGGAQK,KMRGGAQKA,REREGARAP,RQAGGAEAA,AERREREGA,RAPGGGGGAK,KMRGGAQKAG,REREGARAPG,RQAGGAEAAG,RKMRGGAQKA	CESC
KIAA1429	c.413C>T	p.S138F	LRGWYNCLTLAIYGSVDRVISHDRD[p.S138F]FPPPPPPPPPPPQPQPSLKRNPKHAD	RVISHDRDF	HNSC
KIAA1429	c.4576G>A	p.D1526N	VLSAPESLQNLFNNRTAYVLADVMD[p.D1526N]NQLKSMWFTPFQAEEIDTDLDLVKVD	VMDNQLKSM,MDNQLKSMW,VLADVMDNQL,DVMDNQLKSM,VMDNQLKSMW,MDNQLKSMWF	HNSC
KIAA1549	c.3816G>T	p.L1272F	DGERLSAVKSSDLINKMDLQRAAII[p.L1272F]FGYRIQGVIAQPVDRVKRPSPESQSN	RAAIIFGYR,LQRAAIIFG,QRAAIIFGY,AAIIFGYRI,FGYRIQGVI,IIFGYRIQGV,RAAIIFGYRI,IFGYRIQGVI,LQRAAIIFGY,MDLQRAAIIF	LUAD
KIAA1751	c.189G>C	p.L63F	LQEAEDDVDPGHSSSVKELDTDADK[p.L63F]FKKKTAEDRTQAFHLRQNLSALDKMH	KFKKKTAEDR,KELDTDADKF	LUSC
KIAA1751	c.291G>C	p.K97N	TQAFHLRQNLSALDKMHEEQELFTE[p.K97N]NMRGELRACRQRRDLIDKQQEAVAAE	EQELFTENM,EEQELFTEN,FTENMRGELR,NMRGELRACR,EEQELFTENM,TENMRGELRA	KIRC
KIAA1755	c.324A>C	p.Q108H	CLRDEVVVHLAPLNPLLLRQGDFYL[p.Q108H]HVEPQEEQSVCIMIKCLSLDLCTVDK	RQGDFYLHV,LLRQGDFYLH,RQGDFYLHVE	LUAD
KIAA1804	c.1420G>A	p.V474M	AALQQKSQEELLKRREQQLAEREID[p.V474M]MLERELNILIFQLNQEKPKVKKRKGK	MLERELNIL,REIDMLERE,QLAEREIDML,MLERELNILI,QQLAEREIDM,REIDMLEREL,IDMLERELNI	CRC
KIAA1804	c.1429C>T	p.R477W	QQKSQEELLKRREQQLAEREIDVLE[p.R477W]WELNILIFQLNQEKPKVKKRKGKFKR	EWELNILIF,EIDVLEWEL,DVLEWELNI,LEWELNILI,WELNILIFQ,VLEWELNILI,AEREIDVLEW,REIDVLEWEL,LEWELNILIF,WELNILIFQL	CRC
KIAA1967	c.1243delC	p.P415fs	TGIDLSGCTKWWRFAEFQYLQPGPP[p.P415fs]GGFRQWWCTCRMSGPSCLLWRSGRPCASRKLQRQLPQPRRHKGKRSLLNRHLMPWSKQQTLLDGTQKLQRPPHSRKRTLISQRPLHPP*	RQWWCTCRM,RMSGPSCLL,TLLDGTQKL,QTLLDGTQK,MSGPSCLLW,LWRSGRPCA,RSGRPCASR,SGRPCASRK,ASRKLQRQL,KGKRSLLNR,RSLLNRHLM,KLQRPPHSR,LQRPPHSRK,HSRKRTLIS,RTLISQRPL,SCLLWRSGR,MPWSKQQTL,PPHSRKRTL,LQPGPPGGF,CRMSGPSCL,RQLPQPRRH,RRHKGKRSL,KRSLLNRHL,LLNRHLMPW,LLNRHLMPWS,HLMPWSKQQT,LMPWSKQQTL,RSGRPCASRK,KLQRPPHSRK,MSGPSCLLWR,YLQPGPPGGF,RMSGPSCLLW,SLLNRHLMPW,SGRPCASRKL,LQRQLPQPRR,RQLPQPRRHK,KGKRSLLNRH,LNRHLMPWSK,LQRPPHSRKR,HSRKRTLISQ,RTLISQRPLH,GFRQWWCTCR,KLQRQLPQPR,MPWSKQQTLL,RPPHSRKRTL,FQYLQPGPPG,FRQWWCTCRM,RQWWCTCRMS,CRMSGPSCLL,RRHKGKRSLL,GKRSLLNRHL,KRSLLNRHLM,KRTLISQRPL	STAD
KIAA2022	c.1034G>T	p.C345F	NVRDKTTLLMQEDAQFNFFPSVFTT[p.C345F]FPKRESKSGALKQSSDFSQFKVPDVS	SVFTTFPKR,TTFPKRESK,PSVFTTFPK,FFPSVFTTF,FTTFPKRESK,NFFPSVFTTF,FPSVFTTFPK	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KIAA2026	c.1720C>T	p.R574C	PAKMILDNHDISVEMGVKSNYEIRI[p.R574C]CRPCEIKKTDCCKENLEKPRSPGEVT	RICRPCEIK,ICRPCEIKK,SNYEIRICR,YEIRICRPC,RICRPCEIKK,KSNYEIRICR,EIRICRPCEI	UCEC
KIAA2026	c.2069delA	p.K690fs	LEQSLQSHKKLKLTKMRAKKKKKKK[p.K690fs]RN*	RAKKKKKKKR	STAD
KIDINS220	c.2552A>G	p.N851S	SNINGHDYMRNIVHLPVFLNSRGLS[p.N851S]SARKFLVTSATNGDVPCSDTTGIQED	FLNSRGLSS,GLSSARKFL,SARKFLVTS,NSRGLSSAR,LSSARKFLV,RGLSSARKF,FLNSRGLSSA,GLSSARKFLV,NSRGLSSARK,RGLSSARKFL,SARKFLVTSA,SRGLSSARKF	TGCT
KIF13A	c.3345delA	p.K1115fs	LNCVRERWSDALIKRREYLDEQIKK[p.K1115fs]SAIKQRKQRTMWSGKPSLWSSG*	TMWSGKPSL,KQRTMWSGK,MWSGKPSLW,KQRKQRTMW,RTMWSGKPS,SAIKQRKQR,IKQRKQRTM,YLDEQIKKSA,TMWSGKPSLW,KSAIKQRKQR,AIKQRKQRTM,KQRKQRTMWS,RKQRTMWSGK,KQRTMWSGKP,RTMWSGKPSL,QIKKSAIKQR,IKQRKQRTMW	STAD
KIF14	c.1793G>A	p.R598Q	VFTLVMTQTKTEFVEGEEHDHRITS[p.R598Q]QINLIDLAGSERCSTAHTNGDRLKEG	RITSQINLI,SQINLIDLA,HRITSQINL,HRITSQINLI,SQINLIDLAG	CRC
KIF15	c.754G>C	p.E252Q	TSMNRESSRSHAVFTITIESMEKSN[p.E252Q]QIVNIRTSLLNLVDLAGSERQKDTHA	SMEKSNQIV,KSNQIVNIR,ESMEKSNQI,QIVNIRTSLL,ESMEKSNQIV,IESMEKSNQI,MEKSNQIVNI,NQIVNIRTSL	LUAD
KIF16B	c.434G>A	p.R145Q	GLIPRICEGLFSRINETTRWDEASF[p.R145Q]QTEVSYLEIYNERVRDLLRRKSSKTF	SFQTEVSYL,ASFQTEVSY,DEASFQTEV,QTEVSYLEIY,FQTEVSYLEI,EASFQTEVSY,ASFQTEVSYL,DEASFQTEVS	CRC
KIF18A	c.49C>T	p.R17C	MSVTEEDLCHHMKVVV[p.R17C]CVRPENTKEKAAGFHKVVHVVDKHIL	HMKVVVCVR,VVCVRPENTK,CVRPENTKEK,HHMKVVVCVR	CRC
KIF1B	c.3958C>T	p.R1320W	TVTIIHEKGSELHWKDVRELVVGRI[p.R1320W]WNKPEVDEAAVDAILSLNIISAKYLK	LVVGRIWNK,RELVVGRIW	BRCA
KIF20B	c.160G>A	p.E54K	NFDGIKLDLSHEFSLVAPNTEANSF[p.E54K]KSKDYLQVCLRIRPFTQSEKELESEG	KSKDYLQVC,FKSKDYLQV,NTEANSFKSK,SFKSKDYLQV,KSKDYLQVCL,EANSFKSKDY	UCEC
KIF20B	c.2971G>A	p.E991K	NEIETATRSITNNVSQIKLMHTKID[p.E991K]KLRTLDSVSQISNIDLLNLRDLSNGS	LMHTKIDKL,KLMHTKIDK,KLRTLDSVS,TKIDKLRTL,KLMHTKIDKL,HTKIDKLRTL,LMHTKIDKLR	CRC
KIF23	c.1048G>A	p.E350K	KEQITISQLSLVDLAGSERTNRTRA[p.E350K]KGNRLREAGNINQSLMTLRTCMDVLR	RTNRTRAKG,RTRAKGNRL,RTRAKGNRLR,RAKGNRLREA	BLCA
KIF23	c.449G>A	p.R150Q	SPGEGGLLPRCLDMIFNSIGSFQAK[p.R150Q]QYVFKSNDRNSMDIQCEVDALLERQK	FQAKQYVFK,SFQAKQYVF,IGSFQAKQY,SFQAKQYVFK,KQYVFKSNDR,SIGSFQAKQY,GSFQAKQYVF	UCEC
KIF25	c.7T>A	p.W3R	MT[p.W3R]RTSGQLQREKQARPGSGAVLAFPDDK	MTRTSGQLQ,RTSGQLQREK,MTRTSGQLQR	PRAD
KIF26B	c.3194delC	p.S1065fs	SLQSSRESLNSCGFVEGKPRPMGSP[p.S1065fs]GWASPACPRPRSTSHPALLPRDAKSTPRRGSCRLPPHCLPRARIPAWRLGSPCCSPRCVRPRLE*	RLPPHCLPR,TSHPALLPR,RSTSHPALL,RGSCRLPPH,RARIPAWRL,STPRRGSCR,KPRPMGSPG,RPMGSPGWA,CPRPRSTSH,RPRSTSHPA,HPALLPRDA,TPRRGSCRL,LPRARIPAW,IPAWRLGSP,SPRCVRPRL,LPPHCLPRA,RLPPHCLPRA,STSHPALLPR,RPRSTSHPAL,KSTPRRGSCR,RARIPAWRLG,WASPACPRPR,LPRARIPAWR,RLGSPCCSPR,KPRPMGSPGW,RPMGSPGWAS,SPACPRPRST,IPAWRLGSPC,MGSPGWASPA	STAD
KIF26B	c.3337G>A	p.V1113M	RCKVYTQKGVLPSPAPLPPSSKDSG[p.V1113M]MASRESLLQPEVRTPPVGMSPQVLKK	GMASRESLL,SGMASRESL,SSKDSGMASR,LPPSSKDSGM,SGMASRESLL	BRCA
KIF26B	c.3341C>T	p.A1114V	CKVYTQKGVLPSPAPLPPSSKDSGV[p.A1114V]VSRESLLQPEVRTPPVGMSPQVLKKS	SSKDSGVVSR	CRC
KIF26B	c.6097G>A	p.A2033T	SKEAMCFNAKLKILEHRQQRIAEVR[p.A2033T]TKYEWLMKELEATKQYLMLDPNKWLS	RTKYEWLMK,RIAEVRTKY,EVRTKYEWL,AEVRTKYEW,QQRIAEVRTK,RTKYEWLMKE,RQQRIAEVRT,QRIAEVRTKY,AEVRTKYEWL,TKYEWLMKEL,IAEVRTKYEW	LIHC
KIF27	c.2775G>T	p.K925N	LDACNLKRRKGSFGSIDHLQKLDEQ[p.K925N]NKWLDEEVEKVLNQRQELEELEADLK	KLDEQNKWL,EQNKWLDEEV,LQKLDEQNKW	UCEC

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KIF9	c.1438G>A	p.G480R	ISAIQKAGLVDVDGHLVGEPEGQNF[p.G480R]RLGVAPFSTKPGKKAKSKKTFKEPLS	NFRLGVAPF,GQNFRLGVA,RLGVAPFSTK,QNFRLGVAPF,GEPEGQNFRL	LUAD
KIF9	c.1781G>A	p.R594Q	IRPDTPPSKPVAFEEFKNEQGSEIN[p.R594Q]QIFKENKSILNERRKRASETTQHINA	GSEINQIFK,QGSEINQIFK,EQGSEINQIF,NQIFKENKSI,NEQGSEINQI	UCEC
KIRREL	c.1003delC	p.P335fs	VDPKPTTTDIGSDVTLTCVWVGNPP[p.P335fs]SLSPGPKRTQIWS*	VWVGNPPSL,SPGPKRTQI,CVWVGNPPSL,SPGPKRTQIW	STAD
KIRREL	c.1810G>T	p.G604C	VDLKQDLRCDTIDTREEYEMKDPTN[p.G604C]CYYNVRAHEDRPSSRAVLYADYRAPG	EMKDPTNCY,PTNCYYNVR,MKDPTNCYY,YEMKDPTNC,DPTNCYYNV,EMKDPTNCYY,YEMKDPTNCY	LUAD
KIRREL2	c.1947delC	p.V649fs	PPSPLGPPGTPTFYDFNPHLGMVPP[p.V649fs]ADFTEPGQAISPHPTLELSPATSNPHPLGPQIWPPGLPPSHMLPSPHLATRVSRLTCDIFPMEESWDLQLAIMDCSDF*	HMLPSPHLA,RLTCDIFPM,HLATRVSRL,ATRVSRLTC,LPSPHLATR,ESWDLQLAI,HPTLELSPA,NPHPLGPQI,SPHLATRVS,FPMEESWDL,LAIMDCSDF,LGMVPPADF,GQAISPHPT,QAISPHPTL,SHMLPSPHL,VSRLTCDIF,MEESWDLQL,EPGQAISPH,EESWDLQLA,DIFPMEESW,AISPHPTLEL,HLATRVSRLT,IFPMEESWDL,MLPSPHLATR,ESWDLQLAIM,NPHLGMVPPA,SPATSNPHPL,WPPGLPPSHM,LPSPHLATRV,QLAIMDCSDF,HLGMVPPADF,ADFTEPGQAI,GQAISPHPTL,HMLPSPHLAT,RVSRLTCDIF,SRLTCDIFPM,EESWDLQLAI,HPTLELSPAT,NPHPLGPQIW,FPMEESWDLQ,MEESWDLQLA	STAD
KIT	c.1669T>G	p.W557G	VAGMMCIIVMILTYKYLQKPMYEVQ[p.W557G]GKVVEEINGNNYVYIDPTQLPYDHKW	PMYEVQGKV,VQGKVVEEI,EVQGKVVEEI,KPMYEVQGKV	TGCT
KIT	c.2446G>C	p.D816H	RDLAARNILLTHGRITKICDFGLAR[p.D816H]HIKNDSNYVVKGNARLPVKWMAPESI	HIKNDSNYV,RHIKNDSNY,CDFGLARHI,HIKNDSNYVV,ARHIKNDSNY,RHIKNDSNYV	TGCT
KIT	c.2446G>T	p.D816Y	RDLAARNILLTHGRITKICDFGLAR[p.D816Y]YIKNDSNYVVKGNARLPVKWMAPESI	ICDFGLARY,YIKNDSNYV,RYIKNDSNY,DFGLARYIK,CDFGLARYI,YIKNDSNYVV,KICDFGLARY,RYIKNDSNYV,ARYIKNDSNY	TGCT
KIT	c.2447A>T	p.D816V	RDLAARNILLTHGRITKICDFGLAR[p.D816V]VIKNDSNYVVKGNARLPVKWMAPESI	VIKNDSNYV,RVIKNDSNY,CDFGLARVI,RVIKNDSNYV,VIKNDSNYVV,ARVIKNDSNY	LAML,TGCT
KIT	c.2464A>T	p.N822Y	NILLTHGRITKICDFGLARDIKNDS[p.N822Y]YVVKGNARLPVKWMAPESIFNCVYT	KNDSYYVVK,SYYVVKGNA,RDIKNDSYY,YYVVKGNAR,DIKNDSYYV,IKNDSYYVV,YYVVKGNARL,LARDIKNDSY,SYYVVKGNAR,DIKNDSYYVV,DSYYVVKGNA	TGCT
KIT	c.2466T>G	p.N822K	NILLTHGRITKICDFGLARDIKNDS[p.N822K]KYVVKGNARLPVKWMAPESIFNCVYT	KNDSKYVVK,RDIKNDSKY,IKNDSKYVV,KYVVKGNARL,LARDIKNDSK	TGCT
KLC2	c.1703delC	p.T568fs	SFGKLRDALRRSSEMLVKKLQGGTP[p.T568fs]RSPLTPG*	TPRSPLTPG,LQGGTPRSPL	STAD
KLF3	c.312delA	p.I104fs	SLKFPSSHRRASPGLSMPSSSPPIK[p.I104fs]NTHPLLQACSPSACRCPCHQ*	LLQACSPSA,QACSPSACR,PPIKNTHPL,SPSACRCPC,LQACSPSAC,SPPIKNTHPL	STAD
KLF3	c.671_672insC	p.S224fs	GIEPQRTDYYPEEMSPPLMNSVSPP[p.S224fs]ASIVARESPFGHRAAWEETFTCGIPGYSKEAEDTQM*	LMNSVSPPA,SVSPPASIV,TFTCGIPGY,NSVSPPASI,FTCGIPGYS,SPFGHRAAW,SIVARESPF,RESPFGHRA,HRAAWEETF,SKEAEDTQM,WEETFTCGI,PLMNSVSPPA,FTCGIPGYSK,VARESPFGHR,ETFTCGIPGY,NSVSPPASIV,ASIVARESPF,LMNSVSPPAS,MNSVSPPASI,RESPFGHRAA,GHRAAWEETF,YSKEAEDTQM	STAD
KLF4	c.1300A>C	p.K434Q	GRRSWPRKRTATHTCDYAGCGKTYT[p.K434Q]QSSHLKAHLRTHTGEKPYHCDWDGCG	KTYTQSSHL,TQSSHLKAH,KTYTQSSHLK,QSSHLKAHLR,GKTYTQSSHL,TQSSHLKAHL	BRCA
KLF5	c.1255G>C	p.E419Q	LRTHTGEKPYKCTWEGCDWRFARSD[p.E419Q]QLTRHYRKHTGAKPFQCGVCNRSFSR	RSDQLTRHY,FARSDQLTR,DQLTRHYRK,WRFARSDQL,RSDQLTRHYR,ARSDQLTRHY	LUAD,LUSC
KLF5	c.353C>T	p.S118L	EKYLTPQLPPVPIIPEHKKYRRDSA[p.S118L]LVVDQFFTDTEGLPYSINMNVFLPDI	KYRRDSALV,SALVVDQFF,KKYRRDSAL,YRRDSALVV,KYRRDSALVV,HKKYRRDSAL,KKYRRDSALV,RDSALVVDQF	BLCA
KLHDC2	c.962G>C	p.W321S	DAWTYCISKNEWIQFNHPYTEKPRL[p.W321S]SHTACASDEGEVIVFGGCANNLLVHH	KPRLSHTAC,KPRLSHTACA,TEKPRLSHTA	TGCT

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KLHDC7A	c.1903G>A	p.E635K	DRWDFAPPLPSDTFALAHTATVRAK[p.E635K]KIFVTGGSLRFLLFRFSAQEQRWWAG	HTATVRAKK,TVRAKKIFV,RAKKIFVTG,KIFVTGGSL,KIFVTGGSLR,TVRAKKIFVT,RAKKIFVTGG,HTATVRAKKI,KKIFVTGGSL	SKCM
KLHL13	c.637G>A	p.E213K	FLISGVTLDNCVEVGRIANTYNLTE[p.E213K]MDKYVNSFVLKNFPALLSTGEFLKLP	NLTEMDKYV,EMDKYVNSF,ANTYNLTEM,TEMDKYVNS,EMDKYVNSFV,NTYNLTEMDK,TEMDKYVNSF,IANTYNLTEM,MDKYVNSFVL	UCEC
KLHL14	c.693delC	p.P231fs	KYLVEDVLLLNFEEMRALLDSLPPP[p.P231fs]WSRSWRSSRCPCCGWSTTARPACSMRLTS*	WSRSWRSSR,SWRSSRCPC,TARPACSMR,DSLPPPWSR,TTARPACSM,RPACSMRLT,LLDSLPPPW,LPPPWSRSW,TTARPACSMR,RSWRSSRCPC,SWRSSRCPCC,SSRCPCCGWS,STTARPACSM,TARPACSMRL,RPACSMRLTS,ALLDSLPPPW,SLPPPWSRSW,RSSRCPCCGW	STAD
KLHL15	c.554A>G	p.D185G	DNFVPLMSRPDFLSYLSFEKLMSYL[p.D185G]GNDHLSRFPEIELYEAVQSWLRHDRR	MSYLGNDHL,LMSYLGNDH,LGNDHLSRF,FEKLMSYLG,LMSYLGNDHL,YLGNDHLSRF,SYLGNDHLSR	BLCA
KLHL28	c.97G>A	p.E33K	YMLANLTHLHSEQLLQGLNLLRQHH[p.E33K]KLCDIILRVGDVKIHAHKVVLASVSP	KLCDIILRV,LNLLRQHHK,NLLRQHHKL,RQHHKLCDI,GLNLLRQHHK,RQHHKLCDII	UCEC
KLHL5	c.976C>T	p.R326C	QLSQVVEACCKFLMKQLHPSNCLGI[p.R326C]CSFADAQGCTDLHKVAHNYTMEHFME	SNCLGICSF	CRC
KLK2	c.169C>A	p.P57T	EKHSQPWQVAVYSHGWAHCGGVLVH[p.P57T]TQWVLTAAHCLKKNSQVWLGRHNLFE	VLVHTQWVL,GVLVHTQWV,HTQWVLTAA,TQWVLTAAH,VHTQWVLTAA	CRC
KLK2	c.481G>A	p.E161K	VKVLGLPTQEPALGTTCYASGWGSI[p.E161K]KPEEFLRPRSLQCVSLHLLSNDMCAR	YASGWGSIK,SIKPEEFLR,GSIKPEEFLR,GWGSIKPEEF	CESC
KLK6	c.359G>A	p.R120H	QSSVVRAVIHPDYDAASHDQDIMLL[p.R120H]HLARPAKLSELIQPLPLERDCSANTT	MLLHLARPA,LLHLARPAK,DIMLLHLAR,IMLLHLARPA,LLHLARPAKL,MLLHLARPAK,HDQDIMLLHL	GBM
KPNA4	c.86G>A	p.R29Q	NEKLDNQRLKNFKNKGRDLETMRRQ[p.R29Q]QNEVVVELRKNKRDEHLLKRRNVPHE	QQNEVVVEL,TMRRQQNEV,RRQQNEVVV,RQQNEVVVE,TMRRQQNEVV,ETMRRQQNEV,MRRQQNEVVV,RQQNEVVVEL	CRC
KPRP	c.1659_1660insC	p.E553fs	YCGPSSYNQGQESGAGCGPGDVFPE[p.E553fs]PEGSGWPWRPRQCLCWSERGSKECLFLKER*	GSKECLFLK,WPWRPRQCL,RPRQCLCWS,SERGSKECL,FPEPEGSGW,EPEGSGWPW,CLCWSERGSK,RGSKECLFLK,EGSGWPWRPR,SERGSKECLF	HNSC
KRAS	c.176C>G	p.A59G	PTIEDSYRKQVVIDGETCLLDILDT[p.A59G]GGQEEYSAMRDQYMRTGEGFLCVFAI	LDTGGQEEY,GGQEEYSAM,ILDTGGQEEY	MM
KRAS	c.180_181TC>AA	p.Q61K	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61K]KEEYSAMRDQYMRTGEGFLCVFAINNT	LDTAGKEEY,AGKEEYSAM,ILDTAGKEEY,DTAGKEEYSA	CRC,THCA
KRAS	c.182A>G	p.Q61R	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61R]REEYSAMRDQYMRTGEGFLCVFAINN	LDTAGREEY,AGREEYSAM,ILDTAGREEY,AGREEYSAMR,DTAGREEYSA	MM,TGCT
KRAS	c.182A>T	p.Q61L	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61L]LEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGLEEY,AGLEEYSAM,ILDTAGLEEY,LLDILDTAGL,DTAGLEEYSA	CRC,LUAD,TGCT
KRAS	c.183A>C	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	LUAD,PAAD,STAD
KRAS	c.183A>T	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	MM,TGCT
KRAS	c.34G>A	p.G12S	MTEYKLVVVGA[p.G12S]SGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGASGV,KLVVVGASGV,YKLVVVGASG	CRC,STAD
KRAS	c.34G>C	p.G12R	MTEYKLVVVGA[p.G12R]RGVGKSALTIQLIQNHFVDEYDPTIE	ARGVGKSAL,KLVVVGARGV,VVVGARGVGK,EYKLVVVGAR,GARGVGKSAL,RGVGKSALTI	MM,PAAD,TGCT
KRAS	c.34G>T	p.G12C	MTEYKLVVVGA[p.G12C]CGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGACGV,VVGACGVGK,KLVVVGACGV,VVVGACGVGK	CRC,LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KRAS	c.35G>A	p.G12D	MTEYKLVVVGA[p.G12D]DGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGADGV,VVGADGVGK,KLVVVGADGV,VVVGADGVGK	CESC,CRC,GBM,KIRP,LAML,LUAD,MM,PAAD,STAD,UCEC,UCS
KRAS	c.35G>C	p.G12A	MTEYKLVVVGA[p.G12A]AGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGAAGV,VVGAAGVGK,YKLVVVGAA,KLVVVGAAGV,VVVGAAGVGK,YKLVVVGAAG,GAAGVGKSAL	CRC,LUAD,MM,TGCT,UCEC
KRAS	c.35G>T	p.G12V	MTEYKLVVVGA[p.G12V]VGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGAVGV,VVGAVGVGK,YKLVVVGAV,KLVVVGAVGV,VVVGAVGVGK,GAVGVGKSAL	BRCA,CESC,CRC,LUAD,OV,PAAD,TGCT,UCEC,UCS
KRAS	c.37G>T	p.G13C	MTEYKLVVVGAG[p.G13C]CVGKSALTIQLIQNHFVDEYDPTIED	VVGAGCVGK,KLVVVGAGCV,VVVGAGCVGK	LUAD
KRAS	c.38G>A	p.G13D	MTEYKLVVVGAG[p.G13D]DVGKSALTIQLIQNHFVDEYDPTIED	VVGAGDVGK,KLVVVGAGDV,VVVGAGDVGK	CESC,CLL,CRC,DLBCL,LUAD,MM,STAD,UCEC
KRAS	c.436G>A	p.A146T	PSRTVDTKQAQDLARSYGIPFIETS[p.A146T]TKTRQRVEDAFYTLVREIRQYRLKKI	ETSTKTRQR,GIPFIETSTK,ETSTKTRQRV	CRC,MM,TGCT
KRBA1	c.2515A>G	p.R839G	DRLATALAGLAQEVATMRTQVNRLG[p.R839G]GRPQGPGPMGQASWMWTLPRGPRWAH	RTQVNRLGG,TQVNRLGGR,RTQVNRLGGR	TGCT
KRT2	c.896T>G	p.L299W	KRTAAENDFVTLKKDVDNAYMIKVE[p.L299W]WQSKVDLLNQEIEFLKVLYDAEISQI	YMIKVEWQS,MIKVEWQSK,IKVEWQSKV,VEWQSKVDL,NAYMIKVEW,MIKVEWQSKV,YMIKVEWQSK,VEWQSKVDLL	KIRC
KRT4	c.462_463insC	p.F154fs	RGNKSISMSVAGSRQGACFGGAGGF[p.F154fs]RHWWLWWWIWGLLQW*	WLWWWIWGL,GGFRHWWLW,GFRHWWLWW,FRHWWLWWW,RHWWLWWWI,HWWLWWWIW,LWWWIWGLL,WWIWGLLQW,CFGGAGGFR,GGAGGFRHW,WLWWWIWGLL,AGGFRHWWLW,GFRHWWLWWW,RHWWLWWWIW,WWLWWWIWGL,WWWIWGLLQW,FGGAGGFRHW	KIRC
KRT6B	c.590T>C	p.L197P	NKFASFIDKVRFLEQQNKVLDTKWT[p.L197P]PLQEQGTKTVRQNLEPLFEQYINNLR	VLDTKWTPL,KVLDTKWTPL	CRC
KRT8	c.175T>G	p.S59A	TQKSYKVSTSGPRAFSSRSYTSGPG[p.S59A]ARISSSSFSRVGSSNFRGGLGGGYGG	RSYTSGPGA,GARISSSSF,SYTSGPGAR,YTSGPGARI,RSYTSGPGAR,SYTSGPGARI,GARISSSSFS	ACC,KIRP,LIHC
KRTAP1-1	c.346A>G	p.I116V	CGTGCGIGGGIGYGQEGSSGAVSTR[p.I116V]VRWCRPDCRVEGTCLPPCCVVSCTPP	VSTRVRWCR,STRVRWCRP,RVRWCRPDC,GAVSTRVRW,AVSTRVRWCR,STRVRWCRPD,RVRWCRPDCR,SGAVSTRVRW	TGCT
KRTAP27-1	c.372G>T	p.M124I	ACQSESSSAGLACVSQPCQSESTQQ[p.M124I]IGFVAQSCQPASLKGNSCPPKTSKSK	CQSESTQQI,ESTQQIGFV,SESTQQIGF,QSESTQQIGF,QQIGFVAQSC,SESTQQIGFV	LUAD
KRTAP4-11	c.144C>G	p.S48R	TCCRPSCCETTCCRTTYCRPSCCVS[p.S48R]RCCRPQCCQSVCCQPTCCRPRCCISS	VSRCCRPQC	GBM,PRAD
KRTAP4-5	c.220A>T	p.S74C	VCYQPTCCHPSCCISSCCRPYCCES[p.S74C]CCCRPCCCQTTCCRTTCCRTTCCCPS	CESCCCRPC	KIRP
KRTAP4-5	c.272G>T	p.C91F	CRPYCCESSCCRPCCCQTTCCRTTC[p.C91F]FRTTCCCPSCCVSSCCRPQCCQSVCC	TCCRTTCFR,TTCCRTTCFR	LUAD

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KRTAP4-8	c.188C>G	p.T63S	TCYRPSYSVSCCCRPQCCQSVCCQP[p.T63S]SCCRPSCCVSSCCKPQCCQSVCCQPT	SVCCQPSCCR	TGCT
KRTAP4-9	c.53A>T	p.D18V	MVSSCCGSVCSDQGCGQ[p.D18V]VLCQETCCRPSCCETTCCRTTCCRPS	CSDQGCGQV,SDQGCGQVL,QVLCQETCCR	PRAD
KRTAP5-1	c.578C>A	p.S193Y	GSCGGSKGGCGSCGGCKGGCGSCGG[p.S193Y]YKGGCGSGCGGCGSGCGVPVCCCSCS	GGCGSCGGY,KGGCGSCGGY	LUAD
KSR2	c.1664C>T	p.T555M	FNLPASHYYKYKQQFIFPDVVPVPE[p.T555M]MPTRAPQVILHPVTSNPILEGNPLLQ	MPTRAPQVI,FPDVVPVPEM,MPTRAPQVIL,PEMPTRAPQV	HNSC
L1CAM	c.1894C>A	p.R632S	LVVGSPGPVPRLVLSDLHLLTQSQV[p.R632S]SVSWSPAEDHNAPIEKYDIEFEDKEM	LLTQSQVSV,QVSVSWSPA,TQSQVSVSW,SQVSVSWSP,HLLTQSQVSV,SQVSVSWSPA,LTQSQVSVSW	LUAD
L1CAM	c.557C>T	p.T186M	PPSAEPLRIYWMNSKILHIKQDERV[p.T186M]MMGQNGNLYFANVLTSDNHSDYICHA	MMGQNGNLY,VMMGQNGNL,HIKQDERVM,IKQDERVMM,VMMGQNGNLY,MMGQNGNLYF,RVMMGQNGNL,LHIKQDERVM	CRC
L2HGDH	c.1321_1323delCCT	p.P441del	VEDFVFDAGVGDIGNRILHVRNAPS[p.P441del]AATSSIAISGMIADEVQQRFEL*	HVRNAPSAA,SAATSSIAI,APSAATSSI,LHVRNAPSA,ILHVRNAPSA,HVRNAPSAAT,NAPSAATSSI,APSAATSSIA,LHVRNAPSAA	TGCT
L3MBTL4	c.485G>T	p.W162L	HPVGWCEKTKHELHIPKGYRKDKFV[p.W162L]LMDYLKACKLQNAPKKLFRNRSPNGP	VLMDYLKAC,LMDYLKACK,KFVLMDYLK,KDKFVLMDY,YRKDKFVLM,LMDYLKACKL,VLMDYLKACK,KGYRKDKFVL,RKDKFVLMDY	LUAD
LACTB	c.13A>C	p.M5L	MYRL[p.M5L]LSAVTARAAAPGGLASSCGRRGVHQR	LLSAVTARA,RLLSAVTAR,YRLLSAVTA,RLLSAVTARA,LLSAVTARAA,MYRLLSAVTA,LSAVTARAAA	ACC
LALBA	c.121G>A	p.A41T	AILAKQFTKCELSQLLKDIDGYGGI[p.A41T]TLPELICTMFHTSGYDTQAIVENNES	TLPELICTM,IDGYGGITL,GYGGITLPEL,TLPELICTMF,ITLPELICTM	CRC
LAMA1	c.3088G>T	p.D1030Y	NTCDPETGECVCPPHTQGVKCEECE[p.D1030Y]YGHWGYDAEVGCQACNCSLVGSTHHR	GVKCEECEY,CEYGHWGYDA,EECEYGHWGY	LUAD
LAMA4	c.1673C>T	p.A558V	SLSTSADSLTTPRLTLSELDDIIKN[p.A558V]VSGIYAEIDGAKSELQVKLSNLSNLS	ELDDIIKNV,NVSGIYAEI,IIKNVSGIY,DIIKNVSGI,IKNVSGIYA,IIKNVSGIYA,DIIKNVSGIY,KNVSGIYAEI,SELDDIIKNV	CRC
LAMA4	c.1915G>A	p.E639K	NGLVQKALDASNVYENIVNYVSEAN[p.E639K]KTAEFALNTTDRIYDAVSGIDTQIIY	VNYVSEANK,YVSEANKTA,EANKTAEFA,SEANKTAEF,IVNYVSEANK,EANKTAEFAL,VSEANKTAEF,SEANKTAEFA	BLCA
LAMA4	c.3879G>A	p.M1293I	PNGLLFYYASGSDVFSISLDNGTVI[p.M1293I]IDVKGIKVQSVDKQYNDGLSHFVISS	SLDNGTVII,VIIDVKGIK,TVIIDVKGI,VIIDVKGIKV,TVIIDVKGIK,ISLDNGTVII	LUSC
LAMA5	c.6668T>G	p.L2223R	SSMAWARLHRLNASIADLQSQLRSP[p.L2223R]RGPRHETAQQLEVLEQQSTSLGQDAR	QLRSPRGPR,LQSQLRSPR,SPRGPRHET,SQLRSPRGPR,QLRSPRGPRH,DLQSQLRSPR,SPRGPRHETA	KIRP
LAMB4	c.1762G>T	p.G588W	GLAPLGSETFGQSPAVHVVLGEPVP[p.G588W]WNPVTWTGPGFARVLPGAGLRFAVNN	GEPVPWNPV,VVLGEPVPW,HVVLGEPVPW,EPVPWNPVTW	LUAD
LAMB4	c.3715G>T	p.G1239W	EADFKDLRGNVSEIERILKHPVFPS[p.G1239W]WKFLKVKDYHDSVRRQIMQLNEQLKA	VFPSWKFLK,KHPVFPSWK,FPSWKFLKV,HPVFPSWKF,LKHPVFPSW,WKFLKVKDY,PVFPSWKFLK,KHPVFPSWKF,VFPSWKFLKV,SWKFLKVKDY,HPVFPSWKFL,ILKHPVFPSW	LUAD
LAMC3	c.521_522CC>AG	p.P174Q	KRSRADGPWEPYQFYSASCQKTYGR[p.P174Q]QEGQYLRPGEDERVAFCTSEFSDISPL	TYGRQEGQY,YGRQEGQYL,KTYGRQEGQY,TYGRQEGQYL,RQEGQYLRPG	TGCT
LARP1	c.668_669insC	p.A223fs	PRHIPANRGEIKGSESATYVPVAPP[p.A223fs]HPSLATRDQTGACLARPG*	APPHPSLAT,SLATRDQTGA,ATYVPVAPPH,ATRDQTGACL,VPVAPPHPSL	STAD

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LARP4B	c.487delA	p.T163fs	PENSETGGNESQPDSQEDPREVLKK[p.T163fs]HWNSAYLGRTLLVTCILYHRWIVTSMCQSQRWLTSTTSRSSALMWT*	CILYHRWIV,VLKKHWNSA,YLGRTLLVT,ILYHRWIVT,VTSMCQSQR,AYLGRTLLV,RTLLVTCIL,LYHRWIVTS,SAYLGRTLL,RWLTSTTSR,STTSRSSAL,TTSRSSALM,LKKHWNSAY,TLLVTCILY,HWNSAYLGR,LVTCILYHR,YHRWIVTSM,KKHWNSAYL,NSAYLGRTL,SMCQSQRWL,CQSQRWLTS,SQRWLTSTT,TSRSSALMW,TSMCQSQRW,SAYLGRTLLV,RTLLVTCILY,LYHRWIVTSM,STTSRSSALM,VLKKHWNSAY,LLVTCILYHR,IVTSMCQSQR,EVLKKHWNSA,NSAYLGRTLL,LKKHWNSAYL,WNSAYLGRTL,CQSQRWLTST,SQRWLTSTTS,REVLKKHWNS,TTSRSSALMW	STAD
LARS	c.554_555insC	p.P185fs	MKSLGLSDEEIVKFSEAEHWLDYFP[p.P185fs]ATGYSGFKKNGFEGRLASFLHHH*	ATGYSGFKK,RLASFLHHH,GFEGRLASF,FPATGYSGF,LDYFPATGY,FEGRLASFL,WLDYFPATGY,YFPATGYSGF,NGFEGRLASF,AEHWLDYFPA,FKKNGFEGRL	KIRC
LAT2	c.53T>G	p.L18W	MSSGTELLWPGAALLVL[p.L18W]WGVAASLCVRCSRPGAKRSEKIYQQR	AALLVLWGV,VLWGVAASL,LLVLWGVAA,GAALLVLWGV,ALLVLWGVAA,LVLWGVAASL,WPGAALLVLW	GBM
LBX1	c.526C>T	p.R176W	SPADRDQIAQQLGLTNAQVITWFQN[p.R176W]WRAKLKRDLEEMKADVESAKKLGPSG	VITWFQNWR,QVITWFQNW,WFQNWRAKL,TWFQNWRAK,ITWFQNWRA,ITWFQNWRAK,QVITWFQNWR,TWFQNWRAKL,WFQNWRAKLK,NWRAKLKRDL,AQVITWFQNW	CRC
LCP1	c.1334_1335insC	p.P445fs	SDALVIFQLYEKIKVPVDWNRVNKP[p.P445fs]AIPQTGRQYEEA*	RVNKPAIPQT	KIRC
LHCGR	c.47T>A	p.L16Q	MKQRFSALQLLKLLL[p.L16Q]QLQPPLPRALREALCPEPCNCVPDGA	QLLKLLLQL,LLLQLQPPL,QLQPPLPRA,KLLLQLQPPL,QLQPPLPRAL,LQLLKLLLQL,LQLQPPLPRA	TGCT
LILRA1	c.1228C>T	p.H410Y	SPVTSAHSGTYRCYGSLSSNPYLLS[p.H410Y]YPSDSLELMVSGAAETLSPPQNKSDS	SSNPYLLSY,LLSYPSDSL,SYPSDSLEL,YPSDSLELM,NPYLLSYPS,LSSNPYLLSY,YLLSYPSDSL,SYPSDSLELM,LSYPSDSLEL,YPSDSLELMV	BLCA
LILRB1	c.1417_1419delCTC	p.L479del	GLGRHLGVVIGILVAVILLLLLLLL[p.L479del]FLILRHRRQGKHWTSTQRKADFQHPAGA	ILLLLLLLF	BLCA
LILRB5	c.1792T>C	p.S598P	TKDRQAEEDRQMDTERVLSSPGPQA[p.S598P]PPPPPRSLPLTLPRCRLLHLKPPRM*	APPPPPRSL,PPPPPRSLPL	PRAD
LIM2	c.448T>A	p.S150T	IMAFAHQPTFSRISRPFSAGIMFFS[p.S150T]TTLFVVLALAIYTGVTVSFLGRRFGD	GIMFFSTTL,MFFSTTLFV,FFSTTLFVV,IMFFSTTLF,FSTTLFVVL,STTLFVVLA,TTLFVVLAL,IMFFSTTLFV,MFFSTTLFVV,GIMFFSTTLF,FFSTTLFVVL,FSAGIMFFST,FSTTLFVVLA,STTLFVVLAL,TTLFVVLALA,AGIMFFSTTL	LUAD
LIMK2	c.608G>A	p.R203H	TTVQVKEVNRMHISPNNRNAIHPGD[p.R203H]HILEINGTPVRTLRVEEVEDAISQTS	NAIHPGDHI,HPGDHILEI,AIHPGDHIL,HILEINGTPV	GBM
LIN9	c.547C>T	p.R183W	FCVCLKESFPNLKTRKLTRVEWGKI[p.R183W]WRLMGKPRRCSSAFFEEERSALKQKR	RVEWGKIWR,IWRLMGKPR,VEWGKIWRL,WGKIWRLMGK,KIWRLMGKPR,IWRLMGKPRR,VEWGKIWRLM	UCEC
LIN9	c.691G>A	p.E231K	QKRQKIRLLQQRKVADVSQFKDLPD[p.E231K]KIPLPLVIGTKVTARLRGVHDGLFTG	SQFKDLPDK,LPDKIPLPL,KDLPDKIPL,VSQFKDLPDK,SQFKDLPDKI,FKDLPDKIPL,LPDKIPLPLV	CESC
LINGO2	c.1228C>A	p.P410T	PDTIRERSFKDFHSTALSFYFTCKK[p.P410T]TKIREKKLQHLLVDEGQTVQLECSAD	KTKIREKKL,FTCKKTKIR,FYFTCKKTKI,SFYFTCKKTK,TCKKTKIREK,YFTCKKTKIR	HNSC
LIPJ	c.707C>A	p.P236Q	GSKLCPLQIFDKICLNILFMMFGYD[p.P236Q]QKNLNMSRLDVYFSHNPAGTSVQNML	FMMFGYDQK,DQKNLNMSR,MMFGYDQKN,MMFGYDQKNL,LFMMFGYDQK,FGYDQKNLNM	LUAD
LLGL2	c.2864_2865insG	p.P955fs	PRCLVDSAETKNHRPGNGAGPKKAP[p.P955fs]EPSQELRDSE*	KKAPEPSQEL	BLCA
LMLN	c.595G>T	p.G199C	PVIVPEEHLQQCRVYRGGKWPHGAV[p.G199C]CVPDQEGISDADFVLYVGALATERCS	GKWPHGAVC,GKWPHGAVCV	LUSC
LMX1B	c.844_846delCAG	p.Q285del	RHQQQQEQQNSQRLGQGEPGPGQGL[p.Q285del]QEVLSSRMEGMMASYTPLAPPQQQIVAM	LQEVLSSRM,GLQEVLSSRM	THCA

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LOC100132247	c.1594A>C	p.T532P	ADDNLKTPSERQLTALPPSADDNIK[p.T532P]PPAERLRGPLPPSADDNLKTPSERQL	DNIKPPAER,NIKPPAERLR,PPAERLRGPL	LIHC
LOC151174	c.268C>T	p.P90S	AEGIAMLLGTAGPSRLPAAPDASQA[p.P90S]SLRSPWALSVAAALCSPVSCHPCGRH	SLRSPWALS,APDASQASL,SQASLRSPW,ASLRSPWAL,SLRSPWALSV,SQASLRSPWA,ASQASLRSPW	CESC
LOC401296	c.430C>A	p.L144M	CVLAPGSGSRPTPHIVYSVPAARTC[p.L144M]MGAPGSLSPCHLCVHICAHTYSGTPV	AARTCMGAPG,RTCMGAPGSL,VPAARTCMGA,YSVPAARTCM	TGCT
LOC554223	c.438_458delGCGGGCGCCGTGGATGGAGCA	p.RAPWMEQ147del	LSVGDVDDTQCVRLDSDATSPRMEP[p.RAPWMEQ147del]EGPEYWEEETGTAKAKAQFYRVNLRTLSGYYNQSEA*	RMEPEGPEY,RMEPEGPEYW	PRAD
LOC649330	c.278G>A	p.G93E	AGEDGRMIASQVVDINLAAEPKVNR[p.G93E]ENAGVKRSAAEMYGSSFDLDYGFQRD	KVNRENAGV,VNRENAGVK,KVNRENAGVK,RENAGVKRSA	SKCM
LPHN2	c.2716T>A	p.F906I	EFIFLIGIDKTKYAIACPIFAGLLH[p.F906I]IFFLAAFAWMCLEGVQLYLMLVEVFE	GLLHIFFLA,LLHIFFLAA,HIFFLAAFA,IFAGLLHIF,IFFLAAFAW,LHIFFLAAF,FAGLLHIFF,GLLHIFFLAA,IFAGLLHIFF,IFFLAAFAWM,CPIFAGLLHI,LLHIFFLAAF,PIFAGLLHIF,HIFFLAAFAW	TGCT
LPHN3	c.2220G>T	p.E740D	FPENMGHGSTIQLSANTLKQNGRNG[p.E740D]DIRVAFVLYNNLGPYLSTENASMKLG	DIRVAFVLY,KQNGRNGDI,RNGDIRVAF,GDIRVAFVL,GRNGDIRVAF,GDIRVAFVLY	LUAD
LPHN3	c.2477G>A	p.R826H	VFTVKHIKQSEENFNPNCSFWSYSK[p.R826H]HTMTGYWSTQGCRLLTTNKTHTTCSC	YSKHTMTGY,CSFWSYSKH,HTMTGYWST,FWSYSKHTM,SKHTMTGYW,SFWSYSKHTM,SYSKHTMTGY,WSYSKHTMTG,YSKHTMTGYW	PRAD
LPHN3	c.3548G>A	p.R1183Q	SGSRTPGRYSTGSQSRIRRMWNDTV[p.R1183Q]QKQSESSFITGDINSSASLNREGLLN	RMWNDTVQK,VQKQSESSF,TVQKQSESSF,RMWNDTVQKQ,VQKQSESSFI	CRC
LPIN1	c.2921C>T	p.S974L	SDTFSNFTFWREPLPPFENQDIHSA[p.S974L]LA*	FENQDIHSAL	BLCA
LPPR2	c.556G>T	p.A186S	TDQGACAGSPSLVAAARRAFPCKDA[p.A186S]SLCAYAVTYTAMYVTLVFRVKGSRLV	SLCAYAVTY,DASLCAYAV,CKDASLCAY,SLCAYAVTYT,RAFPCKDASL,ASLCAYAVTY,FPCKDASLCA,KDASLCAYAV	ACC
LPPR4	c.1579C>A	p.R527S	LKIQPGAVPGCNNSMPGGPRVSIQS[p.R527S]SPGSSQLVHIPEETQENISTSPKSSS	RVSIQSSPG,IQSSPGSSQ,QSSPGSSQLV,IQSSPGSSQL,SPGSSQLVHI	LUAD
LRBA	c.6307G>A	p.E2103K	VSLSTPAQLVAPSVVVKGTLSVTSS[p.E2103K]KLYFEVDEEDPNFKKIDPKILAYTEG	LSVTSSKLY,TLSVTSSKL,GTLSVTSSK,TSSKLYFEV,SVTSSKLYF,VTSSKLYFEV,KGTLSVTSSK,TLSVTSSKLY,LSVTSSKLYF	UCEC
LRCH2	c.2150A>G	p.D717G	SIHVPSPAVPKLSMAKCRRNVENFL[p.D717G]GACKKLGVSQERLCLPHHILEERGLV	FLGACKKLGV	KIRC
LRFN5	c.396C>A	p.N132K	NSNRLTKITNDMFSGLSNLHHLILN[p.N132K]KNQLTLISSTAFDDVFALEELDLSYN	ILNKNQLTL,NLHHLILNK,ILNKNQLTLI,SNLHHLILNK,LILNKNQLTL	LUAD
LRIG1	c.70C>G	p.L24V	MARPVRGGLGAPRRSPCLLLLWL[p.L24V]VLLRLEPVTAAAGPRAPCAAACTCAG	LLLLWLVLL,LLWLVLLRL,LVLLRLEPV,LLLWLVLLR,LLLWLVLLRL,WLVLLRLEPV,SPCLLLLWLV	ACC
LRIG1	c.76C>G	p.L26V	MARPVRGGLGAPRRSPCLLLLWLLL[p.L26V]VRLEPVTAAAGPRAPCAAACTCAGDS	LLLLWLLLV,LLWLLLVRL,LLLVRLEPV,VRLEPVTAA,CLLLLWLLLV,LLLWLLLVRL,WLLLVRLEPV	ACC
LRP1	c.3172C>A	p.P1058T	TCDGDNDCGDYSDETHANCTNQATR[p.P1058T]TPGGCHTDEFQCRLDGLCIPLRWRCD	ATRTPGGCH,ATRTPGGCHT,TPGGCHTDEF	KIRP,PRAD
LRP1	c.4462_4463insG	p.G1488fs	GSGHMEVLRGHEFLSHPFAVTLYGG[p.G1488fs]GGLLD*	TLYGGGGLL	STAD

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LRP1	c.4462delG	p.G1488fs	GSGHMEVLRGHEFLSHPFAVTLYGG[p.G1488fs]RSTGLTGEQTHWLRPTSGPATMSPWYRGPTPSPLTCRCTTPPASPWLPIPVRPMGARAPAPTCVSSTTTGPCPAPAPTS*	WLRPTSGPA,PVRPMGARA,FAVTLYGGR,PATMSPWYR,TTPPASPWL,TTGPCPAPA,RPTSGPATM,PPASPWLPI,RPMGARAPA,YRGPTPSPL,CTTPPASPW,WLPIPVRPM,GPATMSPWY,TLYGGRSTGL,GLTGEQTHWL,TMSPWYRGPT,WYRGPTPSPL,HWLRPTSGPA,GARAPAPTCV,SGPATMSPWY,PFAVTLYGGR,LTGEQTHWLR,CTTPPASPWL,TTTGPCPAPA,SPWYRGPTPS,TPPASPWLPI,LPIPVRPMGA,IPVRPMGARA,RPMGARAPAP,APAPTCVSST,WLRPTSGPAT,LRPTSGPATM,TSGPATMSPW,RCTTPPASPW,GEQTHWLRPT	STAD
LRP10	c.15_17delCCT	p.L11del	MLLATLLLLL[p.L11del]GGALAHPDRIIFPNHACEDPPAVLLEVQ	TLLLLLGGA	PRAD
LRP11	c.275C>G	p.P92R	QQERPQEELELELRAGGGPQEDCPG[p.P92R]RGSGGYSAMPDAIIRTKDSLAAGASF	RGSGGYSAM,CPGRGSGGY,GRGSGGYSAM	ACC
LRP12	c.928G>T	p.G310C	CTWLIDTGDHRKVILRFTDFKLDGT[p.G310C]CYGDYVKIYDGLEENPHKLLRVLTAF	GTCYGDYVK,KLDGTCYGDY,TDFKLDGTCY,TCYGDYVKIY	TGCT
LRP1B	c.10687G>T	p.G3563C	FDCADGSDERNCETSCSKDQFRCSN[p.G3563C]CQCIPAKWKCDGHEDCKYGEDEKSCE	CSNCQCIPAK	LUAD
LRP1B	c.4174C>T	p.L1392F	SLRTTLIAGAMEHPRAIALDPRYGI[p.L1392F]FFWTDWDANFPRIESASMSGAGRKTI	RYGIFFWTD,ALDPRYGIF,YGIFFWTDW,DPRYGIFFW,GIFFWTDWDA,IALDPRYGIF,RYGIFFWTDW,FFWTDWDANF,ALDPRYGIFF	UCS
LRP2	c.12117G>C	p.M4039I	FGTCPQHCRNTKGSYECVCADGFTS[p.M4039I]ISDRPGKRCAAEGSSPLLLPDNVRI	TSISDRPGK,DGFTSISDR,SISDRPGKR,FTSISDRPGK,TSISDRPGKR	LUAD
LRP2	c.1547C>T	p.A516V	IDMVNLDGSYRVTLITENLGHPRGI[p.A516V]VVDPTVGYLFFSDWESLSGEPKLERA	IVVDPTVGY,LGHPRGIVV,VVDPTVGYLF,IVVDPTVGYL,GIVVDPTVGY,HPRGIVVDPT	LUSC
LRP2	c.2210C>T	p.S737L	IFSSQVAIRGIPFTLSTQEDVMVPV[p.S737L]LGNPSFFVGIDFDAQDSTIFFSDMSK	VLGNPSFFV,VPVLGNPSF,QEDVMVPVL,VPVLGNPSFF,MVPVLGNPSF,TQEDVMVPVL	CRC
LRP2	c.7295G>T	p.R2432I	NHSPPFQTINVERTVMSLDYDSVSD[p.R2432I]IIYFTQNLASGVGQISYATLSSGIHT	SVSDIIYFT,IIYFTQNLA,DIIYFTQNL,LDYDSVSDI,YDSVSDIIY,DSVSDIIYFT,DIIYFTQNLA,LDYDSVSDII,YDSVSDIIYF,SDIIYFTQNL	UCEC
LRP2	c.9127C>T	p.R3043C	CGDYSDERGCLYQTCQQNQFTCQNG[p.R3043C]CCISKTFVCDEDNDCGDGSDELMHLC	CQNGCCISK	CRC
LRP5	c.4825T>C	p.S1609P	LSAEDSCPPSPATERSYFHLFPPPP[p.S1609P]PPCTDSS*	HLFPPPPPPC	PRAD
LRP6	c.2024G>A	p.R675Q	NNNNVAIPLTGVKEASALDFDVTDN[p.R675Q]QIYWTDISLKTISRAFMNGSALEHVV	FDVTDNQIY,QIYWTDISL,NQIYWTDISL,QIYWTDISLK	CRC
LRRC16A	c.679G>A	p.D227N	LDHRDLIPIIAALEYNQWFTKLSSK[p.D227N]NLKLSTDVCEQILRVVSRSNRLEELV	KLSSKNLKL,FTKLSSKNLK,TKLSSKNLKL	BLCA
LRRC16B	c.2359C>T	p.R787W	AVDKELQVILESMVSLTQELCPVAM[p.R787W]WVAEGHNKMLSNVAERVTVPRNFIRG	ELCPVAMWV,WVAEGHNKM,QELCPVAMW,AMWVAEGHNK,MWVAEGHNKM,ELCPVAMWVA,WVAEGHNKML,QELCPVAMWV	PRAD
LRRC18	c.652C>T	p.R218W	RRLENLYVVEEKDLCAACLRKCQNA[p.R218W]WDNLNRIKNMATTTPRKTIFPNLISP	NAWDNLNRI,CLRKCQNAW,RKCQNAWDNL	CRC
LRRC31	c.68A>C	p.K23T	RKKTSSEGETKPQTSTVNKFLR[p.K23T]ASNAESRKEDNDLKTSDSQPSDWIQK	FLRASNAES,RASNAESRK,STVNKFLRA,FLRASNAESR	CRC
LRRC37A2	c.305C>G	p.T102S	ELEQPHTQQGPEKLAGNAIYTKPSF[p.T102S]SQEHKAAVSVLTPFSKGAPSTSSPAK	FSQEHKAAV,SQEHKAAVSV	PRAD
LRRC37A3	c.1217C>A	p.A406D	ETPGQPPEHHEVTVSPPGHHQTHHL[p.A406D]DSPSVSVKPPDVQLTIAAEPSAEVGT	HLDSPSVSV,HLDSPSVSVK,QTHHLDSPSV,HQTHHLDSPS	CESC

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LRRC43	c.1674delC	p.D558fs	KEPAKEWKVLKKKKEPPKELRQDPP[p.D558fs]SSRCWAGAW*	SSRCWAGAW,ELRQDPPSSR,RQDPPSSRCW	STAD
LRRC7	c.4166G>A	p.R1389H	VPPDTITKKAGSHIQTLMGSQSLQH[p.R1389H]HSREQQPYEGNINKVTIQQFQSPLPI	HSREQQPYE,SQSLQHHSR,HHSREQQPY,LMGSQSLQHH,QHHSREQQPY	CRC
LRRCC1	c.17C>T	p.A6V	MEAAA[p.A6V]VVVAAEAEVENEDGDSSCGDVCFMDK	VVVAAEAEV,EAAAVVVAA,MEAAAVVVA,AVVVAAEAEV,MEAAAVVVAA	TGCT
LRRIQ1	c.2375G>T	p.W792L	RKRPVKCPANMTPALDKLEILRCGP[p.W792L]LDTLQQVTTVTFQDLPGCVLSTLAEC	LEILRCGPL,GPLDTLQQV,ILRCGPLDTL	LUAD
LRRIQ3	c.732_733insA	p.K244fs	LIVQRWIRGFLVRKNLSPVFFHKKK[p.K244fs]TAGKNY*	KKKTAGKNY,FFHKKKTAGK,HKKKTAGKNY	PRAD
LRRTM4	c.728C>A	p.S243Y	SKINFAHFPRLFNLRSIYLQWNRIR[p.S243Y]YISQGLTWTWSSLHNLDLSGNDIQGI	LQWNRIRYI,RIRYISQGL,YISQGLTWT,RYISQGLTW,YLQWNRIRY,YLQWNRIRYI,IYLQWNRIRY,YISQGLTWTW,RIRYISQGLT,LQWNRIRYIS,NRIRYISQGL,IRYISQGLTW	LUAD
LRTM2	c.416C>T	p.S139L	DLTNLTELQLRNNSIRTLDRDLLRH[p.S139L]LPLLRHLDLSINGLAQLPPGLFDGLL	LLRHLPLLR,LPLLRHLDL,DLLRHLPLL,RDLLRHLPL,RHLPLLRHL,DLLRHLPLLR,RDLLRHLPLL,LRHLPLLRHL	BLCA
LRTM2	c.526C>G	p.L176V	GLAQLPPGLFDGLLALRSLSLRSNR[p.L176V]VQNLDRLTFEPLANLQLLQVGDNPWE	SLSLRSNRV,VQNLDRLTF,LRSNRVQNL,SLRSNRVQNL,RSNRVQNLDR,RVQNLDRLTF,RSLSLRSNRV	CESC
LSG1	c.1550G>T	p.R517L	ITPREDEDPHRPPTSEELLTAYGYM[p.R517L]LGFMTAHGQPDQPRSARYILKDYVSG	LLTAYGYML,TAYGYMLGF,AYGYMLGFM,GYMLGFMTA,YMLGFMTAH,LTAYGYMLGF,YMLGFMTAHG,TAYGYMLGFM,YGYMLGFMTA	LUSC
LTA4H	c.319T>C	p.F107L	YKGSPMEISLPIALSKNQEIVIEIS[p.F107L]LETSPKSSALQWLTPEQTSGKEHPYL	EISLETSPK,QEIVIEISL,LETSPKSSA,NQEIVIEISL,LETSPKSSAL	KIRC
LTB4R	c.217T>C	p.F73L	QKRSVTALMVLNLALADLAVLLTAP[p.F73L]LFLHFLAQGTWSFGLAGCRLCHYVCG	VLLTAPLFL,LTAPLFLHF,LAVLLTAPL,TAPLFLHFL,AVLLTAPLF,LTAPLFLHFL,DLAVLLTAPL,LLTAPLFLHF,TAPLFLHFLA,LAVLLTAPLF	TGCT
LUC7L3	c.442T>A	p.S148T	GKNEEKIQVLTDKIDVLLQQIEELG[p.S148T]TEGKVEEAQGMMKLVEQLKEERELLR	IEELGTEGKV	TGCT
LUM	c.929G>T	p.R310L	QLEKFDIKSFCKILGPLSYSKIKHL[p.R310L]LLDGNRISETSLPPDMYECLRVANEV	SYSKIKHLL,YSKIKHLLL,SYSKIKHLLL,LSYSKIKHLL	LUSC
LUM	c.988C>T	p.R330C	KIKHLRLDGNRISETSLPPDMYECL[p.R330C]CVANEVTLN*	DMYECLCVA,YECLCVANEV	GBM
LY9	c.205A>C	p.I69L	RASGKDSAPTVVSGILGGSVTLPLN[p.I69L]LSVDTEIENVIWIGPKNALAFARPKE	VTLPLNLSV,SVTLPLNLSV	BRCA
LYPD4	c.191C>A	p.T64K	AVAFHNWKWLLMRNMVCKLQEGCEE[p.T64K]KLVFIETGTARGVVGFKGCSSSSYP	EEKLVFIET,KLQEGCEEKL,KLVFIETGTA,QEGCEEKLVF,CEEKLVFIET	TGCT
LYST	c.2130G>T	p.Q710H	DLLWKWDALKAYQNFVFEEDRLHSI[p.Q710H]HIANHICNLIQKGNIVVQWKLYNYIF	HIANHICNL,HSIHIANHI,EEDRLHSIH,HIANHICNLI,RLHSIHIANH,FEEDRLHSIH,IHIANHICNL,EEDRLHSIHI	KIRC
LZTS1	c.1294_1341delAGGACCCAGGACCTGGAGGGCGCCCTGCGCACCAAGGGCCTGGAGCTG	p.RTQDLEGALRTKGLEL432del	AKASEILGLKAQLKDTRGKLEGLEL[p.RTQDLEGALRTKGLEL432del]EVCENELQRKKNEAELLREKVNLLEQELQELRAQAALARDMGPPTFPEDVPALQRELERLRAELREERQGHDQ	KLEGLELEV,GKLEGLELEV	PAAD
LZTS2	c.298delC	p.P100fs	VPPRKAVPVTSFTYINEDFRTESPP[p.P100fs]AQAVMLRMPESSGHTMPTSAAHHQSSSLSLESWRRTWRRS*	SSLSLESWR,HTMPTSAAH,SWRRTWRRS,ESWRRTWRR,ESSGHTMPT,SPPAQAVML,MPESSGHTM,AAHHQSSSL,TESPPAQAV,HHQSSSLSL,SSSLSLESW,SLESWRRTW,RMPESSGHTM,SSSLSLESWR,SSLSLESWRR,MLRMPESSGH,HTMPTSAAHH,SLESWRRTWR,SAAHHQSSSL,TESPPAQAVM,AHHQSSSLSL,HQSSSLSLES,QSSSLSLESW,LSLESWRRTW,MPTSAAHHQS	CRC
MAEL	c.1033C>T	p.R345C	EAHVPLQDYEASNSVTPKMVVLDAG[p.R345C]CYQKLRVGSSGFSHFNSSNEEQRSNT	VLDAGCYQK,MVVLDAGCY,DAGCYQKLR,VLDAGCYQKL,VVLDAGCYQK,KMVVLDAGCY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MAF	c.158delG	p.G53fs	MKFEVKKEPVETDRIISQCGRLIAG[p.G53fs]ARCPPPP*	CGRLIAGAR,SQCGRLIAGA,RLIAGARCPP	CLL
MAGEC1	c.1826T>A	p.L609H	PQGEDSLSPHYFPQSPPQGEDSMSP[p.L609H]HYFPQSPLQGEEFQSSLQSPVSICSS	GEDSMSPHY,SMSPHYFPQ,SMSPHYFPQS,QGEDSMSPHY,SPHYFPQSPL,GEDSMSPHYF	CLL
MAGEC1	c.714_716delCCC	p.P239del	FQSSPERTQSTFEGFAQSPLQIPVS[p.P239del]SSSSTLLSLFQSFSERTQSTFEGFAQSS	IPVSSSSST,VSSSSSTLL,IPVSSSSSTL	KIRC
MAGEE1	c.1138G>A	p.V380M	SVLPIPGEGLSTSVPPTASDGSDTS[p.V380M]MPPTPGEGASTLVQPTAPDGPGSSVL	ASDGSDTSM,SMPPTPGEGA,TASDGSDTSM	CRC
MAGEE2	c.133delC	p.Q45fs	GDGRGEIQATNASGSPTSMLVVDAP[p.Q45fs]SALRRQSTLSVSTLPRPFRTRMTWRS*	MLVVDAPSA,LVVDAPSAL,TLSVSTLPR,VVDAPSALR,VSTLPRPFR,TLPRPFRTR,PFRTRMTWR,SALRRQSTL,LPRPFRTRM,RPFRTRMTW,LRRQSTLSV,RQSTLSVST,QSTLSVSTL,SVSTLPRPF,SMLVVDAPSA,MLVVDAPSAL,ALRRQSTLSV,RQSTLSVSTL,STLSVSTLPR,LVVDAPSALR,VVDAPSALRR,SVSTLPRPFR,STLPRPFRTR,RPFRTRMTWR,APSALRRQST,LPRPFRTRMT,LSVSTLPRPF,RRQSTLSVST	STAD
MAGI1	c.3467G>T	p.G1156V	KGFGFSLRGGREYNMDLYVLRLAED[p.G1156V]VPAERCGKMRIGDEILEINGETTKNM	YVLRLAEDV,VPAERCGKM,RLAEDVPAER	LUAD
MAGI1	c.3592C>T	p.R1198C	INGETTKNMKHSRAIELIKNGGRRV[p.R1198C]CLFLKRGDGSVPEYDPSSDRHGPATG	GGRRVCLFL,GRRVCLFLK,GGRRVCLFLK,IKNGGRRVCL,KNGGRRVCLF	CRC
MAGI2	c.1348C>A	p.L450M	LSTTLKKSNMGFGFTIIGGDEPDEF[p.L450M]MQVKSVIPDGPAAQDGKMETGDVIVY	EFMQVKSVI,MQVKSVIPD,DEFMQVKSV,MQVKSVIPDG,DEFMQVKSVI	UCEC
MAGI2	c.3130C>A	p.P1044T	PSSEKQSPMAQQSPLAQQSPLAQPS[p.P1044T]TATPNSPIAQPAPPQPLQLQGHENSY	STATPNSPI,STATPNSPIA,SPLAQPSTAT,QQSPLAQPST	LUAD
MAML2	c.1771C>A	p.Q591K	QANQQMPSVLPSQNKPSLLHYTQQQ[p.Q591K]KQQQQQQQQQQQQQQQQQQQQQQQQQ	LLHYTQQQK,SLLHYTQQQK	KIRP
MAMLD1	c.1715A>T	p.Q572L	YLQQPTPTQASSATASSTATATLQL[p.Q572L]LQQQQQQQQQPDHSSFLLQQMMQQPQ	STATATLQLL	TGCT,UCS
MAMSTR	c.484_485insC	p.P162fs	QPHPRMKPSPLTPCPPGVPSPSPPP[p.P162fs]TQVGTSDP*	SPSPPPTQV	STAD
MAN1C1	c.1291_1292insG	p.G431fs	MEAKNMYYEALEAIETYLLNVSPGG[p.G431fs]ADLHCRVARGDSGPQDGAPGLFLRGHDRPWRRGCQGRKEGPLPRARSPDHQDVSRVIRPLRHQTWA*	LLNVSPGGA,RGHDRPWRR,VSRVIRPLR,DGAPGLFLR,DVSRVIRPL,GPQDGAPGL,RPWRRGCQG,RPLRHQTWA,FLRGHDRPW,YLLNVSPGGA,LFLRGHDRPW,QGRKEGPLPR,RARSPDHQDV,VSRVIRPLRH,FLRGHDRPWR,DVSRVIRPLR,VIRPLRHQTW	STAD
MAP1A	c.6187delC	p.P2063fs	GPTVPPRPEPGPSMEPSLTPPAVPP[p.P2063fs]VLLS*	LTPPAVPPV,SLTPPAVPPV	STAD
MAP1B	c.6138G>T	p.E2046D	EGYSYETSTKTTRTPDTSTYCYETA[p.E2046D]DKITRTPQASTYSYETSDLCYTAEKK	ETADKITRT,STYCYETADK,TYCYETADKI	CRC
MAP1S	c.1232C>G	p.S411C	EKMGVGRLDMYVLHPPSAGAERTLA[p.S411C]CVCALLVWHPAGPGEKVVRVLFPGCT	RTLACVCAL,TLACVCALL,AERTLACVC,RTLACVCALL,TLACVCALLV,LACVCALLVW,AERTLACVCA	ACC
MAP2	c.1590G>T	p.K530N	QAVTDSAMTSKTLEKAMTEPSALIE[p.K530N]NSSIQELFEMRVDDKDKIEGVGAATS	SALIENSSI,IENSSIQEL,IENSSIQELF	CRC
MAP2	c.4414_4415insA	p.K1472fs	EPSTVSRDEVRRKKAVYKKAELAKK[p.K1472fs]NRSSGPLSLQEIHFKTCYQIY*	SLQEIHFKT,LSLQEIHFK,KNRSSGPLS,HFKTCYQIY,KKNRSSGPL,NRSSGPLSL,QEIHFKTCY,IHFKTCYQI,KNRSSGPLSL,IHFKTCYQIY,EIHFKTCYQI,AKKNRSSGPL,LQEIHFKTCY	STAD
MAP2K1	c.171G>C	p.K57N	ALQKKLEELELDEQQRKRLEAFLTQ[p.K57N]NQKVGELKDDDFEKISELGAGNGGVV	TQNQKVGEL,TQNQKVGELK,EAFLTQNQKV	CLL

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MAP2K1	c.171G>T	p.K57N	ALQKKLEELELDEQQRKRLEAFLTQ[p.K57N]NQKVGELKDDDFEKISELGAGNGGVV	TQNQKVGEL,TQNQKVGELK,EAFLTQNQKV	LUAD
MAP2K1	c.370C>T	p.P124S	IHLEIKPAIRNQIIRELQVLHECNS[p.P124S]SYIVGFYGAFYSDGEISICMEHMDGG	NSSYIVGFY,SYIVGFYGA,VLHECNSSY,HECNSSYIV,CNSSYIVGF,CNSSYIVGFY,VLHECNSSYI,SYIVGFYGAF,SSYIVGFYGA,QVLHECNSSY	SKCM
MAP2K4	c.551C>T	p.S184L	PYIVQFYGALFREGDCWICMELMST[p.S184L]LFDKFYKYVYSVLDDVIPEEILGKIT	MSTLFDKFY,STLFDKFYK,TLFDKFYKY,ELMSTLFDK,LMSTLFDKF,ICMELMSTL,CMELMSTLF,LMSTLFDKFY,STLFDKFYKY,LFDKFYKYV,TLFDKFYKYV,WICMELMSTL,MSTLFDKFYK,ICMELMSTLF,ELMSTLFDKF	BRCA
MAP2K4	c.752G>T	p.S251I	IHRDIKPSNILLDRSGNIKLCDFGI[p.S251I]IGQLVDSIAKTRDAGCRPYMAPERID	IIGQLVDSI,IKLCDFGII,GIIGQLVDSI	BRCA
MAP2K4	c.783_784delAA	p.T261fs	DRSGNIKLCDFGISGQLVDSIAKTR[p.T261fs]CWL*	SIAKTRCWL	BRCA
MAP2K4	c.860G>A	p.R287H	RDAGCRPYMAPERIDPSASRQGYDV[p.R287H]HSDVWSLGITLYELATGRFPYPKWNS	DVHSDVWSL,RQGYDVHSDV,QGYDVHSDVW,YDVHSDVWSL	CRC
MAP2K5	c.1334A>G	p.Q445R	VQFNDGNAAVVSMWVCRALEERRSQ[p.Q445R]RGPP*	RALEERRSQR	KIRC
MAP3K1	c.2281_2284delATAG	p.I761fs	LNCILGNQTESNNWQELLGRLCLID[p.I761fs]CCWNFLLNFILILSVLMFHKLSLLKSGIRSCCPS*	LIDCCWNFL,FLLNFILIL,FILILSVLM,VLMFHKLSL,LMFHKLSLL,KLSLLKSGI,ILSVLMFHK,MFHKLSLLK,CLIDCCWNF,CWNFLLNFI,NFLLNFILI,ILILSVLMF,CCWNFLLNF,WNFLLNFIL,LSVLMFHKL,CLIDCCWNFL,LIDCCWNFLL,FLLNFILILS,LLNFILILSV,ILSVLMFHKL,VLMFHKLSLL,LILSVLMFHK,LMFHKLSLLK,CWNFLLNFIL,NFLLNFILIL,NFILILSVLM,SVLMFHKLSL,LNFILILSVL,FILILSVLMF,HKLSLLKSGI	BRCA
MAP3K1	c.4036_4038delGTT	p.V1346del	LFIEWMAGGSVAHLLSKYGAFKESV[p.V1346del]INYTEQLLRGLSYLHENQIIHRDVKGAN	SVINYTEQL,AFKESVINY,SVINYTEQLL,KYGAFKESVI,GAFKESVINY,ESVINYTEQL	BRCA
MAP3K1	c.4150_4151insT	p.L1384fs	LHENQIIHRDVKGANLLIDSTGQRL[p.L1384fs]KNCRFWSCSQVGIKRNWCRRVSGTITGDNCIYGT*	WSCSQVGIK,RLKNCRFWS,GIKRNWCRR,VGIKRNWCR,GQRLKNCRF,CRFWSCSQV,SQVGIKRNW,LIDSTGQRLK,RFWSCSQVGI,RLKNCRFWSC,GIKRNWCRRV,GTITGDNCIY,STGQRLKNCR,QVGIKRNWCR,VGIKRNWCRR,GQRLKNCRFW	BRCA
MAP3K1	c.953_954insA	p.L318fs	DGFSPYSPEETNRRVNKVMRARLYL[p.L318fs]TAADRA*	VMRARLYLT,RLYLTAADR,RARLYLTAA,MRARLYLTA,VMRARLYLTA,RLYLTAADRA,KVMRARLYLT,RARLYLTAAD,MRARLYLTAA	BRCA
MAP3K1	c.971C>T	p.P324L	YSPEETNRRVNKVMRARLYLLQQIG[p.P324L]LNSFLIGGDSPDNKYRVFIGPQNCSC	QQIGLNSFL,LYLLQQIGL,LQQIGLNSF,RLYLLQQIGL,QQIGLNSFLI,LLQQIGLNSF,LQQIGLNSFL	GBM
MAP3K12	c.1345_1347delAGG	p.R449del	KLHFEKIKSEGTCLHRLEEELVMRR[p.R449del]EELRHALDIREHYERKLERANNLYMELN	LVMRREELR,ELVMRREEL,ELVMRREELR,MRREELRHAL,EELVMRREEL	STAD
MAP3K4	c.824G>A	p.R275Q	ENTSGFWLNRSNELIWLELQAWHAG[p.R275Q]QTINDQDFFLYTARQAIPDIINEILT	LQAWHAGQT,QAWHAGQTI,GQTINDQDF,LQAWHAGQTI,QTINDQDFFL,GQTINDQDFF,LELQAWHAGQ	CRC
MAP3K7	c.1570G>C	p.E524Q	AYLTLDHQLQPLAPCPNSKESMAVF[p.E524Q]QQHCKMAQEYMKVQTEIALLLQRKQE	MAVFQQHCK,AVFQQHCKM,SMAVFQQHCK,QQHCKMAQEY,MAVFQQHCKM,KESMAVFQQH	HNSC
MAP4K2	c.1021C>G	p.R341G	SRGQHGPAERTPSEIQFHQVKFGAP[p.R341G]GRKETDPLNEPWEEEWTLLGKEELSG	QVKFGAPGR,HQVKFGAPG,QVKFGAPGRK,HQVKFGAPGR,APGRKETDPL	TGCT
MAP4K3	c.1970delC	p.P657fs	LFDYARQMQKLPVAIPAHKLPDRIL[p.P657fs]QGNFLYQQKSLKPNGARSVVL*	RILQGNFLY,FLYQQKSLK,KSLKPNGAR,KPNGARSVV,YQQKSLKPN,SLKPNGARSV,NFLYQQKSLK,KPNGARSVVL,GNFLYQQKSL,YQQKSLKPNG,LPDRILQGNF	HNSC
MAP7D1	c.239_240insC	p.A80fs	ATSSKQLPLEPESPSGQVGPRPAPP[p.A80fs]AGRVPFL*	RPAPPAGRV,APPAGRVPF,PPAGRVPFL,RPAPPAGRVP,APPAGRVPFL	STAD
MAP7D2	c.1459C>T	p.R487C	ERLEKEEQDRLEREELKRKAEEERL[p.R487C]CLEEEARKQEEERKRQEEEKKKQEGE	RKAEEERLCL,EERLCLEEEA	CRC

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MAP7D3	c.922delC	p.Q308fs	PQTKVEESPLEKVETPPKASVDAPP[p.Q308fs]R*	KASVDAPPR	STAD
MAP9	c.1455G>T	p.K485N	QKKAAKREEALASFEAWKAMKEKEA[p.K485N]NKIAAKKRLEEKNKKKTEEENAARKG	AMKEKEANK,KEANKIAAK,KEKEANKIA,AMKEKEANKI,KAMKEKEANK,EANKIAAKKR,KEKEANKIAA	HNSC
MAPK1	c.964G>A	p.E322K	NPHKRIEVEQALAHPYLEQYYDPSD[p.E322K]KPIAEAPFKFDMELDDLPKEKLKELI	YYDPSDKPI,KPIAEAPFK,QYYDPSDKPI,SDKPIAEAPF,KPIAEAPFKF	CESC,HNSC
MAPK13	c.943G>A	p.E315K	ELDVDKRLTAAQALTHPFFEPFRDP[p.E315K]KEETEAQQPFDDSLEHEKLTVDEWKQ	KEETEAQQPF	BRCA
MAPK15	c.1533delG	p.Q511fs	PPRLPPEARPGRRMFSTSALQGAQG[p.Q511fs]VPGLCLEATPKPTGLSATRHWATCPCWRGTMCEPPYSLHLALCSCPSPFPRPLSSLLHPLALPALPGPLKFQGACPGLLGGADEGPAPAPLTSSNKVMSAPN	TMCEPPYSL,PLSSLLHPL,LLHPLALPA,GLSATRHWA,SLHLALCSC,ALPALPGPL,GLCLEATPK,CSCPSPFPR,KFQGACPGL,RGTMCEPPY,HWATCPCWR,EPPYSLHLA,TPKPTGLSA,PPYSLHLAL,CPSPFPRPL,SPFPRPLSS,FPRPLSSLL,APLTSSNKV,SSLLHPLAL,ALCSCPSPF,LQGAQGVPG,AQGVPGLCL,RHWATCPCW,LKFQGACPG,FQGACPGLL,DEGPAPAPL,CEPPYSLHL,GTMCEPPYSL,SLLHPLALPA,LLHPLALPAL,GLSATRHWAT,ALPALPGPLK,PFPRPLSSLL,KFQGACPGLL,ATRHWATCPC,TSALQGAQGV,TPKPTGLSAT,EPPYSLHLAL,SPFPRPLSSL,FPRPLSSLLH,RPLSSLLHPL,LPALPGPLKF,APLTSSNKVM,LALCSCPSPF,LQGAQGVPGL,LEATPKPTGL,WRGTMCEPPY,LSSLLHPLAL,LALPALPGPL,LKFQGACPGL,CEPPYSLHLA	STAD
MAPK4	c.298G>A	p.V100M	DNIVKVYEVLGPKGTDLQGELFKFS[p.V100M]MAYIVQEYMETDLARLLEQGTLAEEH	LFKFSMAYI,ELFKFSMAY,SMAYIVQEY,MAYIVQEYM,FKFSMAYIV,GELFKFSMA,FSMAYIVQEY,ELFKFSMAYI,SMAYIVQEYM,LQGELFKFSM,GELFKFSMAY,FKFSMAYIVQ	BRCA
MAPK7	c.1502C>A	p.A501D	KAALKAALLKSLRSRLRDGPSAPLE[p.A501D]DPEPRKPVTAQERQREREEKRRRRQE	LEDPEPRKPV	KIRP,TGCT
MAPK8IP1	c.651_652insCC	p.L217fs	SSSPLKTGEQTPPHEHICLSDELPP[p.L217fs]PRAAPPPPQIEAPPPTALAAAAQPPRWHLRVVPLLPRLGVGATRIETESTTRPMCD*	RVVPLLPRL,LLPRLGVGA,RLGVGATRI,RWHLRVVPL,RAAPPPPQI,AQPPRWHLR,LAAAAQPPR,EAPPPTALA,APPPTALAA,PPRWHLRVV,VPLLPRLGV,LPRLGVGAT,IEAPPPTAL,AAQPPRWHL,WHLRVVPLL,DELPPPRAA,ETESTTRPM,QPPRWHLRV,ALAAAAQPPR,HLRVVPLLPR,AAQPPRWHLR,RWHLRVVPLL,CLSDELPPPR,EAPPPTALAA,APPPTALAAA,IEAPPPTALA,LAAAAQPPRW,AAAQPPRWHL,LRVVPLLPRL,IETESTTRPM,DELPPPRAAP,QPPRWHLRVV	CRC
MAPKAPK2	c.640_641insC	p.T214fs	ENLLYTSKRPNAILKLTDFGFAKET[p.T214fs]HQPQLFDHSLLYTVLCGSRSAGSREV*	QLFDHSLLY,LLYTVLCGS,QPQLFDHSL,AKETHQPQL,KETHQPQLF,FDHSLLYTV,QLFDHSLLYT,GSRSAGSREV,PQLFDHSLLY,LLYTVLCGSR,YTVLCGSRSA,QPQLFDHSLL,FAKETHQPQL,AKETHQPQLF,HQPQLFDHSL,FDHSLLYTVL	KIRC
11-Mar	c.578G>T	p.R193L	PICKICFQGAEQGELLNPCRCDGSV[p.R193L]LYTHQLCLLKWISERGSWTCELCCYR	VLYTHQLCL,LYTHQLCLL,GSVLYTHQL,VLYTHQLCLL,NPCRCDGSVL	LUAD
S-Mar	c.508C>T	p.R170C	GLPTIPVMLILGKMIRWEDYVLRLW[p.R170C]CKYSNKLQILNSIFPGIGCPVPRIPA	RLWCKYSNK,LWCKYSNKL,YVLRLWCKY,DYVLRLWCK,CKYSNKLQI,RLWCKYSNKL,CKYSNKLQIL	BRCA
MARCKS	c.454delA	p.K152fs	ASSTSSPKAEDGATPSPSNETPKKK[p.K152fs]RSAFPSRSLSS*	KKRSAFPSR,RSAFPSRSL,SAFPSRSLS,TPKKKRSAF,KKKRSAFPSR,RSAFPSRSLS,KRSAFPSRSL,SAFPSRSLSS	KIRC
MARS2	c.1442G>A	p.R481Q	LPKQVADHYDNFRIYKALEAVSSCV[p.R481Q]QQTNGFVQRHAPWKLNWESPVDAPWL	SCVQQTNGF,VQQTNGFVQ,SSCVQQTNGF,QQTNGFVQRH	HNSC
MAS1L	c.970A>G	p.R324G	ISLFLIINSSANPIIYFFVGSLRKK[p.R324G]GLKESLRVILQRALADKPEVGRNKKA	GLKESLRVI,GSLRKKGLK,RKKGLKESL,GLKESLRVIL,VGSLRKKGLK	PRAD,THCA
MAT2A	c.497A>G	p.E166G	YATDETEECMPLTIVLAHKLNAKLA[p.E166G]GLRRNGTLPWLRPDSKTQVTVQYMQD	KLNAKLAGL,KLNAKLAGLR,LAGLRRNGTL,GLRRNGTLPW,HKLNAKLAGL	TGCT
MAX	c.106A>T	p.R36W	SDEEQPRFQSAADKRAHHNALERKR[p.R36W]WDHIKDSFHSLRDSVPSLQGEKASRA	RWDHIKDSF,KRWDHIKDSF	MM

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MAX	c.83A>G	p.H28R	DNDDIEVESDEEQPRFQSAADKRAH[p.H28R]RNALERKRRDHIKDSFHSLRDSVPSL	RAHRNALER,SAADKRAHR,AHRNALERK,DKRAHRNAL,RAHRNALERK,QSAADKRAHR	UCEC
MB21D2	c.931C>G	p.Q311E	EWRLSFARSEVQLKKCISSSLMQAY[p.Q311E]EACKAIIIKLLSRPKAISPYHLRSMM	SLMQAYEAC,MQAYEACKA,LMQAYEACK,QAYEACKAI,YEACKAIII,LMQAYEACKA,MQAYEACKAI,SLMQAYEACK,EACKAIIIKL,QAYEACKAII	HNSC,LUSC
MBD6	c.2194delC	p.P732fs	SVTTATTDPGASSLGKAPSNSGRPP[p.P732fs]NSLALCWVPACWVTCLH*	SLALCWVPA,SGRPPNSLA,VPACWVTCL,PPNSLALCW,SLALCWVPAC,ALCWVPACWV,SGRPPNSLAL,NSLALCWVPA,WVPACWVTCL,RPPNSLALCW,LALCWVPACW	STAD
MBD6	c.2338_2339insG	p.G780fs	LPSLLQPPGPLLSGQLGLQLLPGGG[p.G780fs]SSSTPLRGF*	SSSTPLRGF,LLPGGGSSST,LQLLPGGGSS,GSSSTPLRGF	STAD
MBOAT2	c.128G>A	p.R43Q	AVQLPIDQVNFVVCQLFALLAAIWF[p.R43Q]QTYLHSSKTSSFIRHVVATLLGLYLA	LAAIWFQTY,LLAAIWFQT,AIWFQTYLH,AAIWFQTYL,FQTYLHSSK,LLAAIWFQTY,ALLAAIWFQT,WFQTYLHSSK,LAAIWFQTYL,FQTYLHSSKT	CRC,UCEC
MBOAT7	c.1270C>T	p.R424W	HWFLKMRAYDYMCMGFVLLSLADTL[p.R424W]WYWASIYFCIHFLALAALGLGLALGG	LSLADTLWY,SLADTLWYW,TLWYWASIY,LWYWASIYF,WYWASIYFC,DTLWYWASI,LLSLADTLW,LLSLADTLWY,SLADTLWYWA,LSLADTLWYW,TLWYWASIYF,WYWASIYFCI,DTLWYWASIY,VLLSLADTLW,ADTLWYWASI	HNSC
MC5R	c.325G>A	p.A109T	LVSMSSAWETITIYLLNNKHLVIAD[p.A109T]TFVRHIDNVFDSMICISVVASMCSLL	HLVIADTFV,LVIADTFVR,KHLVIADTF,TFVRHIDNV,VIADTFVRHI,TFVRHIDNVF,HLVIADTFVR,DTFVRHIDNV,NKHLVIADTF	UCEC
MCF2L2	c.2777G>A	p.R926Q	KTMKLMTLSIRQLGRGSHRKFEIAS[p.R926Q]QNGLEKYILQAASKEIRDCWFSEISK	ASQNGLEKY,IASQNGLEK,FEIASQNGL,SQNGLEKYI,IASQNGLEKY,RKFEIASQNG,SQNGLEKYIL	CRC
MCHR1	c.917C>T	p.S306F	QFFLAFALPFVVITAAYVRILQRMT[p.S306F]FSVAPASQRSIRLRTKRVTRTAIAIC	ILQRMTFSV,RMTFSVAPA,RILQRMTFS,LQRMTFSVA,MTFSVAPAS,VRILQRMTF,RILQRMTFSV,ILQRMTFSVA,TFSVAPASQR,YVRILQRMTF,LQRMTFSVAP,QRMTFSVAPA,RMTFSVAPAS	LUSC
MCOLN3	c.421G>A	p.V141I	VYTQSDVYDQLIFAVNQYLQLYNVS[p.V141I]IGNHAYENKGTKQSAMAICQHFYKRG	YLQLYNVSI,NVSIGNHAY,LQLYNVSIG,SIGNHAYENK,QYLQLYNVSI,YNVSIGNHAY	GBM
MECOM	c.2744G>A	p.R915Q	SELLQSVPSMFNFRAPPNALPENLL[p.R915Q]QKGKERYTCRYCGKIFPRSANLTRHL	LLQKGKERY,NALPENLLQK	PRAD
MECOM	c.2905C>T	p.R969C	TGEQPYRCKYCDRSFSISSNLQRHV[p.R969C]CNIHNKEKPFKCHLCDRCFGQQTNLD	NLQRHVCNI,RHVCNIHNK,LQRHVCNIH,HVCNIHNKEK,CNIHNKEKPF	CRC
MED12	c.107T>G	p.L36R	HRPLKRPRLGPPDVYPQDPKQKEDE[p.L36R]RTALNVKQGFNNQPAVSGDEHGSAKN	QKEDERTAL,KQKEDERTAL,RTALNVKQGF,KEDERTALNV	CLL
MED12	c.130G>A	p.G44S	LGPPDVYPQDPKQKEDELTALNVKQ[p.G44S]SFNNQPAVSGDEHGSAKNVSFNPAKI	KQSFNNQPA,TALNVKQSF,QSFNNQPAV,KQSFNNQPAV,LTALNVKQSF,VKQSFNNQPA	CLL
MED12	c.3670C>T	p.L1224F	IRSSCDRHLLAASQNRIVDGAVFAV[p.L1224F]FKAVFVLGDAELKGSGFTVTGGTEEL	AVFAVFKAV,FAVFKAVFV,AVFKAVFVL,VFAVFKAVF,VDGAVFAVF,FAVFKAVFVL,AVFAVFKAVF,IVDGAVFAVF	PRAD
MED12L	c.3875G>A	p.C1292Y	LCTDKELILDPVLSNMQAQKLLQLI[p.C1292Y]YYPHGIKECTEGDNLQRQHIKRLQN	QLIYYPHGI,LIYYPHGIK,AQKLLQLIY,QKLLQLIYY,QAQKLLQLIY,LQLIYYPHGI,QLIYYPHGIK,AQKLLQLIYY	TGCT
MED12L	c.6211C>T	p.P2071S	QDPMRPRQPQVRQQQRLLQMQQPQQ[p.P2071S]SQPQQPPQPQQSSQSQSQTLGLQAMQ	LQMQQPQQS,MQQPQQSQP,LQMQQPQQSQ,MQQPQQSQPQ	KIRC
MED12L	c.6331_6333delCAG	p.Q2115del	LGLQAMQPQQPLFPRQGLQQTQQQQ[p.Q2115del]TAALVRQLQKQLSSNQPQQGVTPYGHPS	QQTQQQQTA,TQQQQTAAL,TQQQQTAALV,LQQTQQQQTA,QQTQQQQTAA	PRAD
MED15	c.104G>T	p.S35I	WRSTAFRQKLVSQIEDAMRKAGVAH[p.S35I]IKSSKDMESHVFLKAKTRDEYLSLVA	GVAHIKSSK,MRKAGVAHI,AHIKSSKDM,AMRKAGVAHI,MRKAGVAHIK,AGVAHIKSSK	THCA
MED16	c.1347C>G	p.H449Q	TAGPAVHLKAMQLSWTSLALVGIDS[p.H449Q]QGKLSVLRLSPSMGHPLEVGLALRHL	DSQGKLSVLR,IDSQGKLSVL,SQGKLSVLRL	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MEF2A	c.295C>T	p.P99S	EPHESRTNSDIVEALNKKEHRGCDS[p.P99S]SDPDTSYVLTPHTEEKYKKINEEFDN	SSDPDTSYV,DSSDPDTSY,DSSDPDTSYV,CDSSDPDTSY	KIRP
MEF2A	c.380G>A	p.R127Q	DTSYVLTPHTEEKYKKINEEFDNMM[p.R127Q]QNHKIAPGLPPQNFSMSVTVPVTSPN	NMMQNHKIA,MMQNHKIAP,MQNHKIAPG,MQNHKIAPGL,MMQNHKIAPG,EEFDNMMQNH	TGCT
MEFV	c.1130G>A	p.R377H	CPRCQDSHERKSPGSLSPQPLPQCK[p.R377H]HHLKQVQLLFCEDHDEPICLICSLSQ	KHHLKQVQL,HHLKQVQLL,HHLKQVQLLF,QPLPQCKHHL,CKHHLKQVQL,KHHLKQVQLL	BRCA
MEGF10	c.3158C>T	p.S1053L	NPYATIKDPPVLIPKSSECGYVEMK[p.S1053L]LPARRDSPYAEINNSTSANRNVYEVE	YVEMKLPAR,LPARRDSPY,KLPARRDSPY,YVEMKLPARR,LPARRDSPYA,SECGYVEMKL	UCEC
MEGF6	c.1178A>G	p.Y393C	RTCIDVDDCADSPCCQQVCTNNPGG[p.Y393C]CECGCYAGYRLSADGCGCEDVDECAS	CECGCYAGY,NPGGCECGCY	THCA
MEGF6	c.1746_1747insC	p.A582fs	DTFGKNCSFSCSCQNGGTCDSVTGA[p.A582fs]LPLPPGCQWN*	LPLPPGCQW,CDSVTGALPL	KIRC
MET	c.3280C>T	p.H1094Y	VVIGPSSLIVHFNEVIGRGHFGCVY[p.H1094Y]YGTLLDNDGKKIHCAVKSLNRITDIG	RGHFGCVYY,HFGCVYYGTL	KIRP
MET	c.3749T>C	p.M1250T	LARDMYDKEYYSVHNKTGAKLPVKW[p.M1250T]TALESLQTQKFTTKSDVWSFGVLLWE	KLPVKWTAL,VKWTALESL,TALESLQTQK,AKLPVKWTAL,LPVKWTALES	KIRP
METTL15	c.157C>G	p.Q53E	VWPNRIHTTAEKYREYEAREQTDQT[p.Q53E]EAQELHRSQDRDFETMAKLHIPVMVD	REQTDQTEA	BRCA
METTL16	c.599G>A	p.R200Q	EIIYDFCMCNPPFFANQLEAKGVNS[p.R200Q]QNPRRPPPSSVNTGGITEIMAEGGEL	SQNPRRPPP,SQNPRRPPPS	CRC
METTL21A	c.521G>A	p.R174Q	EETFTDLLQTLEHLCSNHSVILLAC[p.R174Q]QIRYERDNNFLAMLERQFTVRKVHYD	ILLACQIRY,LACQIRYER,VILLACQIRY,SVILLACQIR,LLACQIRYER	CRC
METTL6	c.168C>A	p.F56L	DFKQQKLEQEAQKNWDLFYKRNSTN[p.F56L]LFKDRHWTTREFEELRSCREFEDQKL	FYKRNSTNL,KRNSTNLFK,YKRNSTNLF,LFYKRNSTNL,FYKRNSTNLF,YKRNSTNLFK,LFKDRHWTTR	CRC
METTL9	c.170A>T	p.Y57F	LYVNMTSGPGGPAAAAGGRKENHQW[p.Y57F]FVCNREKLCESLQAVFVQSYLDQGTQ	QWFVCNREK,NHQWFVCNR,GRKENHQWF,KENHQWFVC,HQWFVCNREK,ENHQWFVCNR	CLL
MEX3C	c.1600C>A	p.R534S	IWTPFEPVNPLSGFGSDPSGNMKTQ[p.R534S]SRGSQPSTPRLSPTFPESIEHPLARR	TQSRGSQPS,KTQSRGSQPS,TQSRGSQPST	TGCT
MEX3C	c.537_545delCGCGGCGGC	p.179_182AAAA>A	IPGGSLGSVLLPAARFDAREAAAAA[p.179_182AAAA>A]GVLYGGDDAQGMMAAMLSHAYGPGGCGAAAAALN	EAAAAAGVL,REAAAAAGV,EAAAAAGVLY,REAAAAAGVL	ACC
MFF	c.19_20AG>TT	p.S7F	MSKGTS[p.S7F]FDTSLGRVSRAAFPSPTAAEMAEISRI	TSFDTSLGR,KGTSFDTSL,GTSFDTSLGR,TSFDTSLGRV,SKGTSFDTSL	TGCT
MFF	c.484C>T	p.R162C	TTPQNEEIRAVGRLKRERSMSENAV[p.R162C]CQNGQLVRNDSLWHRSDSAPRNKISR	RSMSENAVC,SENAVCQNG,NAVCQNGQLV	CRC
MFGE8	c.508G>A	p.D170N	GASRLASHEYLKAFKVAYSLNGHEF[p.D170N]NFIHDVNKKHKEFVGNWNKNAVHVNL	SLNGHEFNF,HEFNFIHDV,SLNGHEFNFI,YSLNGHEFNF,EFNFIHDVNK,HEFNFIHDVN	UCEC
MFSD5	c.839G>A	p.R280Q	FEAWYIHEHVERHDFPAEWIPATFA[p.R280Q]QAAFWNHVLAVVAGVAAEAVASWIGL	WIPATFAQA,AQAAFWNHV,QAAFWNHVL,IPATFAQAA,ATFAQAAFW,FAQAAFWNHV,AQAAFWNHVL,WIPATFAQAA,QAAFWNHVLA,IPATFAQAAF,AEWIPATFAQ	CRC
MGA	c.7304G>A	p.R2435Q	WSDKLQKEAEAFAYYRRTHTANERR[p.R2435Q]QRGEMRDLFEKLKITLGLLHSSKVSK	HTANERRQR,NERRQRGEM,RQRGEMRDL,RQRGEMRDLF	OV
MGAT4B	c.1330A>C	p.T444P	STSLKTYQHFTLEKAYLREDFFWAF[p.T444P]PPAAGDFIRFRFFQPLRLERFFFRSG	FFWAFPPAA,AFPPAAGDF,DFFWAFPPA,FPPAAGDFI,AFPPAAGDFI,WAFPPAAGDF,PPAAGDFIRF,REDFFWAFPP,EDFFWAFPPA	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MGAT4C	c.1034C>T	p.T345M	LAQKNVIRFKPSLFQHMGYYSSYKG[p.T345M]MENKLKDDDFEEESFDIPDNPPASLY	SSYKGMENK,SYKGMENKL,GYYSSYKGM,YSSYKGMENK,SYKGMENKLK,MGYYSSYKGM,SSYKGMENKL,MENKLKDDDF	PRAD
MGST2	c.304delA	p.K102fs	FATCLGLVYIYGRHLYFWGYSEAAK[p.K102fs]NGSPVSD*	EAAKNGSPV,SEAAKNGSPV	STAD
MGST3	c.429_430insT	p.G143fs	SIALLGLVGTTVCSAFQHLGWVKSG[p.G143fs]FGQWTQMLPLKNYRGLKTLIHFK*	GQWTQMLPL,GLKTLIHFK,QMLPLKNYR,GFGQWTQML,RGLKTLIHF,QWTQMLPLK,PLKNYRGLK,TQMLPLKNY,LPLKNYRGL,HLGWVKSGF,WVKSGFGQW,SGFGQWTQM,KNYRGLKTL,WTQMLPLKNY,MLPLKNYRGL,GQWTQMLPLK,RGLKTLIHFK,TQMLPLKNYR,GWVKSGFGQW,QHLGWVKSGF,KSGFGQWTQM,SGFGQWTQML,FGQWTQMLPL,LKNYRGLKTL,KNYRGLKTLI,YRGLKTLIHF	KIRC
MICA	c.952delG	p.G318fs	HPVPSGKVLVLQSHWQTFHVSAVAA[p.G318fs]LLFLLLLFSMSVVVRRKHQLQRVQSS*	VSAVAALLF,AVAALLFLL,LLLLFSMSV,LLLFSMSVV,LLFSMSVVV,HVSAVAALL,SMSVVVRRK,FSMSVVVRR,ALLFLLLLF,LFLLLLFSM,VVRRKHQLQ,LFSMSVVVR,SAVAALLFL,VVVRRKHQL,FHVSAVAAL,VAALLFLLL,HQLQRVQSS,SAVAALLFLL,AVAALLFLLL,LLFLLLLFSM,FLLLLFSMSV,LLLLFSMSVV,LLLFSMSVVV,LLFSMSVVVR,FSMSVVVRRK,AALLFLLLLF,VVRRKHQLQR,HVSAVAALLF,LFSMSVVVRR,SVVVRRKHQL,FHVSAVAALL	CESC
MIER2	c.391C>T	p.L131F	ESEGGDVAPNLPDMTLDKEQIAKDL[p.L131F]FSGEEEEETQSSADDLTPSVTSHEAS	KEQIAKDLF	TGCT
MKI67	c.3241C>A	p.R1081S	REPAGDGKSIRTFKESPKQILDPAA[p.R1081S]SVTGMKKWPRTPKEEAQSLEDLAGFK	AASVTGMKK,DPAASVTGM,SVTGMKKWPR,AASVTGMKKW	LUAD
MKI67	c.4991_4992insCA	p.T1664fs	VGVKEELLAVGKLTQTSGETTHTHT[p.T1664fs]KSQQEMVRA*	HTKSQQEMV,HTHTKSQQEM,HTKSQQEMVR	STAD
MKI67	c.4992_4993insCA	p.T1664fs	VGVKEELLAVGKLTQTSGETTHTHT[p.T1664fs]QSQQEMVRA*	HTQSQQEMV,THTQSQQEM,HTHTQSQQEM,HTQSQQEMVR	UCEC
MKI67	c.6637C>G	p.H2213D	AQPLEDLAGLKELFQTPICTDKPTT[p.H2213D]DEKTTKIACRSPQPDPVGTPTIFKPQ	CTDKPTTDEK	CLL
MKL1	c.920delC	p.P307fs	HHNYQAILPAPPKSAGEALGSSGTP[p.P307fs]QYAASPLPIAAPARAPLGPVGWHVRTAPH*	PLGPVGWHV,QYAASPLPI,GWHVRTAPH,LGSSGTPQY,YAASPLPIA,IAAPARAPL,TPQYAASPL,SPLPIAAPA,LPIAAPARA,ALGSSGTPQY,YAASPLPIAA,APARAPLGPV,PQYAASPLPI,ARAPLGPVGW,APLGPVGWHV	STAD
MKLN1	c.1455C>A	p.F485L	CMLFHSKNRCLYVFGGQRSKTYLND[p.F485L]LFSYDVDSDHVDIISDGTKKDSGMVP	YLNDLFSYD,TYLNDLFSY,RSKTYLNDL,KTYLNDLFS,SKTYLNDLF,KTYLNDLFSY,YLNDLFSYDV,RSKTYLNDLF	UCEC
MKRN3	c.1343C>A	p.P448H	PEGWGDEPPGPGGGSFSAYWHQLVE[p.P448H]HVRMGEGNMLYKSIKKELVVLRLASL	YWHQLVEHV,HVRMGEGNM,HQLVEHVRM,AYWHQLVEHV,HVRMGEGNML,YWHQLVEHVR,SAYWHQLVEH,WHQLVEHVRM	LUAD
MKRN3	c.809G>T	p.G270V	YYASRGVCFRGESCMYLHGDICDMC[p.G270V]VLQTLHPMDAAQREEHMRACIEAHEK	CVLQTLHPM,CDMCVLQTL,MCVLQTLHPM	LUSC
MLL2	c.1939_1940insC	p.P647fs	ASRLSPPPEDSPMSPPPEESPMSPP[p.P647fs]T*	EESPMSPPT	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MLL2	c.1940delC	p.P647fs	EASRLSPPPEDSPMSPPPEESPMSP[p.P647fs]HLRYRAYPPCLWCHACLHRLRNLPCPHRLRSLPRPLHLRLHASPHHLRTPPHPHHLRTHLLPHHRRTRSCPCRWRSHPCCHYLRSRNSAPGPRGRTCHPGLRSRTCPPGLRSHTYLRRLRSHTCPPSLRSHAYALCLRSHTCPPRLRDHICPLSLRNCTCPPRLRSRTCLLCLRSHACPPNLRNHTCPPSLRSHACPPGLRNRICPLSLRSHPCPLGLKSPLRSQANALHLRSCPCSLPLGNHPYLPCLESQPCLSLGNHLCPLCPRSCRCPHLGSHPCRLS*	RLHASPHHL,SLRSHAYAL,RLRDHICPL,SLGNHLCPL,RLRSRTCLL,GLRNRICPL,SLRSHPCPL,HLRSCPCSL,HLGSHPCRL,HLRTHLLPH,GLRSHTYLR,RTHLLPHHR,SQANALHLR,RYRAYPPCL,HLRYRAYPP,RLRNLPCPH,RLRSLPRPL,RSLPRPLHL,HLRLHASPH,HLRTPPHPH,RTPPHPHHL,RTRSCPCRW,RWRSHPCCH,RSHPCCHYL,HYLRSRNSA,RSRNSAPGP,RGRTCHPGL,RSRTCPPGL,RSHTYLRRL,HTYLRRLRS,RLRSHTCPP,RSHTCPPSL,RSHAYALCL,RSHTCPPRL,RSRTCLLCL,RSHACPPNL,RNHTCPPSL,RSHACPPGL,RNRICPLSL,RSHPCPLGL,RSQANALHL,RSCPCSLPL,SPMSPHLRY,SLPLGNHPY,ESPMSPHLR,PMSPHLRYR,NLPCPHRLR,SLPRPLHLR,LLPHHRRTR,SHAYALCLR,DHICPLSLR,MSPHLRYRA,SPHLRYRAY,LPRPLHLRL,RPLHLRLHA,SPHHLRTPP,HPHHLRTHL,LPHHRRTRS,APGPRGRTC,CPLGLKSPL,LPLGNHPYL,CPRSCRCPH,CPHLGSHPC,YLRSRNSAP,NLRNHTCPP,WRSHPCCHY,RDHICPLSL,LESQPCLSL,EESPMSPHL,PPSLRSHAY,CPPRLRDHI,CPPGLRNRI,ESPMSPHLRY,CSLPLGNHPY,SLPLGNHPYL,SLPRPLHLRL,GLKSPLRSQA,YLPCLESQPC,RLRNLPCPHR,RLRSLPRPLH,RLHASPHHLR,GLRSHTYLRR,RSHAYALCLR,CLRSHTCPPR,SLRNCTCPPR,RSRTCLLCLR,RSHPCPLGLK,RSLPRPLHLR,RTHLLPHHRR,RSHPCCHYLR,RTCHPGLRSR,RSHTCPPSLR,RSHTCPPRLR,CTCPPRLRSR,RSHACPPNLR,RSHACPPGLR,RSQANALHLR,RYRAYPPCLW,LWCHACLHRL,HLRYRAYPPC,RNLPCPHRLR,HLRLHASPHH,HLRTPPHPHH,RTPPHPHHLR,HLRTHLLPHH,HLLPHHRRTR,RTRSCPCRWR,RSCPCRWRSH,RWRSHPCCHY,RSRNSAPGPR,RGRTCHPGLR,GLRSRTCPPG,RSRTCPPGLR,RSHTYLRRLR,HTYLRRLRSH,RLRSHTCPPS,SLRSHAYALC,RLRDHICPLS,RLRSRTCLLC,RNHTCPPSLR,SLRSHACPPG,GLRNRICPLS,RNRICPLSLR,SLRSHPCPLG,KSPLRSQANA,MSPHLRYRAY,SPMSPHLRYR,CLWCHACLHR,CPHRLRSLPR,HPCCHYLRSR,HACPPGLRNR,LPCPHRLRSL,RPLHLRLHAS,SPHHLRTPPH,HPHHLRTHLL,LPHHRRTRSC,PPRLRSRTCL,SPLRSQANAL,CPRSCRCPHL,YLRSRNSAPG,YLRRLRSHTC,HAYALCLRSH,LRYRAYPPCL,RAYPPCLWCH,HRLRSLPRPL,LRSLPRPLHL,LHLRLHASPH,LRLHASPHHL,LRTPPHPHHL,HHLRTHLLPH,WRSHPCCHYL,CHYLRSRNSA,LRSHTYLRRL,LRSHTCPPSL,LRSHAYALCL,LRSHTCPPRL,LRNCTCPPRL,LRSHACPPNL,LRNHTCPPSL,LRSHACPPGL,LRNRICPLSL,LSLRSHPCPL,LRSQANALHL,SQANALHLRS,LHLRSCPCSL,LRSCPCSLPL,LSLGNHLCPL,CPPGLRSHTY,CPPSLRSHAY	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MLL2	c.1966delC	p.L656fs	EDSPMSPPPEESPMSPPPEVSRLSP[p.L656fs]CLWCHACLHRLRNLPCPHRLRSLPRPLHLRLHASPHHLRTPPHPHHLRTHLLPHHRRTRSCPCRWRSHPCCHYLRSRNSAPGPRGRTCHPGLRSRTCPPGLRSHTYLRRLRSHTCPPSLRSHAYALCLRSHTCPPRLRDHICPLSLRNCTCPPRLRSRTCLLCLRSHACPPNLRNHTCPPSLRSHACPPGLRNRICPLSLRSHPCPLGLKSPLRSQANALHLRSCPCSLPLGNHPYLPCLESQPCLSLGNHLCPLCPRSCRCPHLGSHPCRLS*	RLHASPHHL,SLRSHAYAL,RLRDHICPL,SLGNHLCPL,RLRSRTCLL,GLRNRICPL,SLRSHPCPL,HLRSCPCSL,HLGSHPCRL,HLRTHLLPH,GLRSHTYLR,RTHLLPHHR,SQANALHLR,RLRNLPCPH,RLRSLPRPL,RSLPRPLHL,HLRLHASPH,HLRTPPHPH,RTPPHPHHL,RTRSCPCRW,RWRSHPCCH,RSHPCCHYL,HYLRSRNSA,RSRNSAPGP,RGRTCHPGL,RSRTCPPGL,RSHTYLRRL,HTYLRRLRS,RLRSHTCPP,RSHTCPPSL,RSHAYALCL,RSHTCPPRL,RSRTCLLCL,RSHACPPNL,RNHTCPPSL,RSHACPPGL,RNRICPLSL,RSHPCPLGL,RSQANALHL,RSCPCSLPL,SLPLGNHPY,NLPCPHRLR,SLPRPLHLR,LLPHHRRTR,SHAYALCLR,DHICPLSLR,EVSRLSPCL,LPRPLHLRL,RPLHLRLHA,SPHHLRTPP,HPHHLRTHL,LPHHRRTRS,APGPRGRTC,CPLGLKSPL,LPLGNHPYL,CPRSCRCPH,CPHLGSHPC,YLRSRNSAP,NLRNHTCPP,VSRLSPCLW,WRSHPCCHY,RDHICPLSL,LESQPCLSL,PPSLRSHAY,CPPRLRDHI,CPPGLRNRI,CSLPLGNHPY,RLSPCLWCHA,SLPLGNHPYL,SLPRPLHLRL,GLKSPLRSQA,YLPCLESQPC,RLRNLPCPHR,RLRSLPRPLH,RLHASPHHLR,GLRSHTYLRR,RSHAYALCLR,CLRSHTCPPR,SLRNCTCPPR,RSRTCLLCLR,RSHPCPLGLK,RSLPRPLHLR,RTHLLPHHRR,RSHPCCHYLR,RTCHPGLRSR,RSHTCPPSLR,RSHTCPPRLR,CTCPPRLRSR,RSHACPPNLR,RSHACPPGLR,RSQANALHLR,LWCHACLHRL,RNLPCPHRLR,HLRLHASPHH,HLRTPPHPHH,RTPPHPHHLR,HLRTHLLPHH,HLLPHHRRTR,RTRSCPCRWR,RSCPCRWRSH,RWRSHPCCHY,RSRNSAPGPR,RGRTCHPGLR,GLRSRTCPPG,RSRTCPPGLR,RSHTYLRRLR,HTYLRRLRSH,RLRSHTCPPS,SLRSHAYALC,RLRDHICPLS,RLRSRTCLLC,RNHTCPPSLR,SLRSHACPPG,GLRNRICPLS,RNRICPLSLR,SLRSHPCPLG,KSPLRSQANA,CLWCHACLHR,CPHRLRSLPR,HPCCHYLRSR,HACPPGLRNR,LPCPHRLRSL,RPLHLRLHAS,SPHHLRTPPH,HPHHLRTHLL,LPHHRRTRSC,PPRLRSRTCL,SPLRSQANAL,CPRSCRCPHL,YLRSRNSAPG,YLRRLRSHTC,HAYALCLRSH,HRLRSLPRPL,LRSLPRPLHL,LHLRLHASPH,LRLHASPHHL,LRTPPHPHHL,HHLRTHLLPH,WRSHPCCHYL,CHYLRSRNSA,LRSHTYLRRL,LRSHTCPPSL,LRSHAYALCL,LRSHTCPPRL,LRNCTCPPRL,LRSHACPPNL,LRNHTCPPSL,LRSHACPPGL,LRNRICPLSL,LSLRSHPCPL,LRSQANALHL,SQANALHLRS,LHLRSCPCSL,LRSCPCSLPL,LSLGNHLCPL,CPPGLRSHTY,CPPSLRSHAY	STAD
MLL2	c.7061delC	p.P2354fs	APLTPRASQVEPQSPGLGLRPQEPP[p.P2354fs]LPRLWHLLLQVTQTSFALAPTLTHMLSPH*	RLWHLLLQV,ALAPTLTHM,LQVTQTSFA,VTQTSFALA,QVTQTSFAL,QTSFALAPT,LPRLWHLLL,LLQVTQTSF,GLRPQEPPL,TQTSFALAP,TSFALAPTL,FALAPTLTH,RLWHLLLQVT,ALAPTLTHML,LLQVTQTSFA,LQVTQTSFAL,LLLQVTQTSF,QVTQTSFALA,QTSFALAPTL,RPQEPPLPRL,FALAPTLTHM,TQTSFALAPT	STAD
MLL3	c.1066C>A	p.Q356K	IDQAPERSKEDANCAVCDSPGDLLD[p.Q356K]KFFCTTCGQHYHGMCLDIAVTPLKRA	LLDKFFCTT,SPGDLLDKF,SPGDLLDKFF	LUAD
MLL3	c.1179C>A	p.N393K	GMCLDIAVTPLKRAGWQCPECKVCQ[p.N393K]KCKQSGEDSKMLVCDTCDKGYHTFCL	KCKQSGEDSK	LUAD
MLL3	c.13488delT	p.F4496fs	TSGCHRFRCTNIYHFTCAIKAQCMF[p.F4496fs]LRTKLCFAPCTNQREFMSKN*	FLRTKLCFA,AIKAQCMFL,AQCMFLRTK,MFLRTKLCF,RTKLCFAPC,CFAPCTNQR,AIKAQCMFLR,KAQCMFLRTK,CTNQREFMSK,CMFLRTKLCF,RTKLCFAPCT,FLRTKLCFAP,AQCMFLRTKL,FAPCTNQREF	STAD
MLL5	c.197A>G	p.Y66C	YPHQLYTSSSHHSHSYIGLPYADHN[p.Y66C]CGARPPPTPPASPPPSVLISKNEVGI	LPYADHNCGA	TGCT
MLXIPL	c.2368A>C	p.S790R	NWKFWVFSILIRPLFESFNGMVSTA[p.S790R]RVHTLRQTSLAWLDQYCSLPALRPTV	STARVHTLR,RVHTLRQTS,GMVSTARVH,VSTARVHTL,MVSTARVHTL,VSTARVHTLR,RVHTLRQTSL,SFNGMVSTAR	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MMAA	c.976C>T	p.R326C	RIQAEYVSALKLLRKRSQVWKPKVI[p.R326C]CISARSGEGISEMWDKMKDFQDLMLA	CISARSGEGI	CRC
MMP3	c.190delA	p.I64fs	ENYYDLKKDVKQFVRRKDSGPVVKK[p.I64fs]SEKCRSSLDWR*	KSEKCRSSL,KCRSSLDWR,KKSEKCRSSL,SEKCRSSLDW	STAD
MMRN1	c.2751C>A	p.F917L	QALQLQVLNSRFKALEAKSIHLSIN[p.F917L]LFSLNKTLHEVLTMCHNASTSVSELN	HLSINLFSL,NLFSLNKTL,SINLFSLNK,SIHLSINLF,KSIHLSINL,LSINLFSLNK,KSIHLSINLF,AKSIHLSINL,IHLSINLFSL	UCEC
MMRN1	c.3037G>T	p.A1013S	RSLPGSLANVVKSQKQVKSLPKKIN[p.A1013S]SLKKPTVNLTTVLIGRTQRNTDNIIY	SLPKKINSL,SLKKPTVNL,KSLPKKINS,LPKKINSLK,SLPKKINSLK,KSLPKKINSL,KINSLKKPTV	LUAD
MMS19	c.3013G>A	p.D1005N	ALTRLPTPVLLPYKPQVIRALAKPL[p.D1005N]NDKKRLVRKEAVSARGEWFLLGSPGS	ALAKPLNDK,LAKPLNDKK,RALAKPLNDK,ALAKPLNDKK	TGCT
MN1	c.1415C>T	p.S472L	APPYMNVAKRPRFDFPGSAGVDRCA[p.S472L]LWNGSMHNGALDNHLSPSAYPGLPGE	RCALWNGSM	BLCA
MOCOS	c.2545T>C	p.S849P	NQHVFQKLSESRETKVNFGMYLMHA[p.S849P]PLDLSSPCFLSVGSQVLPVLKENVEG	GMYLMHAPL,YLMHAPLDL,FGMYLMHAPL,YLMHAPLDLS,MYLMHAPLDL,APLDLSSPCF,LMHAPLDLSS	KIRC
MOCS2	c.65delC	p.P22fs	MSSLEISSSCFSLETKLPLSP[p.P22fs]H*	LETKLPLSPH	STAD
MOGAT2	c.197_198insG	p.Q66fs	TRFWLLTVLYAAWWYLDRDKPRQGG[p.Q66fs]PAHPGHQVLDYMEVHEGLFPHLAGQDC*	HQVLDYMEV,GLFPHLAGQ,DYMEVHEGL,KPRQGGPAH,GPAHPGHQV,RQGGPAHPG,YMEVHEGLF,HPGHQVLDY,EVHEGLFPH,HEGLFPHLA,DYMEVHEGLF,EVHEGLFPHL,GPAHPGHQVL,RQGGPAHPGH,AHPGHQVLDY,HQVLDYMEVH,LDYMEVHEGL,MEVHEGLFPH,HPGHQVLDYM	LUAD
MORC1	c.337G>T	p.D113Y	KRLSTLKFIGQYGNGLKSGSMRIGK[p.D113Y]YFILFTKKEETMTCVFFSQTFCEEES	SMRIGKYFI,RIGKYFILF,KYFILFTKK,SGSMRIGKY,MRIGKYFIL,GSMRIGKYF,IGKYFILFTK,MRIGKYFILF,GSMRIGKYFI,SMRIGKYFIL,KSGSMRIGKY,SGSMRIGKYF	CRC
MORC2	c.2219G>A	p.R740H	SDSAGEEDSADLKRAQKDKGLHVEV[p.R740H]HVNREWYTGRVTAVEVGKHVVRWKVK	VEVHVNREW,HVNREWYTGR,VEVHVNREWY	CRC
MPDZ	c.2410C>A	p.L804I	VRIGVAKPLPLSPEEGYVSAKEDSF[p.L804I]IYPPHSCEEAGLADKPLFRADLALVG	SAKEDSFIY,KEDSFIYPP,VSAKEDSFIY,YVSAKEDSFI	CRC
MPDZ	c.4745delA	p.K1582fs	KLTIHAENPDSQAVPSAAGAASGEK[p.K1582fs]RTAPSL*	GEKRTAPSL	STAD
MPRIP	c.1052delC	p.A351fs	SSDTRQGRSEKRAFPRKRDFTNEAP[p.A351fs]QLLSQTPRLPPCLHTEEPSHWTGGPRSPP*	FTNEAPQLL,QLLSQTPRL,SQTPRLPPC,RDFTNEAPQL,SQTPRLPPCL,CLHTEEPSHW,NEAPQLLSQT	STAD
MR1	c.137C>T	p.S46L	DSRTHSLRYFRLGVSDPIHGVPEFI[p.S46L]LVGYVDSHPITTYDSVTRQKEPRAPW	VPEFILVGY,GVPEFILVGY,VPEFILVGYV	CRC
MRPL47	c.700C>A	p.L234I	LRLEREKRARIKARKENLERKKAKI[p.L234I]ILKKFPHLAEAQKSSLV*	ILKKFPHLA,RKKAKIILK,IILKKFPHL,KAKIILKKF,RKKAKIILKK,KIILKKFPHL,LERKKAKIIL,KKAKIILKKF	CRC
MRPS25	c.355_357delGAG	p.E119del	SNKEIMEHIRKILGKNEETLREEEE[p.E119del]KKQLSHPANFGPRKYCLRECICEVEGQV	REEEEKKQL	TGCT
MS4A4A	c.295G>A	p.V99M	ALMSLSMGITMMCMASNTYGSNPIS[p.V99M]MYIGYTIWGSVMFIISGSLSIAAGIR	ISMYIGYTI,TYGSNPISM,SMYIGYTIW,MYIGYTIWG,YGSNPISMY,NPISMYIGY,ISMYIGYTIW,MYIGYTIWGS,TYGSNPISMY,NTYGSNPISM	BRCA
MS4A8B	c.8C>T	p.S3L	MN[p.S3L]LMTSAVPVANSVLVVAPHNGYPVTPG	NLMTSAVPV,LMTSAVPVA,NLMTSAVPVA,MNLMTSAVPV	CRC,UCEC
MSH4	c.1392G>T	p.K464N	KNCNTPLLRAYYGSLEDKRFGIILE[p.K464N]NIKTVINDDARYMKGCLNMRTQKCYA	IILENIKTV,RFGIILENI,GIILENIKTV,RFGIILENIK,KRFGIILENI	CRC
MSH4	c.2188G>A	p.E730K	YVPAEYSSFRIAKQIFTRISTDDDI[p.E730K]KTNSSTFMKEMKEIAYILHNANDKSL	KTNSSTFMK,IKTNSSTFM	UCEC

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MSH6	c.1727A>C	p.D576A	GHTRAYGVCFVDTSLGKFFIGQFSD[p.D576A]ARHCSRFRTLVAHYPPVQVLFEKGNL	FSDARHCSR,DARHCSRFR,GQFSDARHC,SDARHCSRF,FSDARHCSRF,KFFIGQFSDA,FFIGQFSDAR,QFSDARHCSR,GQFSDARHCS,ARHCSRFRTL	TGCT
MSH6	c.3254_3255insC	p.T1085fs	LANYSRGGDGPMCRPVILLPEDTPP[p.T1085fs]LLRA*	LLPEDTPPL,LPEDTPPLL,ILLPEDTPPL,LLPEDTPPLL	CRC,STAD
MSH6	c.3284G>A	p.R1095H	GDGPMCRPVILLPEDTPPFLELKGS[p.R1095H]HHPCITKTFFGDDFIPNDILIGCEEE	GSHHPCITK,KGSHHPCITK,ELKGSHHPCI,SHHPCITKTF,LELKGSHHPC	CRC
MSLNL	c.202A>C	p.T68P	MTSARRRTDVGPRVAFTYPCTQLSP[p.T68P]PRAHRHLPVHTVTYPCTQLSPTRAHS	QLSPPRAHR,SPPRAHRHL,TQLSPPRAH,PPRAHRHLPV	PRAD
MST1	c.1304delA	p.N435fs	AETPHKPQFTFTSEPHAQLEENFCR[p.N435fs]TQMGIAMGPGATRWTQGPHSTTVPCDAALMTSRHQSWTPQTRCSLRSVARGWIGWISGVPSCAWLGAIRATHPGQSACGIGRASISAGGL*	GWIGWISGV,WISGVPSCA,RTQMGIAMG,QTRCSLRSV,RCSLRSVAR,AIRATHPGQ,HQSWTPQTR,HPGQSACGI,EENFCRTQM,CRTQMGIAM,SLRSVARGW,ISGVPSCAW,RATHPGQSA,SLRSVARGWI,SVARGWIGWI,QTRCSLRSVA,RGWIGWISGV,AIRATHPGQS,WTPQTRCSLR,VPSCAWLGAI,FCRTQMGIAM,LEENFCRTQM,CSLRSVARGW,RSVARGWIGW,WISGVPSCAW	KIRP
MST1R	c.1390A>G	p.M464V	FNGLLGPVQVTALYVTRLDNVTVAH[p.M464V]VGTMDGRILQVELVRSLNYLLYVSNF	VTVAHVGTM,RLDNVTVAHV	KIRC
MTG1	c.315delA	p.L105fs	LNKMDLADLTEQQKIMQHLEGEGLK[p.L105fs]MSFLPTV*	HLEGEGLKM,LKMSFLPTV,GEGLKMSFL,GLKMSFLPTV,LEGEGLKMSF	STAD
MTG1	c.981delC	p.H327fs	DFLQTFRRGLLGSVMLDLDVLRGHP[p.H327fs]RLRLCPELVRVGRAGGMWPPRPPDLGG*	RLCPELVRV,RLRLCPELV,RAGGMWPPR,MWPPRPPDL,VLRGHPRLR,RGHPRLRLC,LVRVGRAGG,HPRLRLCPE,RVGRAGGMW,GMWPPRPPDL,RLRLCPELVR,VLRGHPRLRL,LVRVGRAGGM,DLDVLRGHPR,DVLRGHPRLR,HPRLRLCPEL	STAD
MTIF2	c.326delA	p.N109fs	STKSKKVVEVWIGMTIEELARAMEK[p.N109fs]TQIMYMKLY*	AMEKTQIMY,KTQIMYMKL,RAMEKTQIM,TQIMYMKLY,MEKTQIMYM,KTQIMYMKLY,RAMEKTQIMY,MEKTQIMYMK,ARAMEKTQIM,AMEKTQIMYM	STAD
MTMR9	c.577delA	p.K193fs	DEALRKVATFRHGGRFPVLSYYHKK[p.K193fs]MGW*	SYYHKKMGW,VLSYYHKKM,LSYYHKKMGW	KICH
MTOR	c.4379T>C	p.L1460P	YAMKHFGELEIQATWYEKLHEWEDA[p.L1460P]PVAYDKKMDTNKDDPELMLGRMRCLE	APVAYDKKM,HEWEDAPVA,KLHEWEDAPV,HEWEDAPVAY	KIRC
MTOR	c.4448G>T	p.C1483F	DALVAYDKKMDTNKDDPELMLGRMR[p.C1483F]FLEALGEWGQLHQQCCEKWTLVNDET	LMLGRMRFL,RFLEALGEW,LGRMRFLEA,RMRFLEALG,ELMLGRMRF,GRMRFLEAL,MLGRMRFLEA,RMRFLEALGE,ELMLGRMRFL,LGRMRFLEAL,MRFLEALGEW	KIRC
MTOR	c.6644C>A	p.S2215Y	EDLRQDERVMQLFGLVNTLLANDPT[p.S2215Y]YLRKNLSIQRYAVIPLSTNSGLIGWV	LLANDPTYL,LANDPTYLR,TYLRKNLSI,TLLANDPTY,TLLANDPTYL,LLANDPTYLR,LANDPTYLRK,NTLLANDPTY,YLRKNLSIQR	UCEC
MTUS2	c.3013C>T	p.R1005W	YPKQRTAAARNGFPPKPDPQAREAE[p.R1005W]WQLVLRLKERCEQQTRQLGVAQGELK	EAEWQLVLR,REAEWQLVL,AEWQLVLRL,DPQAREAEW,AEWQLVLRLK	STAD
MUC16	c.15355C>T	p.P5119S	LPNFSSTSDKILATSKDSKDTKEIF[p.P5119S]SSINTEETNVKANNSGHESHSPALAD	DTKEIFSSI,KEIFSSINT,KDTKEIFSSI	SKCM
MUC16	c.18466G>A	p.A6156T	PDISPEASSSHSNSPPLTISTHKTI[p.A6156T]TTQTGPSGVTSLGQLTLDTSTIATSA	TTQTGPSGV,ITTQTGPSGV	STAD
MUC16	c.25817G>A	p.R8606H	ESISSSPHPVTALLTLGPVKTTDML[p.R8606H]HTSSEPETSSPPNLSSTSAEILATSE	MLHTSSEPET	CRC
MUC16	c.31355_31356insC	p.P10452fs	GIMEHITKIPNEAAHRGTIRPVKGP[p.P10452fs]SDIHFACQS*	RPVKGPSDI,VKGPSDIHF	KICH
MUC16	c.33014C>T	p.T11005I	VLPEVPGMVTSLVASSRAVTSTTLP[p.T11005I]ILTLSPGEPETTPSMATSHGAEASST	AVTSTTLPI,LPILTLSPG,RAVTSTTLPI	CLL
MUC16	c.33778C>G	p.P11260A	IDSWVAHPGTEASSVVPTLTVSTGE[p.P11260A]AFTNISLVTHPAESSSTLPRTTSRFS	STGEAFTNI,EAFTNISLV,LTVSTGEAF,GEAFTNISL,TLTVSTGEAF,GEAFTNISLV	KIRC

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MUC16	c.34782C>A	p.N11594K	YEPETTATWLTHPAETSTTVSGTIP[p.N11594K]KFSHRGSDTAPSMVTSPGVDTRSGVP	TTVSGTIPK,GTIPKFSHR,STTVSGTIPK,TTVSGTIPKF	LUSC
MUC16	c.38321G>A	p.R12774H	SGCRLTLLRSEKDGAATGVDAICTH[p.R12774H]HLDPKSPGVDREQLYWELSQLTNGIK	HLDPKSPGV,AICTHHLDPK	HNSC
MUC17	c.13244G>A	p.R4415H	LVYGLVGAGVVLMLIILVALLMLVF[p.R4415H]HSKREVKRQKYRLSQLYKWQEEDSGP	LLMLVFHSK,VFHSKREVK,LMLVFHSKR,MLVFHSKREV,ALLMLVFHSK,LVFHSKREVK,HSKREVKRQK,LLMLVFHSKR,VFHSKREVKR	BRCA
MUC17	c.229G>A	p.V77M	CQQLSQHVRTGSAANTATGTTSTNV[p.V77M]MEPRMYLSCSTNPEMTSIESSVTSDT	NVMEPRMYL,TSTNVMEPR,MEPRMYLSC,STNVMEPRMY,TTSTNVMEPR,NVMEPRMYLS,ATGTTSTNVM	GBM
MUC17	c.3680_3681insC	p.R1227fs	PTAEVTSMPTSTPGERSTPLTSMPV[p.R1227fs]STHASGQF*	TSMPVSTHA,VSTHASGQF,MPVSTHASG,LTSMPVSTHA,MPVSTHASGQ	KIRC
MUC17	c.3683delA	p.H1228fs	TAEVTSMPTSTPGERSTPLTSMPVR[p.H1228fs]PRQWPVLRLAPFQHLPLTPAHL*	FQHLPLTPA,HLPLTPAHL,LTSMPVRPR,PVRPRQWPV,RPRQWPVLR,RQWPVLRLA,WPVLRLAPF,LRLAPFQHL,LAPFQHLPL,RLAPFQHLPL,VLRLAPFQHL,QWPVLRLAPF,PVRPRQWPVL,MPVRPRQWPV,RPRQWPVLRL,FQHLPLTPAH,TSMPVRPRQW,RQWPVLRLAP	KIRC
MUC17	c.6836C>A	p.T2279N	STEATSSPTTAEGTSIPTSTLSEGT[p.T2279N]NPLTSIPVSHTLVANSEVSTLSTTPV	TLSEGTNPL,TLSEGTNPLT,GTNPLTSIPV,STLSEGTNPL,SEGTNPLTSI,NPLTSIPVSH	TGCT
MUC2	c.4703C>T	p.T1568M	TTTVTPTPTPTGTQTPTTTPITTTTTVT[p.T1568M]MVTPTPTPTGTQTPTSTPITTTTTVT	TTPITTTTTM,TPITTTTTMV,TTTTMVTPT,TTMVTPTPT,MVTPTPTPT,TTTPITTTTM,TTPITTTTMV,TMVTPTPTPT,TPITTTTMVT	TGCT
MUC2	c.4739C>A	p.T1580N	TQTPTTTPITTTTTTVTPTPTPTGTQ[p.T1580N]NPTSTPITTTTTTVTPTPTPTGTQTPT	TQNPTSTPI,TQNPTSTPIT	TGCT
MUC2	c.4745C>G	p.T1582R	TPTTTPITTTTTTVTPTPTPTGTQTP[p.T1582R]RSTPITTTTTTVTPTPTPTGTQTPTTT	TQTPRSTPI,GTQTPRSTPI,TPRSTPITTT	KIRP
MUC2	c.4790C>T	p.T1597I	TPTPTGTQTPTSTPITTTTTTVTPTP[p.T1597I]IPTGTQTPTTTPITTTTTTVTPTPTPT	TTTVTPTPI,TTTTVTPTPI,TTVTPTPIPT	TGCT
MUC2	c.5111C>T	p.T1704I	TTTTTVTPTPTPTGTQTPTSTPITT[p.T1704I]ITTVTPTPTPTGTQTPTPTPISTTTT	TTITTVTPT,TPITTITTV,STPITTITTV,TPITTITTVT,TPTSTPITTI	TGCT
MUC2	c.5117C>T	p.T1706M	TTTVTPTPTPTGTQTPTSTPITTTT[p.T1706M]MVTPTPTPTGTQTPTPTPISTTTTVT	TPITTTTMV,TTTTMVTPT,TTMVTPTPT,MVTPTPTPT,STPITTTTMV,TSTPITTTTM,TMVTPTPTPT,TPITTTTMVT	TGCT
MUC2	c.5143G>A	p.G1715S	PTGTQTPTSTPITTTTTVTPTPTPT[p.G1715S]STQTPTPTPISTTTTVTPTPTPTGTQ	STQTPTPTPI	TGCT
MUC2	c.5165C>T	p.T1722I	TSTPITTTTTVTPTPTPTGTQTPTP[p.T1722I]IPISTTTTVTPTPTPTGTQTPTTTPI	IPISTTTTV,TQTPTPIPI,TPIPISTTT,TPIPISTTTT,IPISTTTTVT	KIRP
MUC5B	c.2041A>G	p.S681G	YMGIFLVIETHGMAVSWDRKTSVFI[p.S681G]GLHQDYKGRVCGLCGNFDDNAINDFA	KTSVFIGLH,FIGLHQDYK,VFIGLHQDY,RKTSVFIGL,GLHQDYKGRV,VFIGLHQDYK,SVFIGLHQDY	ACC
MUC5B	c.2045A>G	p.D682G	MGIFLVIETHGMAVSWDRKTSVFIR[p.D682G]RHQDYKGRVCGLCGNFDDNAINDFAT	FIRRHQDYK,KTSVFIRRH,VFIRRHQDY,VFIRRHQDYK,SVFIRRHQDY	ACC,KIRP

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MUC6	c.4707_4708insA	p.P1569fs	ITPNPTSTRTRTPVAHTNSATSSRP[p.P1569fs]TTTLHHTLPTYREQSLLFHRSHDGNILQDHHYLSNPITPSDHTSHSRSTFLHLFGDSKYSHSHHPYPCTDGHFCLHPLNANRHDSSTDNAQGHRVHPHSANNDADHQRDQPSPELIKHSQNLYIPTFTHFLHTPC*	CTDGHFCLH,YLSNPITPS,YIPTFTHFL,FLHLFGDSK,CLHPLNANR,TYREQSLLF,SRSTFLHLF,KYSHSHHPY,SQNLYIPTF,LYIPTFTHF,SSRPTTTLH,TSHSRSTFL,HSRSTFLHL,RSTFLHLFG,RVHPHSANN,TLHHTLPTY,LHLFGDSKY,LIKHSQNLY,FTHFLHTPC,LPTYREQSL,HPHSANNDA,ELIKHSQNL,HTSHSRSTF,TSSRPTTTL,HRSHDGNIL,GNILQDHHY,HHYLSNPIT,SKYSHSHHP,AQGHRVHPH,IKHSQNLYI,HPYPCTDGH,IPTFTHFLH,TTLHHTLPTY,STDNAQGHRV,LIKHSQNLYI,TLHHTLPTYR,TSHSRSTFLH,TFLHLFGDSK,PTYREQSLLF,HSRSTFLHLF,HSQNLYIPTF,NLYIPTFTHF,LYIPTFTHFL,ATSSRPTTTL,SSRPTTTLHH,HTSHSRSTFL,RVHPHSANND,HQRDQPSPEL,FLHLFGDSKY,SKYSHSHHPY,ELIKHSQNLY,RPTTTLHHTL,LPTYREQSLL,HPYPCTDGHF,EQSLLFHRSH,FHRSHDGNIL,SHSRSTFLHL,HLFGDSKYSH,YSHSHHPYPC,KHSQNLYIPT,SQNLYIPTFT,YPCTDGHFCL,REQSLLFHRS,QDHHYLSNPI,IPTFTHFLHT	KIRC
MUC6	c.5930C>A	p.P1977H	AHTTSASSSRLPTPFTTHSPPTGSS[p.P1977H]HFSSTGPMTATSFQTTTTYPTPSHPQ	SHFSSTGPM,SSHFSSTGPM,HSPPTGSSHF,SHFSSTGPMT	TGCT
MUC6	c.6000C>G	p.H2000Q	SSPFSSTGPMTATSFQTTTTYPTPS[p.H2000Q]QPQTTLPTHVPPFSTSLVTPSTHTVI	TPSQPQTTL,SQPQTTLPT,SQPQTTLPTH,QPQTTLPTHV	TGCT
MUC6	c.6387_6389delCTC	p.2129_2130SS>S	SPITTQLPHLSSATTPVSTTNQLSS[p.2129_2130SS>S]FSPSPSAPSTVSSYVPSSHSSPQTSSPS	STTNQLSSF,NQLSSFSPS,VSTTNQLSSF,NQLSSFSPSP	STAD
MUC7	c.1007C>T	p.S336L	PNSSPTTLAPDTSETSAAPTHQTTT[p.S336L]LVTTQTTTTKQPTSAPGQNKISRFLL	APTHQTTTL,HQTTTLVTT,LVTTQTTTTK,APTHQTTTLV,HQTTTLVTTQ	UCEC
MVK	c.412delC	p.P138fs	YLSICRKQRALPSLDIVVWSELPPG[p.P138fs]RAWAPAPPTRCVWQQPS*	RAWAPAPPT,APAPPTRCV,SELPPGRAW,RAWAPAPPTR,VVWSELPPGR,WAPAPPTRCV,LPPGRAWAPA,APAPPTRCVW,SELPPGRAWA	STAD
MXRA5	c.970G>T	p.D324Y	EEDGGSQLILEKFQLPQWSISLNMT[p.D324Y]YEHGNMVNLVCDIKKPMDVYKIHLNQ	WSISLNMTY,MTYEHGNMV,NMTYEHGNM,YEHGNMVNL,NMTYEHGNMV,TYEHGNMVNL,QWSISLNMTY,LNMTYEHGNM,YEHGNMVNLV	LUAD
MYB	c.1443delA	p.R481fs	ESSLDPPKVLPPARHSTIPLVILRK[p.R481fs]NGARPAP*	VILRKNGAR,ILRKNGARPA,LVILRKNGAR	STAD
MYBPC2	c.1937G>A	p.R646H	TNPVGEDVASIFLQVVDVPDPPEAV[p.R646H]HITSVGEDWAILVWEPPMYDGGKPVT	PEAVHITSV,VPDPPEAVHI	UCEC
MYD88	c.719T>C	p.M240T	TCVWSIASELIEKRLARRPRGGCRR[p.M240T]TVVVVSDDYLQSKECDFQTKFALSLS	TVVVVSDDY,RPRGGCRRT,RTVVVVSDDY,TVVVVSDDYL,RPRGGCRRTV	CLL
MYD88	c.752G>A	p.S251N	EKRLARRPRGGCRRMVVVVSDDYLQ[p.S251N]NKECDFQTKFALSLSPGAHQKRLIPI	YLQNKECDF,VVSDDYLQNK,NKECDFQTKF	DLBCL
MYD88	c.818T>C	p.L273P	YLQSKECDFQTKFALSLSPGAHQKR[p.L273P]PIPIKYKAMKKEFPSILRFITVCDYT	HQKRPIPIK,RPIPIKYKA,QKRPIPIKY,AHQKRPIPIK,QKRPIPIKYK,HQKRPIPIKY,SPGAHQKRPI,RPIPIKYKAM	CLL,DLBCL
MYEF2	c.967A>G	p.K323E	LFDRPMHVKMDDKSVPHEEYRSHDG[p.K323E]ETPQLPRGLGGIGMGLGPGGQPISAS	ETPQLPRGL,RSHDGETPQL,GETPQLPRGL	TGCT
MYEOV	c.807delG	p.L269fs	CSTWGLPLRVAGSWLTVVTVEALGG[p.L269fs]GAWELGGLARWGPLCTHPQCQVLLLSSSTTSSSSSSSSSSLVEDVLCAKWFICPASFNPQNDSMR*	ALGGGAWEL,SLVEDVLCA,GLARWGPLC,LVEDVLCAK,KWFICPASF,SSSSSSSLV,CAKWFICPA,DVLCAKWFI,HPQCQVLLL,VEALGGGAW,WELGGLARW,CQVLLLSSS,SFNPQNDSM,SLVEDVLCAK,SS5SSSSSSLV,SFNPQNDSMR,VTVEALGGGA,EALGGGAWEL,LARWGPLCTH,CQVLLLSSST,AKWFICPASF,ASFNPQNDSM,WELGGLARWG	STAD
MYEOV	c.905T>A	p.L302H	RRTGQVGPTMHPPPVSGASPLLLHH[p.L302H]HLLLLLIIILTC*	LLLHHHLLL,LLHHHLLLL,SPLLLHHHL,LHHHLLLLL,LLLHHHLLL,LLHHHLLLLL,SPLLLHHHLL,LHHHLLLLLI,HHHLLLLLII	TGCT
MYH10	c.3271_3272insC	p.L1091fs	MISDLEERLKKEEKTRQELEKAKRK[p.L1091fs]PRRGDDRPAGPDRRAAGAD*	KAKRKPRRG,RPAGPDRRA,KPRRGDDRPA,RPAGPDRRAA	LUAD

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MYH11	c.2977G>A	p.E993K	EEEAARQKLQLEKVTAEAKIKKLED[p.E993K]KILVMDDQNNKLSKERKLLEERISDL	KLEDKILVM,KKLEDKILVM	HNSC
MYH11	c.3787_3789delAAG	p.K1263del	KENADLAGELRVLGQAKQEVEHKKK[p.K1263del]LEAQVQELQSKCSDGERARAELNDKVHK	VEHKKKLEA,KQEVEHKKKL	STAD
MYH13	c.931G>A	p.D311N	HIFYQIMSNKKPELIDLLLISTNPF[p.D311N]NFPFVSQGEVTVASIDDSEELLATDN	LISTNPFNF,STNPFNFPF,TNPFNFPFV,NPFNFPFVS,STNPFNFPFV,LLISTNPFNF,ISTNPFNFPF	CRC
MYH4	c.2369C>T	p.T790M	TKVFFKAGLLGTLEEMRDEKLAQLI[p.T790M]MRTQAICRGFLMRVEFRKMMERRESI	KLAQLIMRT,QLIMRTQAI,IMRTQAICR,AQLIMRTQA,DEKLAQLIM,LIMRTQAICR,IMRTQAICRG,RDEKLAQLIM,AQLIMRTQAI,MRTQAICRGF	LUAD
MYH6	c.2540C>T	p.T847M	AFMGVKNWPWMKLYFKIKPLLKSAE[p.T847M]MEKEMATMKEEFGRIKETLEKSEARR	LLKSAEMEK,KPLLKSAEM,KSAEMEKEM,AEMEKEMAT,EMEKEMATM,IKPLLKSAEM,LKSAEMEKEM,AEMEKEMATM	BRCA
MYH7	c.4459G>A	p.A1487T	ESQSELESSQKEARSLSTELFKLKN[p.A1487T]TYEESLEHLETFKRENKNLQEEISDL	TYEESLEHL,ELFKLKNTY,LKNTYEESL,KLKNTYEESL,NTYEESLEHL,TELFKLKNTY	KIRP
MYH7	c.5065C>T	p.R1689C	NDDLKENIAIVERRNNLLQAELEEL[p.R1689C]CAVVEQTERSRKLAEQELIETSERVQ	AELEELCAV,EELCAVVEQ,AELEELCAVV,EELCAVVEQT	CRC
MYH8	c.2354C>T	p.A785V	KFGHTKVFFKAGLLGLLEEMRDEKL[p.A785V]VQIITRTQAVCRGFLMRVEYQKMLQR	KLVQIITRT,VQIITRTQA,DEKLVQIIT,VQIITRTQAV,EMRDEKLVQI	TGCT
MYH8	c.3016C>A	p.H1006N	LTEEMAGLDETIAKLSKEKKALQET[p.H1006N]NQQTLDDLQAEEDKVNILTKAKTKLE	LQETNQQTL,ALQETNQQTL	LUAD
MYH8	c.3143G>A	p.R1048Q	LTKAKTKLEQQVDDLEGSLEQEKKL[p.R1048Q]QMDLERAKRKLEGDLKLAQESTMDME	KLQMDLERA,LEQEKKLQM,LQMDLERAK,QEKKLQMDL,KLQMDLERAK	CRC
MYH8	c.3349C>T	p.R1117C	NLISKIEDEQAVEIQLQKKIKELQA[p.R1117C]CIEELGEEIEAERASRAKAEKQRSDL	KIKELQACI,KKIKELQAC,KKIKELQACI,KELQACIEEL	LUAD
MYO18A	c.627delC	p.P209fs	PRPGHRSRAPELVTKKFPVDLRLPP[p.P209fs]WCPCPHLPSGSWSCNDGPLETLASPCGAQPCWIGAPRARPVGVWSTLLSLVQAPRTWPWGWCQEIDWWRLMGTMWRASPGMRLWR*	GVWSTLLSL,RLMGTMWRA,TMWRASPGM,VWSTLLSLV,VQAPRTWPW,WWRLMGTMW,RARPVGVWS,GTMWRASPG,MWRASPGMR,QPCWIGAPR,CWIGAPRAR,LLSLVQAPR,ETLASPCGA,CPHLPSGSW,APRARPVGV,RPVGVWSTL,SLVQAPRTW,QEIDWWRLM,WRASPGMRL,RASPGMRLW,LPPWCPCPH,SPCGAQPCW,WPWGWCQEI,GVWSTLLSLV,WIGAPRARPV,TMWRASPGMR,TLLSLVQAPR,RASPGMRLWR,TWPWGWCQEI,DWWRLMGTMW,MWRASPGMRL,RARPVGVWST,GTMWRASPGM,WWRLMGTMWR,FPVDLRLPPW,APRARPVGVW,RPVGVWSTLL,GSWSCNDGPL,VGVWSTLLSL,LSLVQAPRTW,LVQAPRTWPW,CQEIDWWRLM,IDWWRLMGTM,WRASPGMRLW,LETLASPCGA,LPPWCPCPHL	STAD
MYO1D	c.326C>T	p.T109M	AAYKAMKRRSKDTCIVISGESGAGK[p.T109M]MEASKYIMQYIAAITNPSQRAEVERV	GAGKMEASK,AGKMEASKY,GKMEASKYI,KMEASKYIM,SGAGKMEASK,GAGKMEASKY,MEASKYIMQY,GKMEASKYIM,GESGAGKMEA	GBM
MYO1D	c.736G>A	p.E246K	LQKSLSSYNYIHVGAQLKSSINDAA[p.E246K]KFRVVADAMKVIGFKPEEIQTVYKIL	KSSINDAAK,SINDAAKFR,KFRVVADAM,DAAKFRVVA,SSINDAAKF,SINDAAKFRV,SSINDAAKFR,AAKFRVVADA,KFRVVADAMK,KSSINDAAKF,AKFRVVADAM	CRC
MYO3A	c.1573A>C	p.N525H	AVVGAQISEYLLEKSRVIHQAIGEK[p.N525H]HFHIFYYIYAGLAEKKKLAHYKLPEN	AIGEKHFHI,IGEKHFHIF,KHFHIFYYI,HFHIFYYIY,HQAIGEKHF,GEKHFHIFY,EKHFHIFYY,HFHIFYYIY,QAIGEKHFHI,IHQAIGEKHF,AIGEKHFHIF	CRC
MYO3A	c.1574A>G	p.N525S	AVVGAQISEYLLEKSRVIHQAIGEK[p.N525S]SFHIFYYIYAGLAEKKKLAHYKLPEN	AIGEKSFHI,KSFHIFYYI,GEKSFHIFY,SFHIFYYIY,HQAIGEKSF,IGEKSFHIF,EKSFHIFYY,KSFHIFYYI,SFHIFYYIY,IGEKSFHIFY,GEKSFHIFYY,QAIGEKSFHI,IHQAIGEKSF,HQAIGEKSFH,AIGEKSFHIF	KIRC,OV

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MYO5B	c.1214C>T	p.A405V	KLVTTSETYVKTMSLQQVINARNAL[p.A405V]VKHIYAQLFGWIVEHINKALHTSLKQ	VINARNALV,LVKHIYAQL,RNALVKHIY,VKHIYAQLF,ALVKHIYAQL,QVINARNALV,VINARNALVK,RNALVKHIYA,LVKHIYAQLF,ARNALVKHIY	BRCA
MYO5B	c.2123G>T	p.R708L	VLETIRISAAGYPSRWAYHDFFNRY[p.R708L]LVLVKKRELANTDKKAICRSVLENLI	FFNRYLVLV,DFFNRYLVL,FNRYLVLVK,HDFFNRYLV,AYHDFFNRYL,HDFFNRYLVL	LUAD
MYO6	c.2742_2743insA	p.Q914fs	EQIQKEYDALVKSSEELLSALQKKK[p.Q914fs]TAGRGSRKAEAYSRRNGKGKKKT*	KTAGRGSRK,LQKKKTAGR,GSRKAEAYS,EAYSRRNGK,YSRRNGKGK,RGSRKAEAY,KTAGRGSRKA,GSRKAEAYSR,AYSRRNGKGK,YSRRNGKGKK	GBM
MYO6	c.3538G>A	p.D1180N	IPARQREIEMNRQQRFFRIPFIRPA[p.D1180N]NQYKDPQSKKKGWWYAHFDGPWIARQ	FIRPANQYK,IPFIRPANQY	CRC
MYO7B	c.6119C>A	p.P2040H	KQTSEPSYPDVILIAINRHGVLLIH[p.P2040H]HKTKDLLTTYPFTKISSWSSGSTYFH	VLLIHHKTK,LLIHHKTKDL,GVLLIHHKTK,RHGVLLIHHK,HKTKDLLTTY	LUAD
MYO9A	c.500G>A	p.R167Q	QPQQKDFDDLCSLPDLNEKTLLENL[p.R167Q]QNRFKHEKIYTYVGSILIVINPFKFL	LQNRFKHEK,TLLENLQNR,LLENLQNRF,KTLLENLQNR,TLLENLQNRF,LQNRFKHEKI	CRC
MYO9A	c.6536G>A	p.R2179Q	FLRAMGLQERKETIRGVYSVIDQLS[p.R2179Q]QTHLNTLERLIFHLVRIALQEDTNRM	SVIDQLSQT,QTHLNTLER,LSQTHLNTL,QLSQTHLNTL	CRC
MYO9B	c.281G>T	p.R94L	KESGGEEWVLDANDSPVHRVLLWPR[p.R94L]LAQDEHPQEDGYYFLLQERNADGTIK	RVLLWPRLA,HRVLLWPRL	LUAD
MYOCD	c.1478C>T	p.T493M	AGSLPDTFNDASPSFGLHPSPVHVC[p.T493M]MEESLMSSLNGGSVPSELDGLDSEKD	HPSPVHVCM,MEESLMSSL,CMEESLMSSL,VHVCMEESLM	HNSC
MYOCD	c.678delC	p.G226fs	ENDRNDSASQPSHQSDAGKQGLGPP[p.G226fs]APP*	GKQGLGPPA	STAD
MYOCD	c.910_912delCAG	p.Q310del	AYARLLQQQQLFLQLQILSQQQQQQ[p.Q310del]HRFSYLGMHQAQLKEPNEQMVRNPNSSS	SQQQQQQHRF	PRAD
MYOF	c.495_496insG	p.G165fs	PGMGGDGEEDEGDEDRLDNAVRGPG[p.G165fs]AQGASWDGVGSSACSEAHQSKEQPADAVK*	GPGAQGASW,SACSEAHQSK,AVRGPGAQGA	LUAD
MYOM1	c.188G>A	p.R63Q	VYTQGSTAYSSRSSAAHRRESEAFR[p.R63Q]QASASSSQQQASQHALSSEVSRKAAS	AFRQASASS,RESEAFRQA,SEAFRQASA,RQASASSSQ,AFRQASASSS,RESEAFRQAS,RQASASSSQQ,SEAFRQASAS	HNSC
MYOM2	c.2962G>A	p.D988N	DHSKLYLKNPDKEDLGTYSVSVSDT[p.D988N]NGVSSSFVLDPEELERLMALSNEIKN	VSVSDTNGV,DTNGVSSSF,NGVSSSFVL,SVSVSDTNGV,DTNGVSSSFV,SDTNGVSSSF	CESC
MYOZ2	c.751G>A	p.E251K	LSGRRSFNRTPKGWISENIPIVITT[p.E251K]KPTDDTTVPESEDL*	TTKPTDDTTV	CRC
MYT1	c.676G>A	p.E226K	AAEGAASEEGEKGLFIQPEDAEEVV[p.E226K]KVTTERSQDLCPQSLEDAASEESSKQ	EVVKVTTER,AEEVVKVTT	CRC
MYT1L	c.1052C>A	p.P351Q	SLECLRNQCFDLARKLSETNPQERN[p.P351Q]QQQNMNIRQHVRPEEDFPGRTPDRNY	QERNQQQNM,QQQNMNIRQH	LUAD
N4BP2L2	c.1516C>T	p.R506C	STKNKKRRKKRIFNLVPNFDLLGQS[p.R506C]CIGVKEREKCDLLTKNHGLKITLGEE	LLGQSCIGV,FDLLGQSCI,LLGQSCIGVK	UCEC
NAA11	c.551C>A	p.T184K	RRQMDLKKGGYVVLGSRENQETQGS[p.T184K]KLSDSEEACQQKNPATEESGSDSKEP	NQETQGSKL	LUAD
NAA16	c.1542delT	p.H514fs	CISAYQRLGRYGDALKKCHEVERHF[p.H514fs]LR*	HEVERHFLR	STAD
NAA25	c.2420C>A	p.S807Y	DIYELDTSGLEDTMEIQERIENSFK[p.S807Y]YLLDQLKDVFSKCKGDLLEVKDGNLK	YLLDQLKDV,RIENSFKYL,IENSFKYLL,KYLLDQLKDV,YLLDQLKDVF,SFKYLLDQLK,QERIENSFKY,NSFKYLLDQL	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
NAB1	c.216G>C	p.L72F	EEFLEIMALVGMASKPLHVRRLQKA[p.L72F]FRDWVTNPGLFNQPLTSLPVSSIPIY	RLQKAFRDW,HVRRLQKAF,LQKAFRDWV,RLQKAFRDWV,HVRRLQKAFR,LHVRRLQKAF,RRLQKAFRDW,LQKAFRDWVT	LUAD
NANOS3	c.548C>T	p.S183L	KTQDTGHRRGGGGGAGFRGAGKSEP[p.S183L]LPSCSPSMST*	RGAGKSEPL,EPLPSCSPSM,FRGAGKSEPL	HNSC
NAP1L3	c.1058C>G	p.P353R	MIQKYDEPILKFLSDVSLKFSKPGQ[p.P353R]RVSYTFEFHFLPNPYFRNEVLVKTYI	RVSYTFEFH,PGQRVSYTF,QRVSYTFEF,SKPGQRVSY,RVSYTFEFHF,SLKFSKPGQR,FSKPGQRVSY,KPGQRVSYTF,GQRVSYTFEF,LKFSKPGQRV	TGCT
NAP1L4	c.854_855CC>AA	p.P285Q	VTVKTIKKKQKHKGRGTVRTITKQV[p.P285Q]QNESFFNFFNPLKASGDGESLDEDSEF	VQNESFFNF,KQVQNESFF,TKQVQNESF,QVQNESFFNF,VQNESFFNFF,ITKQVQNESF,TKQVQNESFF	SKCM
NAPSA	c.362G>A	p.R121Q	DTGSSNLWVPSRRCHFFSVPCWLHH[p.R121Q]QFDPKASSSFQANGTKFAIQYGTGRV	WLHHQFDPK,VPCWLHHQF,HQFDPKASS,WLHHQFDPKA,CWLHHQFDPK,SVPCWLHHQF,QFDPKASSSF,HQFDPKASSS	UCEC
NARS2	c.719C>G	p.P240R	AFLTVSGQLHLEVMSGAFTQVFTFG[p.P240R]RTFRAENSQSRRHLAEFYMIEAEISF	FTFGRTFRA,FTQVFTFGR,VFTFGRTFR,QVFTFGRTF,QVFTFGRTFR,AFTQVFTFGR,TQVFTFGRTF	BRCA
NAT10	c.1178T>C	p.I393T	IQYIHPADAVKLGQAELVVIDEAAA[p.I393T]TPLPLVKSLLGPYLVFMASTINGYEG	AAATPLPLV,AATPLPLVK,EAAATPLPL,TPLPLVKSL,IDEAAATPL,DEAAATPLP,VIDEAAATPL,AAATPLPLVK,EAAATPLPLV,TPLPLVKSLL,DEAAATPLPL	TGCT
NBPF1	c.2428G>A	p.E810K	SSSHVEWEDAVHIIPENESDDEEEE[p.E810K]KKGPVSPRNLQESEEEEVPQESWDEG	KKGPVSPRNL	MM
NBPF14	c.73C>T	p.R25C	MVVSAGPWSSEKAEMNILEINEKL[p.R25C]CPQLAENKQQFGNLKERCFVTQLAGF	KLCPQLAENK	PAAD
NBPF16	c.1347delT	p.D449fs	RELLDEKEPEVLQDSLDRCYSTPSD[p.D449fs]ILNCLT*	RCYSTPSDI,TPSDILNCL,STPSDILNCL,RCYSTPSDIL	PAAD
NBPF3	c.1472A>T	p.D491V	QEEEEDQGPPCPRLSRELPEVVEPE[p.D491V]VLQDSLDRWYSTPFSYPELPDSCQPY	LPEVVEPEV,ELPEVVEPEV	KIRC
NCAM2	c.2092G>T	p.G698C	GYSEPTVYEFSMPPKPNIIKDTLFN[p.G698C]CLGLGAVIGLGVAALLLILVVTDVSC	DTLFNCLGL,TLFNCLGLGA,IIKDTLFNCL,KDTLFNCLGL	LUAD
NCAPD2	c.659G>T	p.R220L	VSLVTGCCYRLLENPTINHQKNRPT[p.R220L]LEAITHLLGVALTRYNHMLSATVKII	TLEAITHLL,KNRPTLEAI,LEAITHLLG,HQKNRPTLEA,RPTLEAITHL,INHQKNRPTL,QKNRPTLEAI,LEAITHLLGV	LUAD
NCAPD3	c.2725delC	p.Q909fs	ASSADADHSPSSQGSSEAPASQPPP[p.Q909fs]RSEVLSCPL*	QPPPRSEVL,RSEVLSCPL,EAPASQPPPR,SQPPPRSEVL	STAD
NCAPH	c.1398delA	p.T466fs	HWRFRPRRKQDAPSQSENKKKSTKK[p.T466fs]ILKLTLKMILTLMYILEKQRLLLF*	KMILTLMYI,MILTLMYIL,YILEKQRLL,ILKLTLKMI,TLKMILTLM,LTLMYILEK,MYILEKQRL,KKSTKKILK,KILKLTLKM,LKMILTLMY,LMYILEKQR,LKLTLKMIL,LTLKMILTL,LEKQRLLLF,KLTLKMILTL,KMILTLMYIL,YILEKQRLLL,ILTLMYILEK,MYILEKQRLL,ILEKQRLLLF,KKKSTKKILK,STKKILKLTL,TLKMILTLMY,TLMYILEKQR,ILKLTLKMIL,KKSTKKILKL,KKILKLTLKM,LTLKMILTLM,LKMILTLMYI,LMYILEKQRL	STAD
NCOA3	c.3759_3760delGC	p.Q1253fs	RSRELLSHHFRQQRVAMMMQQQQQQ[p.Q1253fs]TAAAAAAAAATATATATAATAANPGLQPTS*	QTAAAAAAA,MQQQQQQTA,QQQQQQTAA,QQQQQTAA,QQQTAAAA,QQQTAAAAA,QQTAAAAAA,MMMQQQQQQT,MMQQQQQQTA,ATATATATAA,ATATATAATA,QTAAAAAAAA,TAATAANPGL,MQQQQQQTAA,QQQQQQTAAA,QQQQQTAAAA,QQQQTAAAAA,QQQTAAAAAA,QQTAAAAAAA	PAAD
NCOA4	c.1685G>A	p.R562Q	ADWVLPGKKMGNLSQLSSGEDKWLL[p.R562Q]QKKAQEVLLNSPLQEEHNFPPDHYGL	LLQKKAQEV,LQKKAQEVL,WLLQKKAQEV,LLQKKAQEVL,LQKKAQEVLL	CRC
NCOA7	c.1107G>T	p.E369D	DSRPIVPLEKSTGHTPTKPSGSSVS[p.E369D]DKLKKLDSSRETSHGSPTVTKLSKEP	SSVSDKLKK,GSSVSDKLKK	UCEC
NCOR1	c.4682G>A	p.R1561Q	PGVDPVVSHSPFDPHHRGSTAGEVY[p.R1561Q]QSHLPTHLDPAMPFHRALDPAAAAYL	YQSHLPTHL,EVYQSHLPT,VYQSHLPTHL,EVYQSHLPTH,GEVYQSHLPT	HNSC

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NCR1	c.772C>T	p.R258W	TYLLTTETGLQKDHALWDHTAQNLL[p.R258W]WMGLAFLVLVALVWFLVEDWLSRKRT	LLWMGLAFL,WMGLAFLVL,AQNLLWMGL,LWMGLAFLV,HTAQNLLWM,NLLWMGLAF,NLLWMGLAFL,LLWMGLAFLV,WMGLAFLVLV,AQNLLWMGLA,LWMGLAFLVL,QNLLWMGLAF	UCEC
NDST3	c.1279G>A	p.V427I	LNKKFALEHGIPTDMGYAVAPHHSG[p.V427I]IYPVHVQLYEAWKKVWNIKITSTEEY	GIYPVHVQL,AVAPHHSGI,IYPVHVQLY,VAPHHSGIY,GIYPVHVQLY,AVAPHHSGIY,YAVAPHHSGI,APHHSGIYPV,SGIYPVHVQL	LUAD
NEDD4L	c.570_572delTCC	p.P194del	DMEHGWEVVDSNDSASQHQEELPPP[p.P194del]LPPGWEEKVDNLGRTYYVNHNNRTTQWH	HQEELPPPL,LPPPLPPGW	CLL
NEDD9	c.2392G>A	p.A798T	RNKVMNSSNQLCEQLKTIVMATKMA[p.A798T]TLHYPSTTALQEMVHQVTDLSRNAQL	VMATKMATL,TLHYPSTTA,ATKMATLHY,KMATLHYPS,MATKMATLHY,IVMATKMATL,KMATLHYPST,TLHYPSTTAL,ATKMATLHYP,ATLHYPSTTA,VMATKMATLH,TKMATLHYPS	CRC
NEDD9	c.946G>A	p.A316T	ARRHQSLSPNHPPPQLGQSVGSQND[p.A316T]TYDVPRGVQFLEPPAETSEKANPQER	SVGSQNDTY,DTYDVPRGV,TYDVPRGVQF,QSVGSQNDTY	CRC
NEFH	c.1933G>A	p.E645K	SPVKEEAKSPAEVKSPEKAKSPTKE[p.E645K]KAKSPEKAKSPEKEEAKSPEKAKSPV	KAKSPTKEK,KSPTKEKAK,KEKAKSPEK,KAKSPTKEKA,KEKAKSPEKA	KIRP
NEFH	c.1993_1994insAGGAAG	p.665_666insEE	PTKEEAKSPEKAKSPEKEEAKSPEK[p.665_666insEE]EEAKSPVKAEAKSPEKAKSPVKAEAKSPEKA	EEAKSPVKA,KEEAKSPVKA	ACC,KIRP
NEFH	c.2009T>A	p.V670E	EAKSPEKAKSPEKEEAKSPEKAKSP[p.V670E]EKAEAKSPEKAKSPVKAEAKSPEKAK	KSPEKAEAK,KAKSPEKAEA	TGCT
NEFM	c.638C>T	p.A213V	RFEEEARLRDDTEAAIRALRKDIEE[p.A213V]VSLVKVELDKKVQSLQDEVAFLRSNH	ALRKDIEEV,EVSLVKVEL,RKDIEEVSL,IEEVSLVKV,VSLVKVELDK,EEVSLVKVEL	STAD
NEK1	c.1822C>T	p.R608C	EVYLARLRQIRLQNFNERQQIKAKL[p.R608C]CGEKKEANHSEGQEGSEEADMRRKKI	KAKLCGEKK,QIKAKLCGEK	CRC
NEK11	c.1121G>A	p.R374Q	KLQAADEKARKLKKIVEEKYEENSK[p.R374Q]QMQELRSRNFQQLSVDVLHEKTHLKG	NSKQMQELR,QMQELRSRNF,EKYEENSKQM,KQMQELRSRN	UCEC
NEK2	c.715C>A	p.R239S	PPFTAFSQKELAGKIREGKFRRIPY[p.R239S]SYSDELNEIITRMLNLKDYHRPSVEE	KFRRIPYSY,SYSDELNEI,IPYSYSDEL,SYSDELNEII,KFRRIPYSYS,GKFRRIPYSY,YSYSDELNEI	LUAD
NEK8	c.2070delC	p.V690fs	VTSVSCCHGNTLLAVRSVTDEPVPP[p.V690fs]EAPGFTSGPP*	EPVPPEAPGF	STAD
NELL2	c.509G>A	p.G170D	QTHLNSGVILSIHHLDHRYLELESS[p.G170D]DHRNEVRLHYRSGSHRPHTEVFPYIL	ESSDHRNEV,ESSDHRNEVR,LESSDHRNEV	TGCT
NES	c.1831G>C	p.V611L	LKSLEKENKELLKDVEVVRPLEKEA[p.V611L]LGQLKPTGKEDTQTLQSLQKENQELM	LEKEALGQL,ALGQLKPTGK,KEALGQLKPT	KIRC
NF1	c.2027_2028insC	p.T676fs	PGASLRKGKGNSSMDSAAGCSGTPP[p.T676fs]DLPTSPDQTRSGPVHVSVEP*	QTRSGPVHV,RSGPVHVSV,SPDQTRSGPV	STAD
NF1	c.4974_4977delTCTC	p.F1658fs	AKPYEIVVDLTHTGPSNRFKTDFLS[p.F1658fs]GLLFFLALLTTTSPQSISITVTPGSGSTPSIMSGC*	KTDFLSGLL,FLSGLLFFL,GLLFFLALL,FLALLTTTS,DFLSGLLFF,RFKTDFLSG,TTSPQSISI,STPSIMSGC,SPQSISITV,FKTDFLSGL,TDFLSGLLF,SGLLFFLAL,GSGSTPSIM,KTDFLSGLLF,FLSGLLFFLA,LLFFLALLTT,FLALLTTTSP,LLTTTSPQSI,DFLSGLLFFL,RFKTDFLSGL,TTTSPQSISI,TSPQSISITV,TPGSGSTPSI,FKTDFLSGLL,TDFLSGLLFF,LSGLLFFLAL	GBM
NFASC	c.766G>A	p.V256I	QFEEDQFQPGVWHDHSKYPGSVNSA[p.V256I]ILRLSPYVNYQFRVIAINEVGSSHPS	AILRLSPYV,GSVNSAILR,SAILRLSPY,YPGSVNSAI,NSAILRLSPY,SAILRLSPYV,KYPGSVNSAI,ILRLSPYVNY,YPGSVNSAIL	CRC
NFAT5	c.2716C>G	p.Q906E	QQQQQQQQVMESSAAMVMEMQQSIC[p.Q906E]EAAAQIQSELFPSTASANGNLQQSPV	EMQQSICEA,SICEAAAQI,MQQSICEAA,CEAAAQIQS,QSICEAAAQI,EAAAQIQSEL,MEMQQSICEA,MQQSICEAAA	KIRC

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NFE2L2	c.100C>G	p.R34G	PGLPSQQDMDLIDILWRQDIDLGVS[p.R34G]GEVFDFSQRRKEYELEKQKKLEKERQ	IDLGVSGEVF,LGVSGEVFDF	BLCA
NFE2L2	c.101G>A	p.R34Q	PGLPSQQDMDLIDILWRQDIDLGVS[p.R34Q]QEVFDFSQRRKEYELEKQKKLEKERQ	IDLGVSQEVF,LGVSQEVFDF	LUSC
NFE2L2	c.235G>A	p.E79K	LEKERQEQLQKEQEKAFFAQLQLDE[p.E79K]KTGEFLPIQPAQHIQSETSGSANYSQ	QLDEKTGEFL,LQLDEKTGEF,DEKTGEFLPI	BLCA,HNSC
NFE2L2	c.235G>C	p.E79Q	LEKERQEQLQKEQEKAFFAQLQLDE[p.E79Q]QTGEFLPIQPAQHIQSETSGSANYSQ	AQLQLDEQT,QLDEQTGEF,EQTGEFLPI,QLDEQTGEFL,LQLDEQTGEF,DEQTGEFLPI	HNSC,LUSC
NFE2L2	c.241G>A	p.G81S	KERQEQLQKEQEKAFFAQLQLDEET[p.G81S]SEFLPIQPAQHIQSETSGSANYSQVA	QLDEETSEF,EETSEFLPI,SEFLPIQPA,QLDEETSEFL,LQLDEETSEF,DEETSEFLPI,SEFLPIQPAQ	LUSC
NFE2L2	c.85G>C	p.D29H	LELPPPGLPSQQDMDLIDILWRQDI[p.D29H]HLGVSREVFDFSQRRKEYELEKQKKL	ILWRQDIHL,HLGVSREVF,DIHLGVSREV,IHLGVSREVF	CESC,HNSC,LUSC
NFE2L2	c.88C>T	p.L30F	ELPPPGLPSQQDMDLIDILWRQDID[p.L30F]FGVSREVFDFSQRRKEYELEKQKKLE	ILWRQDIDF,IDFGVSREV,IDFGVSREVF,FGVSREVFDF	LUSC
NFE2L2	c.92G>C	p.G31A	LPPPGLPSQQDMDLIDILWRQDIDL[p.G31A]AVSREVFDFSQRRKEYELEKQKKLEK	DLAVSREVF,WRQDIDLAV,AVSREVFDF,ILWRQDIDLA,IDLAVSREVF,LAVSREVFDF	LUSC
NFIA	c.882G>C	p.L294F	SVTELVRVSQTPIAAGTGPNFSLSD[p.L294F]FESSSYYSMSPGAMRRSLPSTSSTSS	LSDFESSSY,SDFESSSYY,FESSSYYSM,GPNFSLSDF,LSDFESSSYY,SLSDFESSSY,FESSSYYSMS	LUAD
NHEJ1	c.326G>A	p.R109Q	LKDAAHPSEATFSCDCVADALILRV[p.R109Q]QSELSGLPFYWNFHCMLASPSLVSQH	RVQSELSGL,QSELSGLPF,QSELSGLPFY,ALILRVQSEL,VQSELSGLPF,LRVQSELSGL	UCEC
NHLRC1	c.612delT	p.F204fs	DVTITNDCHVVVTDAGDRSIKVFDF[p.F204fs]LARSSLSLEANSPYLGVWRPPLRMGLW*	LSLEANSPY,FLARSSLSL,SLEANSPYL,YLGVWRPPL,RSIKVFDFL,SIKVFDFLA,LGVWRPPLR,EANSPYLGV,FDFLARSSL,ANSPYLGVW,SIKVFDFLAR,DFLARSSLSL,PYLGVWRPPL,RSIKVFDFLA,LARSSLSLEA,VWRPPLRMGL,SLSLEANSPY,YLGVWRPPLR,LSLEANSPYL,LEANSPYLGV,LGVWRPPLRM,EANSPYLGVW	STAD
NHP2L1	c.250C>T	p.R84C	DAEPLEILHLPLLCEDKNVPYVFV[p.R84C]CSKQALGRACGVSRPVIACSVTIKEG	YVFVCSKQAL,NVPYVFVCSK,FVCSKQALGR	GBM
NHS	c.4681G>A	p.D1561N	ATEILKSPILPKPPGELTAESPQST[p.D1561N]NDAHQGSQGAEALSPLSPCSPRVNAE	AESPQSTNDA	TGCT
NID2	c.3103delC	p.R1035fs	EPTQRPPTICERWRENLLEHYGGTP[p.R1035fs]GMTSTCPSAMTWATSSPCSATERATSAGVWTKMAERCRAPAPSQAPPLRVYPPSLHPWSGPRPGQM*	GMTSTCPSA,ATSAGVWTK,SLHPWSGPR,GVWTKMAER,VYPPSLHPW,RVYPPSLHP,MTSTCPSAM,SQAPPLRVY,WTKMAERCR,MTWATSSPC,TSAGVWTKM,HPWSGPRPG,PLRVYPPSL,LEHYGGTPG,EHYGGTPGM,STCPSAMTW,AMTWATSSP,TERATSAGV,CPSAMTWAT,AERCRAPAP,KMAERCRAPA,GMTSTCPSAM,AMTWATSSPC,TSSPCSATER,RATSAGVWTK,RVYPPSLHPW,WTKMAERCRA,RCRAPAPSQA,MTSTCPSAMT,MTWATSSPCS,TSAGVWTKMA,APAPSQAPPL,APSQAPPLRV,LEHYGGTPGM,TERATSAGVW,ATSAGVWTKM,SQAPPLRVYP,CPSAMTWATS,AERCRAPAPS,TSTCPSAMTW	STAD
NINL	c.4096C>T	p.R1366C	VRALQATEEKQRGAEKQSRLLEEKV[p.R1366C]CALNKLVSRIAPAALSV*	LLEEKVCAL,KVCALNKLV,CALNKLVSR,RLLEEKVCAL	CRC
NKD1	c.856_857insC	p.P286fs	AGIENYTSQFGPGSPSVAQKSELPP[p.P286fs]PHLQSHSISLP*	HLQSHSISL,AQKSELPPP,LQSHSISLP,AQKSELPPPH,QKSELPPPHL	STAD
NKD2	c.1315_1317delCAC	p.H447del	GYAVPVIQRHEHHHHHEHHHHHHHH[p.H447del]FHPS*	EHHHHHHHHF	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
NLK	c.570delT	p.C190fs	KKMPNVFQNLVSCKRVFRELKMLCF[p.C190fs]LSMIMYSLPLTYSNLHTLTILKKYMLSQN*	IMYSLPLTY,YSNLHTLTI,KMLCFLSMI,FLSMIMYSL,SMIMYSLPL,MIMYSLPLT,LTYSNLHTL,SLPLTYSNL,NLHTLTILK,HTLTILKKY,LTILKKYML,MLCFLSMIM,RELKMLCFL,LKMLCFLSM,LCFLSMIMY,SNLHTLTIL,LPLTYSNLH,MIMYSLPLTY,KMLCFLSMIM,SMIMYSLPLT,IMYSLPLTYS,FLSMIMYSLP,MLCFLSMIMY,NLHTLTILKK,SNLHTLTILK,CFLSMIMYSL,YSLPLTYSNL,TYSNLHTLTI,ELKMLCFLSM,LSMIMYSLPL,LKMLCFLSMI,YSNLHTLTIL,LHTLTILKKY,RELKMLCFLS,LPLTYSNLHT	STAD
NLRC4	c.1225G>A	p.E409K	SDFIRSLDHCGDLALEGVFSHKFDF[p.E409K]KLQDVSSVNEDVLLTTGLLCKYTAQR	VFSHKFDFK,FSHKFDFKL,FKLQDVSSV,GVFSHKFDFK,VFSHKFDFKL,HKFDFKLQDV	CRC
NLRC4	c.1777G>A	p.D593N	KSALSQEFEAFFQGKSLYINSGNIP[p.D593N]NYLFDFFEHLPNCASALDFIKLDFYG	NIPNYLFDF,INSGNIPNY,IPNYLFDFF,SGNIPNYLF,NSGNIPNYLF,GNIPNYLFDF,NIPNYLFDFF,NYLFDFFEHL,YINSGNIPNY	CRC
NLRC4	c.862C>T	p.R288W	ALIKENHRFKNMVIVTTTTECLRHI[p.R288W]WQFGALTAEVGDMTEDSAQALIREVL	ECLRHIWQF,RHIWQFGAL,WQFGALTAE,WQFGALTAEV,CLRHIWQFGA,TECLRHIWQF,LRHIWQFGAL,RHIWQFGALT,HIWQFGALTA	BRCA
NLRP3	c.469C>T	p.R157C	MKKDYRKKYRKYVRSRFQCIEDRNA[p.R157C]CLGESVSLNKRYTRLRLIKEHRSQQE	RNACLGESV,CLGESVSLNK	LUAD
NLRP4	c.685G>A	p.V229I	LISREWPDPAAPITEIVSQPERLLF[p.V229I]IIDSFEELQGGLNEPDSDLCGDLMEK	SQPERLLFI,FIIDSFEEL,RLLFIIDSF,QPERLLFII,SQPERLLFII,LFIIDSFEEL	CRC
NLRP5	c.1175G>A	p.R392H	LGSVLNNDTKLCKDWAEKQPPFTLI[p.R392H]HSLLRKVLLPESFLIVTVRDVGTEKL	LIHSLLRKV,TLIHSLLRK,FTLIHSLLR,PFTLIHSLL,HSLLRKVLL,PPFTLIHSL,KQPPFTLIH,TLIHSLLRKV,FTLIHSLLRK,QPPFTLIHSL,LIHSLLRKVL	CRC
NLRP5	c.2209C>T	p.R737W	LPINQNLDLIASSFCLQHCPYLRKI[p.R737W]WVDVKGIFPRDESAEACPVVPLWMRD	YLRKIWVDV,IWVDVKGIF,CPYLRKIWV,YLRKIWVDVK,PYLRKIWVDV,WVDVKGIFPR,RKIWVDVKGI,KIWVDVKGIF	GBM
NLRP6	c.1832A>G	p.E611G	CPGVAPEVTEGAKGLEDTEEPEEEE[p.E611G]GGEEPNYPLELLYCLYETQEDAFVRQ	EEGGEEPNY,EEEGGEEPNY	THCA
NME9	c.223G>A	p.E75K	QKMRIEVGLDLLHFALAEADRLDVL[p.E75K]KKYRGKCEPTFLFYAGGELVAVVRGA	KKYRGKCEPT	CRC
NMU	c.53C>A	p.A18E	MLRTESCRPRSPAGQVA[p.A18E]EASPLLLLLLLLAWCAGACRGAPILP	QVAEASPLL,EASPLLLLL,GQVAEASPL,AEASPLLLL,QVAEASPLLL,EASPLLLLL,GQVAEASPLL,AEASPLLLLL	ACC
NMU	c.56C>A	p.A19E	MLRTESCRPRSPAGQVAA[p.A19E]ESPLLLLLLLAWCAGACRGAPILPQ	QVAAESPLL,GQVAAESPL,VAAESPLLL,AESPLLLLL,QVAAESPLLL,GQVAAESPLL,VAAESPLLLL,AESPLLLLLL	ACC
NNMT	c.697G>A	p.E233K	EQKFSSLPLGREAVEAAVKEAGYTI[p.E233K]KWFEVISQSYSSTMANNEGLFSLVAR	YTIKWFEVI,GYTIKWFEV,KEAGYTIKW,AVKEAGYTIK,GYTIKWFEVI,KWFEVISQSY,KEAGYTIKWF	UCEC
NOL9	c.172T>G	p.S58A	PRRRLGSLRWCGRRRLRWRLLQAQA[p.S58A]AGVDWREGARQVSRAAAARRPNTATP	WRLLQAQAA,RWRLLQAQAA	ACC
NOLC1	c.1283C>T	p.T428M	VTTKSPAVKPAAAPKQPVGGGQKLL[p.T428M]MRKADSSSSEEESSSSEEEKTKKMVA	LMRKADSSS,LMRKADSSSS	CRC
NOM1	c.70C>G	p.R24G	MAASRSAGEAGPGGSQGRVVRMK[p.R24G]GRGGRGPRRGPAGGGEKALKRLKLAV	RMKGRGGRG,KGRGGRGPR,QGRVVRMKGR,VVRMKGRGGR,KGRGGRGPRR	ACC
NOS1AP	c.901_903delCAG	p.Q306del	LGTETPLSTHHQMQLLQQLLQQQQQ[p.Q306del]TQVAVAQVHLLKDQLAAEAAARLEAQAR	LQQQQQTQV,LLQQQQQTQV,LQQQQQTQVA	BLCA
NOTCH1	c.7541_7542delCT	p.P2514fs	SYSSPVDNTPSHQLQVPEHPFLTPS[p.P2514fs]RVP*	HPFLTPSRV	CLL

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NOTCH2	c.17_18delCC	p.P6fs	MPALR[p.P6fs]RSAVGAAGALAVLRGPRACIAVSRWL*	ALRRSAVGA,AAGALAVLR,RSAVGAAGA,VLRGPRACI,ALAVLRGPR,MPALRRSAV,SAVGAAGAL,LRRSAVGAA,GAAGALAVL,RACIAVSRW,ALRRSAVGAA,AVGAAGALAV,ALAVLRGPRA,RSAVGAAGAL,GALAVLRGPR,VLRGPRACIA,RACIAVSRWL,MPALRRSAVG,VGAAGALAVL	BLCA
NOTCH2	c.57C>G	p.C19W	MPALRPALLWALLALWLC[p.C19W]WAAPAHALQCRDGYEPCVNEGMCVTY	LLALWLCWA,CWAAPAHAL,ALLALWLCW,WLCWAAPAH,ALLALWLCWA,LLALWLCWAA,ALWLCWAAPA,WLCWAAPAHA,WALLALWLCW,LCWAAPAHAL	ACC
NOTCH2	c.6314G>T	p.R2105L	LSPVICGPNRSFLSLKHTPMGKKSR[p.R2105L]LPSAKSTMPTSLPNLAKEAKDAKGSR	KSRLPSAKS,TPMGKKSRL,RLPSAKSTM,MGKKSRLPSA,KSRLPSAKST,LPSAKSTMPT,SRLPSAKSTM	LUAD
NOTCH2	c.6892C>T	p.R2298W	APAEGTHPGIAPQSRPPEGKHITTP[p.R2298W]WEPLPPIVTFQLIPKGSIAQPAGAPQ	HITTPWEPL,TPWEPLPPI,WEPLPPIVT,TTPWEPLPPI,KHITTPWEPL,WEPLPPIVTF,TPWEPLPPIV	CESC
NOX3	c.1210_1211delTG	p.C404fs	SLPRLAVDGPFGTALTDVFHYPVCV[p.C404fs]RCRGDRSHSLRCSSEIYMVQMQ*	RSHSLRCSS,SLRCSSEIY,VFHYPVCVR,HSLRCSSEI,LRCSSEIYM,SLRCSSEIYM,CVRCRGDRSH,RSHSLRCSSE,HSLRCSSEIY,DVFHYPVCVR,RCRGDRSHSL,CSSEIYMVQM	PRAD
NOX5	c.1401delT	p.P467fs	AVCIMEVNLLPSKVTHLLIKRPPFF[p.P467fs]TIDLVTTCI*	FTIDLVTTC,RPPFFTIDL,IKRPPFFTI,PPFFTIDLV,LLIKRPPFFT,FTIDLVTTCI,LIKRPPFFTI	STAD
NOXA1	c.18C>G	p.D6E	MASLG[p.D6E]ELVRAWHLGAQAVDRGDWARALHLFS	SLGELVRAW,GELVRAWHL,ELVRAWHLGA,ASLGELVRAW,GELVRAWHLG	ACC
NOXO1	c.8_9insG	p.G3fs	MAGP[p.G3fs]PIPSFSARGSPGADQEAPNVCLLCALVRRQRHLRAQELGRIQAAQEDPQGDLPGGGGPAAEI*	FSARGSPGA,LVRRQRHLR,RQRHLRAQE,HLRAQELGR,CLLCALVRR,NVCLLCALV,LPGGGGPAA,ALVRRQRHL,QRHLRAQEL,MAGPPIPSF,QEAPNVCLL,AQELGRIQA,QELGRIQAA,HLRAQELGRI,SFSARGSPGA,LVRRQRHLRA,RQRHLRAQEL,RAQELGRIQA,NVCLLCALVR,LLCALVRRQR,ALVRRQRHLR,APNVCLLCAL,CALVRRQRHL,AQELGRIQAA	KIRC
NPAS2	c.602A>G	p.Q201R	DSITPLLGHLPSDVMDQNLLNFLPE[p.Q201R]REHSEVYKILSSHMLVTDSPSPEYLK	NLLNFLPER,PEREHSEVY,REHSEVYKI,LPEREHSEV,FLPEREHSEV,LPEREHSEVY,REHSEVYKIL	OV
NPC1	c.1351G>A	p.E451K	GADVPFGPPLDIQILHQVLDLQIAI[p.E451K]KNITASYDNETVTLQDICLAPLSPYN	AIKNITASY,LQIAIKNIT,QVLDLQIAIK,IAIKNITASY,LQIAIKNITA	CRC
NPIP	c.812C>T	p.A271V	QPPPPTQQHSIIDNSLSLKTPSELS[p.A271V]VHSPSTLSSTLSG*	LKTPSELSV,SELSVHSPS,LSVHSPSTL,SLKTPSELSV,LKTPSELSVH,SELSVHSPST	PRAD
NPM1	c.859_860insTCTG	p.L287fs	KVEAKFINYVKNCFRMTDQEAIQDL[p.L287fs]CLAVEEVSLRK*	AIQDLCLAV,AVEEVSLRK,EAIQDLCLA,QEAIQDLCL,LAVEEVSLRK,EAIQDLCLAV,QEAIQDLCLA	LAML
NPM1	c.861_862insCTGC	p.L287fs	KVEAKFINYVKNCFRMTDQEAIQDL[p.L287fs]LLAVEEVSLRK*	AIQDLLLAV,LLAVEEVSL,AVEEVSLRK,EAIQDLLLA,QEAIQDLLL,LLLAVEEVSL,LAVEEVSLRK,EAIQDLLLAV,QEAIQDLLA	LAML
NPM1	c.863_864insTCTG	p.W288fs	KVEAKFINYVKNCFRMTDQEAIQDL[p.W288fs]CLAVEEVSLRK*	AIQDLCLAV,AVEEVSLRK,EAIQDLCLA,QEAIQDLCL,LAVEEVSLRK,EAIQDLCLAV,QEAIQDLCLA	LAML
NPR3	c.412T>C	p.Y138H	LFSLVDRVAAARGAKPDLILGPVCE[p.Y138H]HAAAPVARLASHWDLPMLSAGALAAG	ILGPVCEHA,HAAAPVARL,CEHAAAPVA,GPVCEHAAA,ILGPVCEHAA,HAAAPVARLA	STAD
NPSR1	c.704G>A	p.R235Q	YMTIVAFLVYFIPLTIISIMYGIVI[p.R235Q]QTIWIKSKTYETVISNCSDGKLCSSY	IMYGIVIQT,IVIQTIWIK,MYGIVIQTI,QTIWIKSKT,YGIVIQTIW,IMYGIVIQTI,SIMYGIVIQT,VIQTIWIKSK,GIVIQTIWIK,MYGIVIQTIW,QTIWIKSKTY	CRC
NPTX1	c.787G>A	p.A263T	YMYAKVKKSLPEMYAFTVCMWLKSS[p.A263T]TTPGVGTPFSYAVPGQANELVLIEWG	LKSSTTPGV,WLKSSTTPGV,STTPGVGTPF	GBM
NPY1R	c.1111G>A	p.A371T	DYETIAMSTMHTDVSKTSLKQASPV[p.A371T]TFKKINNNDDNEKI*	KQASPVTFK,QASPVTFKK,LKQASPVTF,KQASPVTFKK,SLKQASPVTF	UCEC
NR2C1	c.809G>T	p.S270I	HPSGVKTESAVLMTSDKAESCQGDL[p.S270I]ITLANVVTSLANLGKTKDLSQNSNEM	AESCQGDLI,ITLANVVTSL,GDLITLANVV,AESCQGDLIT	KIRC
NR4A2	c.941G>T	p.R314L	RTVQKNAKYVCLANKNCPVDKRRRN[p.R314L]LCQYCRFQKCLAVGMVKEVVRTDSLK	RNLCQYCRF,KRRRNLCQY,NLCQYCRFQK,CPVDKRRRNL,RRNLCQYCRF	LUAD

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NR5A2	c.238G>A	p.E80K	SHGEQGQMPENMQVSQFKMVNYSYD[p.E80K]KDLEELCPVCGDKVSGYHYGLLTCES	KMVNYSYDK,KDLEELCPV,YSYDKDLEEL	CESC
NRAP	c.979G>A	p.E327K	YEEHRGKGSFPAMITPAYQNAKKAH[p.E327K]KLASDIKYRQDFNKMKGAAHYHSLPA	YQNAKKAHK,KAHKLASDI,KLASDIKYR,HKLASDIKY,YQNAKKAHKL,KAHKLASDIK,AYQNAKKAHK,KKAHKLASDI,AHKLASDIKY	CRC
NRAS	c.181C>A	p.Q61K	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61K]KEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGKEEY,AGKEEYSAM,ILDTAGKEEY,DTAGKEEYSA	CRC,LAML,MM,SKCM,THCA
NRAS	c.182A>G	p.Q61R	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61R]REEYSAMRDQYMRTGEGFLCVFAINN	LDTAGREEY,AGREEYSAM,ILDTAGREEY,AGREEYSAMR,DTAGREEYSA	CLL,MM,OV,SKCM,TGCT,THCA,UCEC
NRAS	c.182A>T	p.Q61L	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61L]LEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGLEEY,AGLEEYSAM,ILDTAGLEEY,LLDILDTAGL,DTAGLEEYSA	CRC,LUAD,MM,SKCM
NRAS	c.183A>C	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	MM
NRAS	c.183A>T	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	LAML
NRAS	c.34G>T	p.G12C	MTEYKLVVVGA[p.G12C]CGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGACGV,VVGACGVGK,KLVVVGACGV,VVVGACGVGK	CRC
NRAS	c.35G>A	p.G12D	MTEYKLVVVGA[p.G12D]DGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGADGV,VVGADGVGK,KLVVVGADGV,VVVGADGVGK	CRC,LAML,MM
NRAS	c.37G>C	p.G13R	MTEYKLVVVGAG[p.G13R]RVGKSALTIQLIQNHFVDEYDPTIED	VVGAGRVGK,RVGKSALTI,KLVVVGAGR,AGRVGKSAL,KLVVVGAGRV,VVVGAGRVGK,GRVGKSALTI	CRC,MM
NRAS	c.38G>A	p.G13D	MTEYKLVVVGAG[p.G13D]DVGKSALTIQLIQNHFVDEYDPTIED	VVGAGDVGK,KLVVVGAGDV,VVVGAGDVGK	LAML
NRG1	c.1441G>T	p.V481L	VSSMTVSMPSMAVSPFMEEERPLLL[p.V481L]LTPPRLREKKFDHHPQQFSSFHHNPA	LLLLTPPRL,LTPPRLREK,LLLTPPRLR,EEERPLLLL,EERPLLLLT,LLTPPRLREK,MEEERPLLLL	LUAD
NRG2	c.737C>T	p.T246M	LKKEVGKILCTDCATRPKLKKMKSQ[p.T246M]MGQVGEKQSLKCEAAAGNPQPSYRWF	KMKSQMGQV,SQMGQVGEK,KLKKMKSQM,MKSQMGQVG,KSQMGQVGEK,KLKKMKSQMG,KMKSQMGQVG,KKMKSQMGQV	CRC
NRG4	c.63_64insG	p.G21fs	ANRSRRALWSQSQVVLPEWGA[p.G21fs]VVM*	VLPEWGAVV,LPEWGAVVM,VVLPEWGAVV,VLPEWGAVVM,QVVLPEWGAV	CLL
NRXN3	c.307C>T	p.R103C	FETPEAYISLPKWNTKRMGSISFDF[p.R103C]CTTEPNGLILFTHGKPQERKDARSQK	CTTEPNGLI	LUAD
NRXN3	c.68C>A	p.P23H	MLGSDDFFYVGGSPSTADLPGS[p.P23H]HVSNNFMGCLKEVVYKNNDIRLELSR	GSHVSNNFM,STADLPGSH,STADLPGSHV,HVSNNFMGCL,LPGSHVSNNF	LUAD
NSMCE1	c.730G>A	p.D244N	YFQSNAEPRCPHCNDYWPHEIPKVF[p.D244N]NPEKERESGVLKSNKKSLRSRQH*	KVFNPEKER,HEIPKVFNP,HEIPKVFNPE	UCEC
NSMCE2	c.91_92insA	p.Q31fs	SNSGSTGFISFSGVESALSSLKNFQ[p.Q31fs]SLYQLWYGHSF*	FQSLYQLWY,YQLWYGHSF,SLKNFQSLY,SSLKNFQSL,NFQSLYQLW,KNFQSLYQL,SLYQLWYGH,SSLKNFQSLY,KNFQSLYQLW,LYQLWYGHSF,NFQSLYQLWY,LSSLKNFQSL,LKNFQSLYQL	KIRC
NT5C3	c.7G>C	p.A3P	MR[p.A3P]PPSMDRAAVARVGAVASASVCALVAG	RPPSMDRAA,PPSMDRAAV,RPPSMDRAAV	TGCT
NT5M	c.616delC	p.P206fs	AEPTPSWEHVLFTACHNQHLQLQPP[p.P206fs]AAGCTRGRTTGRPFWTASGPAELDCASGSSVGL*	LQLQPPAAG,NQHLQLQPPA	STAD
NTM	c.997G>T	p.G333C	IMLFEVKTTALTPWKGPGAVSEVSN[p.G333C]CTSRRAGCVWLLPLLVLHLLLKF*	EVSNCTSRR	LUAD

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NTN4	c.175G>A	p.E59K	CNPRMGNLALGRKLWADTTCGQNAT[p.E59K]KLYCFYSENTDLTCRQPKCDKCNAAY	TTCGQNATK,ATKLYCFYS,CGQNATKLY,NATKLYCFY,KLYCFYSENT,QNATKLYCFY,DTTCGQNATK,GQNATKLYCF	CRC
NUAK1	c.517G>T	p.G173C	RRLSERETRHFFRQIVSAVHYCHKN[p.G173C]CVVHRDLKLENILLDDNCNIKIADFG	AVHYCHKNCV,KNCVVHRDLK,VHYCHKNCVV,HKNCVVHRDL	LUAD
NUB1	c.1118G>A	p.R373Q	RLVHIKGNCGKEKVLFLRLYLLQGI[p.R373Q]QNYHSGNDVEAYEYLNKARQLFKELY	YLLQGIQNY,IQNYHSGNDV	CRC
NUDT15	c.248C>A	p.S83Y	ECAQRETWEEAALHLKNVHFASVVN[p.S83Y]YFIEKENYHYVTILMKGEVDVTHDSE	FASVVNYFI,SVVNYFIEK,HFASVVNYF,VHFASVVNY,ASVVNYFIEK,VHFASVVNYF,HFASVVNYFI,YFIEKENYHY,NVHFASVVNY,VNYFIEKENY	CRC
NUDT21	c.39_40insG	p.W13fs	MSVVPPNRSQTGW[p.W13fs]APGGHSVRQQVHPADEAPHPGAHHQPVPSYQLYFWYKRAPLREGQLCCSQISAHEGRI*	QLYFWYKRA,SYQLYFWYK,YQLYFWYKR,YFWYKRAPL,RSQTGWAPG,SVRQQVHPA,FWYKRAPLR,AHHQPVPSY,PSYQLYFWY,HPGAHHQPV,QPVPSYQLY,HQPVPSYQL,DEAPHPGAH,VPSYQLYFW,YQLYFWYKRA,PSYQLYFWYK,SYQLYFWYKR,LYFWYKRAPL,GAHHQPVPSY,HQPVPSYQLY,YFWYKRAPLR,VPSYQLYFWY,RQQVHPADEA,HHQPVPSYQL,QPVPSYQLYF,REGQLCCSQI,GQLCCSQISA,SQISAHEGRI,DEAPHPGAHH	KIRC
NUF2	c.1019C>T	p.S340L	KESLNLEDQIESDESELKKLKTEEN[p.S340L]LFKRLMIVKKEKLATAQFKINKKHED	NLFKRLMIV,KTEENLFKR,LFKRLMIVK,KKLKTEENL,KLKTEENLF,EENLFKRLM,TEENLFKRL,KLKTEENLFK,NLFKRLMIVK,LFKRLMIVKK,KKLKTEENLF,TEENLFKRLM,EENLFKRLMI	CRC
NUFIP2	c.670delA	p.R224fs	TNGYMGKGADNDGSGSESGYTTPKK[p.R224fs]GKLGAIVPRVVKTLI*	KLGAIVPRV,GAIVPRVVK,VPRVVKTLI,KKGKLGAIV,KLGAIVPRVV,AIVPRVVKTL,SGYTTPKKGK,KGKLGAIVPR,LGAIVPRVVK,TPKKGKLGAI	STAD
NUFIP2	c.86_88delAGC	p.Q29del	KPGQPQPQHHHSHHHPHHHPQQQQQ[p.Q29del]PHHHHHYYFYNHSHNHHHHHHHQQPHQY	HPQQQQQPH	GBM
NUP210	c.403delC	p.L135fs	DAIVDLIHDIQIVSTTRELYLEDSP[p.L135fs]WS*	ELYLEDSPW,RELYLEDSPW	STAD
NUP88	c.905C>T	p.A302V	FLTYISLLHSPGNIGKLLGPLPMHP[p.A302V]VAEDNYGYDACAVLCLPCVPNILVIA	PVAEDNYGY,LLGPLPMHPV,PMHPVAEDNY,HPVAEDNYGY	CRC
NUP93	c.40G>A	p.E14K	MDTEGFGELLQQA[p.E14K]KQLAAETEGISELPHVERNLQEIQQA	LQQAKQLAA,KQLAAETEG,KQLAAETEGI,LLQQAKQLAA,GELLQQAKQL	BRCA
NYAP1	c.1438C>T	p.P480S	DKAVSYTMVYSAVKVTTHSVLPAGP[p.P480S]SLGAGEPKTEKEISVLHGMLCTSSRP	SVLPAGPSL,LPAGPSLGA,VLPAGPSLGA,HSVLPAGPSL	TGCT
NYAP2	c.1310C>T	p.P437L	SSPPPPSTLYRTQSPHGYPKSHSTS[p.P437L]LSPVSMGRSLTPLSLKRPPPYDAVHS	SLSPVSMGR,KSHSTSLSP,YPKSHSTSL,SHSTSLSPV,STSLSPVSM,TSLSPVSMGR,KSHSTSLSPV,HSTSLSPVSM	LUAD
NYAP2	c.590G>A	p.R197Q	RTEASAKPRPHSDEYSKKIPPPKPK[p.R197Q]QNPNTQLSTSFDETYIKKHGPRRTSL	KQNPNTQLS,KPKQNPNTQL,KQNPNTQLST	CESC
NYNRIN	c.339delC	p.G113fs	AFLGAQGLFLDCLCWSTLAYLVPGP[p.G113fs]LAP*	LAYLVPGPL,TLAYLVPGPL	STAD
OBSCN	c.13546C>T	p.R4516W	LLLRSAQPHHAGEVTFACRDAVASA[p.R4516W]WLTVLGLPDPPEDAEVVARSSHTVTL	AVASAWLTV,VASAWLTVL,SAWLTVLGL,AVASAWLTVL,DAVASAWLTV,ACRDAVASAW,ASAWLTVLGL	ACC
OBSCN	c.2721_2722TG>CA	p.A908T	VSEPKVVFAKEQLARRKLQAEAGAS[p.A908T]TTLSCEVAQAQTEVTWYKDGKKLSSSS	LQAEAGAST,AEAGASTTL,LQAEAGASTT,QAEAGASTTL,AEAGASTTLS	TGCT
OBSCN	c.2989_2990insG	p.G997fs	LDVKEPKVVFAKDQVAHSEVQAEAG[p.G997fs]GQCHAELRGGPGPDGGDVVQRWEEAELQLESACRGQGLQTEAGGAAGRQDRCRGLQLRGQGPEGLLPPAHHRAQDDVCKGAVSA*	LLPPAHHRA,AEAGGQCHA,VQRWEEAEL,LQTEAGGAA,EEAELQLES,AELRGGPGP,AELQLESAC,GLLPPAHHRA,VQAEAGGQCH,QRWEEAELQL,LESACRGQGL,LQTEAGGAAG,RQDRCRGLQL,LQLRGQGPEG,EEAELQLESA	STAD
OBSL1	c.4924G>A	p.E1642K	RCAARLIVREVPVTIVRGPHDLEVT[p.E1642K]KGDTATFECELSQALADVTWEKDGNA	VTKGDTATF,LEVTKGDTA,EVTKGDTATF	CESC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ODF2L	c.1221delA	p.K407fs	TTLAALKDEVVSVENELSELQEVEK[p.K407fs]NRKPLLKCIKLRYKSCKKQLK*	KLRYKSCKK,RYKSCKKQL,LLKCIKLRY,ELQEVEKNR,KPLLKCIKL,CIKLRYKSC,VEKNRKPLL,LLKCIKLRYK,VEKNRKPLLK,KNRKPLLKCI,CIKLRYKSCK,RYKSCKKQLK,QEVEKNRKPL,LRYKSCKKQL	KICH
ODF2L	c.880G>A	p.E294K	DQEAKLSETISASNAWKSHYEKIVI[p.E294K]KKTELEVQIETMKKQIINLLEDLKKM	KKTELEVQI,YEKIVIKKT,IVIKKTELEV,KSHYEKIVIK	MM
ODF4	c.181C>T	p.R61C	TGELGQDGRLLSSTLSLSSNRSLGQ[p.R61C]CQNSPLPFQWRITHSFRWMAQVLASE	QCQNSPLPF,SLGQCQNSPL,GQCQNSPLPF,CQNSPLPFQW	GBM
ODZ1	c.1097G>T	p.R366M	HLFGLTWQLQPVEGELYANGVSKGN[p.R366M]MGTESMDTTYSPIGGKVSDKSEKKVF	KGNMGTESM,MGTESMDTTY,YANGVSKGNM,SKGNMGTESM	HNSC
ODZ1	c.7666C>T	p.R2556W	KGIKFAIKDGIVTADIIGVANEDSR[p.R2556W]WLAAILNNAHYLENLHFTIEGRDTHY	WLAAILNNA,NEDSRWLAA,RWLAAILNNA,WLAAILNNAH,NEDSRWLAAI	CRC
ODZ2	c.1882_1883insG	p.W628fs	KAACPVLCSGNGQYSKGTCQCYSGW[p.W628fs]ERCRVRRAHESVHRSFLRGPRLLH*	SFLRGPRLL,RVRRAHESV,SVHRSFLRG,RSFLRGPRL,CYSGWERCR,SGWERCRVR,ESVHRSFLR,AHESVHRSF,HESVHRSFL,WERCRVRRA,RVRRAHESVH,RAHESVHRSF,VHRSFLRGPR,RSFLRGPRLL,SGWERCRVRR,WERCRVRRAH	KIRC
ODZ3	c.653C>A	p.P218Q	SAQHHPSITSLNRNSLTNRRNQSPA[p.P218Q]QPAALPAELQTTPESVQLQDSWVLGS	QPAALPAEL,NQSPAQPAA,SPAQPAALPA,RRNQSPAQPA,NQ5PAQPAAL,AQPAALPAEL	LUAD
OGDH	c.233delT	p.I78fs	NYVEEMYCAWLENPKSVHKSWDIFF[p.I78fs]ATRMPEPHRALPTRVPFP*	RMPEPHRAL,RALPTRVPF,ATRMPEPHR,SWDIFFATR,WDIFFATRM,FATRMPEPH,KSWDIFFATR,ATRMPEPHRA,RALPTRVPFP,FATRMPEPHR,MPEPHRALPT,TRMPEPHRAL,HRALPTRVPF,EPHRALPTRV	GBM
OGDH	c.2844_2845insC	p.Y948fs	VAITRIEQLSPFPFDLLLKEVQKYP[p.Y948fs]QC*	KEVQKYPQC	STAD
OGDHL	c.1279G>A	p.A427T	TKAEQFYRGDAQGKKVMSILVHGDA[p.A427T]TFAGQGVVYETFHLSDLP5YTTNGTV	LVHGDATFA,ATFAGQGVV,TFAGQGVVY,DATFAGQGV,ILVHGDATF,ATFAGQGVVY,ILVHGDATFA,SILVHGDATF	CRC
OGDHL	c.169C>T	p.R57C	RLLPSRLGVQAARLLAAHDVPVFGW[p.R57C]CSRSSGPPATFPSSKGGGGSSYMEEM	CSRSSGPPA,VPVFGWCSR,CSRSSGPPAT,DVPVFGWCSR	UCEC
OGFOD1	c.1430_1431insGTTTTTTT	p.G477fs	SKAEFALDLILYCGCEGWEPEYGGF[p.G477fs]FFLLLTLPKVKMKSC*	FLLLTLPKV,FFLLLTLPK,LTLPKVKMK,EYGGFFFLL,YGGFFFLLL,GFFFLLLTL,LPKVKMKSC,WEPEYGGFF,PEYGGFFFL,EPEYGGFFF,FFFLLLTLPK,GWEPEYGGFF,EYGGFFFLLL,WEPEYGGFFF,GGFFFLLLTL,LLLTLPKVKM,PEYGGFFFLL,EPEYGGFFFL	PAAD
OGFR	c.1670G>C	p.S557T	DEPAESPSETPGPRPAGPAGDEPAE[p.S557T]TPSETPGPRPAGPAGDEPAESPSETP	ETPSETPGPR	ACC
OIT3	c.1522C>A	p.R508S	FVGKDHKEVFLHCRVLVCGVLDERS[p.R508S]SCAQGCHRRMRRGAGGEDSAGLQGQT	VLDERSSCA,RSSCAQGCHR	LUAD
OLFM4	c.396G>T	p.K132N	HVLSQKFEKELSKVREYVQLISVYE[p.K132N]NKLLNLTVRIDIMEKDTISYTELDFE	QLISVYENK,VYENKLLNL,YENKLLNLT,QLISVYENKL,SVYENKLLNL,VQLISVYENK,YENKLLNLTV	CRC
OMA1	c.1334G>A	p.R445Q	MEFVDSLHGQPKMPEWLSTHPSHGN[p.R445Q]QVEYLDRLIPQALKIREMCNCPPLSN	NQVEYLDRL,PSHGNQVEY,STHPSHGNQV,HPSHGNQVEY,NQVEYLDRLI	UCEC
ONECUT1	c.1270T>A	p.L424M	TLHAIFKENKRPSKELQITISQQLG[p.L424M]MELSTVSNFFMNARRRSLDKWQDEGS	QLGMELSTV,ITISQQLGM,MELSTVSNF,ISQQLGMEL,QQLGMELST,QQLGMELSTV,GMELSTVSNF,MELSTVSNFF,SQQLGMELST	KIRC
OOEP	c.301C>T	p.R101C	TSQALLTVDIVDSGNLVEITVFGRP[p.R101C]CVQNRVKSMLLCLAWFHREHRARAEK	ITVFGRPCV,CVQNRVKSM,EITVFGRPCV,VEITVFGRPC	LUAD
OPLAH	c.2699C>A	p.A900D	QQEGAVFLSFKLVQGGVFQEEAVTE[p.A900D]DLRAPGKVPNCSGTRNLHDNLSDLRA	QEEAVTEDL,VTEDLRAPGK,FQEEAVTEDL,EEAVTEDLRA	TGCT

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OPN1LW	c.848C>A	p.P283H	STQKAEKEVTRMVVVMIFAYCVCWG[p.P283H]HYTFFACFAAANPGYAFHPLMAALPA	CVCWGHYTF,VCWGHYTFF,AYCVCWGHY,GHYTFFACF,YCVCWGHYTF,CVCWGHYTFF,FAYCVCWGHY,WGHYTFFACF	LUAD
OPN1MW	c.853G>A	p.A285T	QKAEKEVTRMVVVMVLAFCFCWGPY[p.A285T]TFFACFAAANPGYPFHPLMAALPAFF	CFCWGPYTF,FCWGPYTFF,FCWGPYTFFA,FCFCWGPYTF,CFCWGPYTFF	HNSC
OPRD1	c.80G>T	p.C27F	EPAPSAGAELQPPLFANASDAYPSA[p.C27F]FPSAGANASGPPGARSASSLALAIAI	ASDAYPSAF,AYPSAFPSA,FPSAGANAS,YPSAFPSAG,DAYPSAFPSA,YPSAFPSAGA,NASDAYPSAF,SAFPSAGANA,FPSAGANASG	ACC
OPRM1	c.1058G>A	p.R353H	KICVFIFAFIMPVLIITVCYGLMIL[p.R353H]HLKSVRMLSGSKEKDRNLRRITRMVL	LMILHLKSV,YGLMILHLK,CYGLMILHL,HLKSVRMLS,MILHLKSVR,ILHLKSVRM,LHLKSVRML,GLMILHLKSV,ILHLKSVRML,HLKSVRMLSG,LMILHLKSVR,MILHLKSVRM	CRC
OPRM1	c.1384C>T	p.R462C	NFKRCFREFCIPTSSNIEQQNSTRI[p.R462C]CQNTRDHPSTANTVDRTNHQLENLEA	STRICQNTR,NSTRICQNTR	UCEC
OPTN	c.70delC	p.P24fs	MSHQPLSCLTEKEDSPSESTGNGPP[p.P24fs]TWPTQTWTRLPRRSCCSR*	TQTWTRLPR,QTWTRLPRR,TWPTQTWTR,WPTQTWTRL,PPTWPTQTW,TWPTQTWTRL,RLPRRSCCSR,PTWPTQTWTR,PTQTWTRLPR,TQTWTRLPRR,SESTGNGPPT,ESTGNGPPTW	STAD
OR10A3	c.217T>G	p.F73V	IISLNQSLHVPMYLFLLNLSVVEVS[p.F73V]VSAVITPEMLVVLSTEKTMISFVGCF	NLSVVEVSV,SVVEVSVSA,VEVSVSAVI,VSAVITPEM,SVVEVSVSAV,SVSAVITPEM,VEVSVSAVIT	KIRC
OR10A3	c.278C>A	p.S93Y	VVEVSFSAVITPEMLVVLSTEKTMI[p.S93Y]YFVGCFAQMYFILLFGGTECFLLGAM	LSTEKTMIY,STEKTMIYF,MIYFVGCFA,YFVGCFAQM,KTMIYFVGC,TMIYFVGCF,TEKTMIYFV,TMIYFVGCFA,KTMIYFVGCF,IYFVGCFAQM,VLSTEKTMIY,YFVGCFAQMY,STEKTMIYFV,LSTEKTMIYF	CRC
OR10H4	c.597G>T	p.M199I	VIHHFFCHVLSLLKLACENKTSSVI[p.M199I]IGVMLVCVTALIGCLFLIILSYVFIV	KTSSVIIGV,SVIIGVMLV,IIGVMLVCV,TSSVIIGVM,VIIGVMLVCV,KTSSVIIGVM,SSVIIGVMLV,CENKTSSVII	LUAD
OR10J1	c.470T>A	p.L157Q	DRYVAICNPLRYMVIMNKRLRIQLV[p.L157Q]QGACSIGLIVAITQVTSVFRLPFCAR	QLVQGACSI,RLRIQLVQG,VQGACSIGL,RLRIQLVQGA,IQLVQGACSI,VQGACSIGLI	LUAD
OR10J1	c.731G>A	p.R244Q	VPMGLVFISYVLIISTILKIASVEG[p.R244Q]QKKAFATCASHLTVVIVHYSCASIAY	KIASVEGQK,KIASVEGQKK,ASVEGQKKAF	TGCT
OR10X1	c.892C>A	p.L298I	IVYLKPEASGDDTLIAVPYTVITPF[p.L298I]ISPIIFSLRNKDMKNAFRRMMGNTVA	VITPFISPI,FISPIIFSL,ISPIIFSLR,PYTVITPFI,ITPFISPII,TPFISPIIF,TVITPFISPI,VITPFISPII,FISPIIFSLR,ITPFISPIIF,PFISPIIFSL,VPYTVITPFI	LUAD
OR10Z1	c.615G>C	p.L205F	DTPPVLSLACGDTGPSELRIFILSL[p.L205F]FVLLVSFFFITISYAYILAAILRIPS	RIFILSLFV,FILSLFVLL,ILSLFVLLV,LRIFILSLF,IFILSLFVL,SLFVLLVSF,LFVLLVSFF,FVLLVSFFI,IFILSLFVLL,LSLFVLLVSF,SLFVLLVSFF,LFVLLVSFFF,ELRIFILSLF	LUAD
OR11H12	c.461A>C	p.H154P	LLTVMAFDQYLAICRPLLYPNIMTG[p.H154P]PLCAKLVILCWVCGFLWFLIPIVLIS	IMTGPLCAK,MTGPLCAKL,YPNIMTGPL,GPLCAKLVI,IMTGPLCAKL,LLYPNIMTGP,NIMTGPLCAK,LYPNIMTGPL,MTGPLCAKLV,GPLCAKLVIL,YPNIMTGPLC	GBM
OR13C2	c.25C>G	p.L9V	MEWENHTI[p.L9V]VVEFFLKGLSGHPRLELLFFVLIFIM	TIVVEFFLK,HTIVVEFFL,MEWENHTIV,IVVEFFLKGL,HTIVVEFFLK,MEWENHTIVV,WENHTIVVEF	CESC
OR13G1	c.773G>A	p.R258H	KAFSTCSSHLTVVTLYYSPVIYTYI[p.R258H]HPASSYTFERDKVVAALYTLVTPTLN	VIYTYIHPA,YIHPASSYT,IHPASSYTF,TYIHPASSY,YTYIHPASS,SPVIYTYIH,YTYIHPASSY,YIHPASSYTF,HPASSYTFER	BRCA
OR14A16	c.478G>T	p.G160C	DRSTCVQRATVSWLYGGLIAVMHTA[p.G160C]CTFSLSYCGSNMVHQFFCDIPQLLAI	TACTFSLSY,HTACTFSLS,AVMHTACTF,MHTACTFSL,HTACTFSLSY,VMHTACTFSL,GLIAVMHTAC,IAVMHTACTF	LUAD
OR1M1	c.205G>A	p.V69I	LIILAISIDSHLHTPMYFFLANLSL[p.V69I]IDFCLATNTIPKMLVSLQTGSKAISY	NLSLIDFCL,SLIDFCLAT,FFLANLSLI,LANLSLIDF,NLSLIDFCLA,FLANLSLIDF,YFFLANLSLI,IDFCLATNTI	PRAD
OR2A25	c.240G>A	p.M80I	HTPMYFFLSHLAVVDIACACSTVPQ[p.M80I]ILVNLLHPAKPISFAGCMTQMFLFLS	ILVNLLHPA,CSTVPQILV,TVPQILVNL,VPQILVNLL,ILVNLLHPAK,STVPQILVNL,TVPQILVNLL	LUAD
OR2A25	c.313A>T	p.S105C	MLVNLLHPAKPISFAGCMTQMFLFL[p.S105C]CFAHTECLLLVVMSYDRYVAICHPLR	QMFLFLCFA,FLFLCFAHT,FLCFAHTEC,TQMFLFLCF,LCFAHTECL,MTQMFLFLCF,TQMFLFLCFA,FLCFAHTECL,CFAHTECLLL,QMFLFLCFAH	CLL
OR2A5	c.212C>T	p.S71L	GLIWLDSRLHTPMYFFLSHLAIIDI[p.S71L]LYASNNVPKMLTNLGLNKRKTISFVP	HLAIIDILY,AIIDILYAS,LYASNNVPK,DILYASNNV,ILYASNNVP,HLAIIDILYA,ILYASNNVPK,LYASNNVPKM,SHLAIIDILY,LSHLAIIDIL,IDILYASNNV	SKCM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR2AG2	c.745G>T	p.G249W	TVLRMPSNEGRKKALVTCSSHLIVV[p.G249W]WMFYGAATFMYVLPSSFHSPKQDNII	IVVWMFYGA,WMFYGAATF,HLIVVWMFY,SHLIVVWMF,SSHLIVVWM,CSSHLIVVW,LIVVWMFYGA,WMFYGAATFM,SSHLIVVWMF,VWMFYGAATF,SHLIVVWMFY,IVVWMFYGAA	LUAD
OR2AK2	c.111G>C	p.W37C	LVSAMKTGNQSFGTDFLLVGLFQYG[p.W37C]CINSLLFVVIATLFTVALTGNIMLIH	FQYGCINSL,CINSLLFVV,QYGCINSLL,YGCINSLLF,FQYGCINSLL,CINSLLFVVI,QYGCINSLLF	LUAD
OR2AK2	c.133G>A	p.V45I	NQSFGTDFLLVGLFQYGWINSLLFV[p.V45I]IIATLFTVALTGNIMLIHLIRLNTRL	WINSLLFVI,SLLFVIIAT,LLFVIIATL,VIIATLFTV,IIATLFTVA,LFVIIATLF,WINSLLFVII,SLLFVIIATL,FVIIATLFTV,VIIATLFTVA,IIATLFTVAL,GWINSLLFVI,LLFVIIATLF	BRCA
OR2B11	c.29G>T	p.G10V	MKSDNHSFL[p.G10V]VDSPKAFILLGVSDRPWLELPLFVVL	KSDNHSFLV,FLVDSPKAF,HSFLVDSPK,FLVDSPKAFI,SFLVDSPKAF,MKSDNHSFLV	LUSC
OR2H1	c.859G>A	p.V287I	NPYAQGRGKFFGLFYAVGTPSLNPL[p.V287I]IYTLRNKEIKRALRRLLGKERDSRES	IYTLRNKEI	GBM
OR2H2	c.615G>C	p.L205F	PALIRLSCEDTSYNEIQVAVASVFI[p.L205F]FVVPLSLILVSYGAITWAVLRINSAK	AVASVFIFV,SVFIFVVPL,FIFVVPLSL,FVVPLSLIL,VAVASVFIF,IFVVPLSLI,VASVFIFVV,VAVASVFIFV,AVASVFIFVV,FIFVVPLSLI,FVVPLSLILV,VFIFVVPLSL,IFVVPLSLIL,QVAVASVFIF,ASVFIFVVPL	LUAD
OR2J2	c.700G>T	p.G234W	LIPLILILTTYGAIARAVLSMQSTT[p.G234W]WLQKVFRTCGAHLMVVSLFFIPVMCM	MQSTTWLQK,TTWLQKVFR,QSTTWLQKV,VLSMQSTTW,LSMQSTTWL,STTWLQKVF,VLSMQSTTWL,MQSTTWLQKV,SMQSTTWLQK,STTWLQKVFR,AVLSMQSTTW,QSTTWLQKVF	LUAD
OR2L13	c.318G>T	p.M106I	AYNFLSGQKGISFLGCGVQSFFFLT[p.M106I]IACSEGLLLTSMAYDRYLAICHSLYY	VQSFFFLTI,QSFFFLTIA,LTIACSEGL,IACSEGLLL,FLTIACSEGL,GVQSFFFLTI,LTIACSEGLL,VQSFFFLTIA	LUAD
OR2L13	c.724A>G	p.T242A	CGRVLFAVYHMHSKEGRKKAFTTIS[p.T242A]AHLTVVIFYYAPFVYTYLRPRNLRSP	TISAHLTVV,KAFTTISAH,AHLTVVIFY,FTTISAHLT,TTISAHLTV,SAHLTVVIF,KKAFTTISA,ISAHLTVVI,FTTISAHLTV,TTISAHLTVV,TISAHLTVVI,ISAHLTVVIF,RKKAFTTISA,KAFTTISAHL,SAHLTVVIFY,AHLTVVIFYY,KKAFTTISAH	LUAD
OR2L3	c.199C>A	p.L67I	LSMILLIFLDTHLHTPMYFLLSQLS[p.L67I]IIDLNYISTIVPKMASDFLSGNKSIS	QLSIIDLNY,FLLSQLSII,LLSQLSIIDL,QLSIIDLNYI,YFLLSQLSII,SQLSIIDLNY	LUAD
OR2L3	c.3G>T	p.M1I	[p.M1I]IENYNQTSTDFILLGFFPPSRIGLFL	IENYNQTST	LUAD
OR2L3	c.881A>G	p.K294R	EDKVLAVFYTTLTPMLNPIIYSLRN[p.K294R]REVMGALTRVSQRICSGKM*	IIYSLRNREV,RNREVMGALT,REVMGALTRV	TGCT
OR2L8	c.361C>T	p.R121C	CGIQSFFFLALGGAEALLLASMAYD[p.R121C]CYIAICFPLHYLIRMSKRVCVLMITG	ASMAYDCYI,SMAYDCYIA,MAYDCYIAI,CYIAICFPL,SMAYDCYIAI,AYDCYIAICF,CYIAICFPLH	LUAD
OR2L8	c.513G>T	p.R171S	GSWIIGSINACAHTVYVLHIPYCRS[p.R171S]SAINHFFCDVPAMVTLACMDTWVYEG	RSSAINHFF,IPYCRSSAI,CRSSAINHF,HIPYCRSSAI,SAINHFFCDV,RSSAINHFFC,YCRSSAINHF,LHIPYCRSSA,CRSSAINHFF	LUAD
OR2L8	c.603_604delTG	p.S201fs	FCDVPAMVTLACMDTWVYEGTVFLS[p.S201fs]HHLSRVSLHWYFMFLWPGSLCCLPHEICRREEESLFDLQHPPHCSNFLLCTFCLHLSTSKIPAISNRGQGSGCLLHHPHPNAQPHHL*	FLSHHLSRV,SLHWYFMFL,FMFLWPGSL,FLWPGSLCC,SLCCLPHEI,LLCTFCLHL,SLFDLQHPP,CLHLSTSKI,HLSTSKIPA,LLHHPHPNA,SRVSLHWYF,VSLHWYFMF,WYFMFLWPG,CSNFLLCTF,NFLLCTFCL,VFLSHHLSR,RVSLHWYFM,LSRVSLHWY,HPPHCSNFL,HPHPNAQPH,HPNAQPHHL,YEGTVFLSH,SHHLSRVSL,HLSRVSLHW,CRREEESLF,REEESLFDL,LQHPPHCSN,RGQGSGCLL,GQGSGCLLH,EESLFDLQH,LHWYFMFLW,HLSRVSLHWY,VSLHWYFMFL,FMFLWPGSLC,FLWPGSLCCL,FLLCTFCLHL,HLSTSKIPAI,CLLHHPHPNA,FLSHHLSRVS,TVFLSHHLSR,TFCLHLSTSK,VFLSHHLSRV,RVSLHWYFMF,SLHWYFMFLW,YFMFLWPGSL,TSKIPAISNR,HPPHCSNFLL,LSRVSLHWYF,LQHPPHCSNF,SLFDLQHPPH,YEGTVFLSHH,LSHHLSRVSL,HHLSRVSLHW,SRVSLHWYFM,ICRREEESLF,HCSNFLLCTF,LHLSTSKIPA,GQGSGCLLHH,WPGSLCCLPH	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR2M2	c.284delC	p.A95fs	DLMLICTTVPKMAFNYLSGSKSISM[p.A95fs]VVVSHKFSSIYHCLALNVFFWLLWLMTAILLFATL*	VSHKFSSIY,LALNVFFWL,ALNVFFWLL,NVFFWLLWL,WLLWLMTAI,LLWLMTAIL,LMTAILLFA,VVSHKFSSI,ISMVVVSHK,SMVVVSHKF,KFSSIYHCL,IYHCLALNV,CLALNVFFW,VFFWLLWLM,LWLMTAILL,WLMTAILLF,GSKSISMVV,FSSIYHCLA,MTAILLFAT,TAILLFATL,SSIYHCLAL,SKSISMVVV,HKFSSIYHC,YHCLALNVF,HCLALNVFF,SIYHCLALNV,CLALNVFFW,LALNVFFWLL,NVFFWLLWLM,WLLWLMTAIL,LLWLMTAILL,WLMTAILLFA,LMTAILLFAT,MTAILLFATL,VVVSHKFSSI,SISMVVVSHK,VSHKFSSIYH,ISMVVVSHKF,IYHCLALNVF,YHCLALNVFF,FWLLWLMTAI,LWLMTAILLF,GSKSISMVVV,KFSSIYHCLA,VVSHKFSSIY,KSISMVVVSH,HKFSSIYHCL,FSSIYHCLAL	HNSC
OR2M2	c.531C>A	p.F177L	GSTDGIIDAVATFSFSFCGSREIAH[p.F177L]LFCEFPSLLILSCNDTSIFEEVIFIC	HLFCEFPSL,GSREIAHLF,EIAHLFCEF,REIAHLFCE,HLFCEFPSLL,REIAHLFCEF,LFCEFPSLLI,GSREIAHLFC,CGSREIAHLF,AHLFCEFPSL	LUAD
OR2M2	c.967T>C	p.F323L	TRAFMKILGKGKSESELPHKLYVLL[p.F323L]LAKFFFLISIFFYDVKILALIMYIA	LLLAKFFFL,LLAKFFFLI,KLYVLLLAK,LYVLLLAKF,VLLLAKFFF,VLLLAKFFFL,LLLAKFFFLI,KLYVLLLAKF,LYVLLLAKFF,YVLLLAKFFF,LAKFFFLISI,LPHKLYVLLL	LUAD
OR2M3	c.704G>A	p.R235H	PVAIIIASYARVILAVIHMGSGEGR[p.R235H]HKAFTTCSSHLLVVGMYYGAALFMYI	SGEGRHKAF,HMGSGEGRHK,GSGEGRHKAF,HKAFTTCSSH,GEGRHKAFTT	CRC
OR2M3	c.819G>T	p.M273I	VGMYYGAALFMYIRPTSDRSPTQDK[p.M273I]IVSVFYTILTPMLNPLIYSLRNKEVT	KIVSVFYTI,TQDKIVSVF,TQDKIVSVFY,KIVSVFYTIL,SPTQDKIVSV	HNSC
OR2M5	c.613G>T	p.V205L	DFPSLLILSCNDTSIFEKVLFICCI[p.V205L]LMIVFPVAIIIASYARVILAVIHMGS	FICCILMIV,CILMIVFPV,ILMIVFPVA,LMIVFPVAI,LFICCILMI,KVLFICCIL,VLFICCILM,VLFICCILMI,ILMIVFPVAI,LMIVFPVAII,KVLFICCILM,FICCILMIVF	LUAD
OR2T12	c.551G>A	p.R184H	VATLSFPYCGAHEIDHFFCEAPVLV[p.R184H]HLACADTSVFENAMYICCVLMLLVPF	HLACADTSV,EAPVLVHLA,CEAPVLVHL,HLACADTSVF,CEAPVLVHLA	GBM
OR2T12	c.772A>T	p.M258L	KKAFATCSSHVAVVGLFYGAGIFTY[p.M258L]LRPKSHRSTNHDKVVSAFYTMFTPLL	YGAGIFTYL,GIFTYLRPK,GAGIFTYLR,TYLRPKSHR,YLRPKSHRS,AGIFTYLRPK,FTYLRPKSHR,FYGAGIFTYL,YGAGIFTYLR,YLRPKSHRST	LUAD
OR2T2	c.37T>G	p.F13V	MGMEGLLQNSTN[p.F13V]VVLTGLITHPAFPGLLFAIVFSIFVV	GLLQNSTNV,LLQNSTNVV,STNVVLTGL,LQNSTNVVL,GLLQNSTNVV,LLQNSTNVVL,NSTNVVLTGL,STNVVLTGLI,LQNSTNVVLT	LUSC
OR2T27	c.31G>T	p.D11Y	MEQSNYSVYA[p.D11Y]YFILLGLFSNARFPWLLFALILLVFL	QSNYSVYAY,SVYAYFILL,YAYFILLGL,SNYSVYAYF,NYSVYAYFI,YSVYAYFIL,VYAYFILLG,AYFILLGLF,YSVYAYFILL,NYSVYAYFIL,VYAYFILLGL,YAYFILLGLF,EQSNYSVYAY,QSNYSVYAYF,SNYSVYAYFI	LUAD
OR2T33	c.358C>A	p.R120S	CGVQIFFLPTLGGGECFLLAAMAYD[p.R120S]SYAAVCHPLRYPTLMSWQLCLRMTMS	AMAYDSYAA,MAYDSYAAV,AAMAYDSYA,SYAAVCHPL,LAAMAYDSY,FLLAAMAYDS,AMAYDSYAAV,AAMAYDSYAA,LLAAMAYDSY,SYAAVCHPLR,LAAMAYDSYA,DSYAAVCHPL,MAYDSYAAVC	HNSC
OR2T33	c.494C>A	p.P165Q	LRMTMSCWLLGAADGLLQAVVTLSF[p.P165Q]QYCGAHEIDHFFCETPVLVRLACADT	FQYCGAHEI,TLSFQYCGA,AVVTLSFQY,LSFQYCGAH,SFQYCGAHEI,QAVVTLSFQY,FQYCGAHEID	LUAD
OR2T34	c.737G>T	p.C246F	SSYTLILHLIHRMNSAAGRRKALAT[p.C246F]FSSHMIIVLLLFGASFYTYMLRSSYH	ALATFSSHM,KALATFSSH,ATFSSHMII,GRRKALATF,RKALATFSS,FSSHMIIVL,LATFSSHMI,ALATFSSHMI,ATFSSHMIIV,FSSHMIIVLL,TFSSHMIIVL,KALATFSSHM,AGRRKALATF,RKALATFSSH,LATFSSHMII	LUAD
OR2T4	c.408_409CG>TC	p.V137L	KMLLDQVMGVNKISAPECGMQMFFY[p.V137L]LTLAGSEFFLLATMAYDRYVAICHPLR	GMQMFFYLT,MQMFFYLTL,CGMQMFFYL,GMQMFFYLTL,MQMFFYLTLA,FYLTLAGSEF	LIHC
OR2T6	c.637G>T	p.V213L	ACGDKTTYETVMYVCCVAMLLIPFS[p.V213L]LVTASYTRILITVHQMTSAEGRKKAF	AMLLIPFSL,MLLIPFSLV,LLIPFSLVT,LIPFSLVTA,LVTASYTRI,SLVTASYTR,PFSLVTASY,IPFSLVTAS,AMLLIPFSLV,LLIPFSLVTA,SLVTASYTRI,FSLVTASYTR,IPFSLVTASY,VAMLLIPFSL	LUAD
OR4C12	c.744C>A	p.F248L	LKNNSLEGRCKALSTCISHIIVVVL[p.F248L]LFVPCIFVYLRSVTTLPIDKAVAVFY	IIVVVLLFV,LLFVPCIFV,HIIVVVLLF,VLLFVPCIF,LFVPCIFVY,HIIVVVLLFV,VLLFVPCIFV,LLFVPCIFVY,SHIIVVVLLF,VVLLFVPCIF,LFVPCIFVYL,ISHIIVVVLL	UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR4C12	c.837G>T	p.M279I	FVYLRSVTTLPIDKAVAVFYTMVVP[p.M279I]ILNPVVYTLRNAEVKSAIRKLWRKKV	MVVPILNPV,ILNPVVYTL,VFYTMVVPI,FYTMVVPIL,VPILNPVVY,AVFYTMVVPI,TMVVPILNPV,MVVPILNPVV,ILNPVVYTLR,VFYTMVVPIL,VVPILNPVVY	LUAD
OR4C12	c.925G>T	p.D309Y	VYTLRNAEVKSAIRKLWRKKVTSDN[p.D309Y]Y	RKKVTSDNY,WRKKVTSDNY	LUAD
OR4C16	c.188A>T	p.Y63F	LGNLLIIISVKTSQALKNPMFFFLF[p.Y63F]FLSLSDTCLSTSITPRMIVDALLKKT	PMFFFLFFL,FLSLSDTCL,FFFLFFLSL,NPMFFFLFF,FLFFLSLSDT,FLSLSDTCLS,KNPMFFFLFF,MFFFLFFLSL,NPMFFFLFFL	CLL
OR4C16	c.403A>C	p.S135R	IFILILTAVDRYVDICKPLHYMTII[p.S135R]RQWVCGVLMAVAWVGSCVHSLVQIFL	YMTIIRQWV,IIRQWVCGV,HYMTIIRQW,RQWVCGVLM,TIIRQWVCGV,RQWVCGVLMA,HYMTIIRQWV,LHYMTIIRQW,IRQWVCGVLM	STAD
OR4C16	c.484C>A	p.L162M	WVCGVLMAVAWVGSCVHSLVQIFLA[p.L162M]MSLPFCGPNVINHCFCDLQPLLKQAC	SLVQIFLAM,VQIFLAMSL,FLAMSLPFC,IFLAMSLPF,MSLPFCGPNV,FLAMSLPFCG,QIFLAMSLPF,HSLVQIFLAM,VQIFLAMSLP	LUAD
OR4C3	c.389_390insT	p.H130fs	IADSLYEGRTISYECCMAQLFGAHF[p.H130fs]FGRC*	AQLFGAHFF,LFGAHFFGR,QLFGAHFFGR,MAQLFGAHFF	LUAD
OR4E2	c.677G>A	p.R226Q	TNSGTISLSCFLAVVTSYMVILVSL[p.R226Q]QKHSAEGRQKALSTCSAHFMVVALFF	MVILVSLQK,ILVSLQKHSA,YMVILVSLQK	SKCM
OR4K2	c.761G>T	p.C254F	SSRGSSKALSTCTAHFIVVFLFFGP[p.C254F]FIFIYMWPLSSFLTDKILSVFYTIFT	FLFFGPFIF,FIFIYMWPL,VFLFFGPFI,LFFGPFIFI,FFGPFIFIY,VVFLFFGPF,GPFIFIYMW,VVFLFFGPFI,FLFFGPFIFI,IVVFLFGPF,VFLFFGPFIF,FFGPFIFIYM,FGPFIFIYMW,PFIFIYMWPL,LFFGPFIFIY	LUSC
OR4K5	c.529delT	p.F177fs	VHTLSQLSFTVNLPFCGPNVVDSFF[p.F177fs]VIFLESPNLPAWTLTSLKY*	NVVDSFFVI,FLESPNLPA,PAWTLTSLK,AWTLTSLKY,SPNLPAWTL,LPAWTLTSL,VVDSFFVIF,LESPNLPAW,VVDSFFVIFL,FVIFLESPNL,NLPAWTLTSL,PAWTLTSLKY,ESPNLPAWTL,NVVDSFFVIF,FLESPNLPAW,LESPNLPAWT	STAD
OR4M1	c.122G>A	p.G41E	GLSQTREVQLVLFVIFLSFYLFILP[p.G41E]ENILIICTIRLDPHLTSPMYFLLANL	YLFILPENI,FILPENILI,ILPENILII,YLFILPENIL,FILPENILII,FYLFILPENI,LFILPENILI,ENILIICTIR	SKCM
OR4M2	c.355G>T	p.A119S	FDGCIAQLFFLHFAGASEMFLLTVM[p.A119S]SFDLYTAICRPLHYATIMNQRLCCIL	LTVMSFDLY,LLTVMSFDL,VMSFDLYTA,MSFDLYTAI,MFLLTVMSF,TVMSFDLYT,LLTVMSFDLY,FLLTVMSFDL,TVMSFDLYTA,VMSFDLYTAI,EMFLLTVMSF,MSFDLYTAIC,SEMFLLTVMS	LUAD
OR4M2	c.481G>T	p.A161S	MNQRLCCILVALSWRGGFIHSIIQV[p.A161S]SLIVRLPFCGPNELDSYFCDITQVVR	SIIQVSLIV,IQVSLIVRL,SLIVRLPFC,VSLIVRLPF,HSIIQVSLI,IHSIIQVSL,FIHSIIQVSL,SIIQVSLIVR,HSIIQVSLIV,QVSLIVRLPF	LUAD
OR4M2	c.803C>T	p.S268F	YSHITIVVLMFGPSIYIYARPFDSF[p.S268F]FLDKVVSVFNTLIFPLRNPIIYTLRN	FFLDKVVSV,FLDKVVSVF,YARPFDSFF,IYARPFDSFF,FFLDKVVSVF,YARPFDSFFL,RPFDSFFLDK	SKCM
OR4N2	c.122G>A	p.G41E	GLTQSQDIQLLVFVLVLIFYFIILP[p.G41E]ENFLIIFTIKSDPGLTAPLYFFLGNL	FIILPENFL,IILPENFLI,ILPENFLII,YFIILPENF,ENFLIIFTI,LPENFLIIF,FIILPENFLI,IILPENFLII,FYFIILPENF,YFIILPENFL,ILPENFLIIF,PENFLIIFTI	SKCM
OR4N2	c.448_449insT	p.L150fs	ICRPLHYPTVMNPRTCYAMMLALWL[p.L150fs]WGFCPLHYPGGPHPPLAFLWPKPAGQLLL*	MLALWLWGF,AMMLALWLW,LWLWGFCPL,LWGFCPLHY,YPGGPHPPL,GPHPPLAFL,WPKPAGQLL,LHYPGGPHP,LAFLWPKPA,MMLALWLWGF,MLALWLWGFC,ALWLWGFCPL,FLWPKPAGQL,YAMMLALWLW,HYPGGPHPPL,LWPKPAGQLL,WLWGFCPLHY,WPKPAGQLLL,LHYPGGPHPP,GPHPPLAFLW	BLCA,KIRC
OR4N4	c.448_449insT	p.L150fs	ICRPLHCSTVMNPRACYAMMLALWL[p.L150fs]WGFCPLHYPGGPHPPLAFLWPKPAGQLLL*	MLALWLWGF,AMMLALWLW,LWLWGFCPL,LWGFCPLHY,YPGGPHPPL,GPHPPLAFL,WPKPAGQLL,LHYPGGPHP,LAFLWPKPA,MMLALWLWGF,MLALWLWGFC,ALWLWGFCPL,FLWPKPAGQL,YAMMLALWLW,HYPGGPHPPL,LWPKPAGQLL,WLWGFCPLHY,WPKPAGQLLL,LHYPGGPHPP,GPHPPLAFLW	CLL
OR51A7	c.371T>G	p.L124R	AQEFFIHGFTVMESSVLLIMSLDRF[p.L124R]RAIHNPLRYSSILTSNRVAKMGLILA	IMSLDRFRA,LIMSLDRFR,RFRAIHNPL,MSLDRFRAI,RAIHNPLRY,IMSLDRFRAI,LIMSLDRFRA,MSLDRFRAIH,RFRAIHNPLR,FRAIHNPLRY,LLIMSLDRFR	STAD
OR51B2	c.488C>T	p.S163L	RVIALGVGVFLRGFVSILPVILRLF[p.S163L]LFSYCKSHVITRAFCLHQEIMRLACA	RLFLFSYCK,PVILRLFLF,ILRLFLFSY,LPVILRLFL,FLFSYCKSH,FLFSYCKSHV,ILPVILRLFL,VILRLFLFSY,LPVILRLFLF	SKCM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR51B5	c.197_213delCCACAGACCTGGGGCTG	p.A66fs	GTLLLLIKEDHNLHEPMYFFLAMLA[p.A66fs]GPDHNAHGAGSPLAGSQGDWKCGLLFPGLLYTLTFLSRVWHSACHGL*	MLAGPDHNA,LLFPGLLYT,GLLYTLTFL,LLYTLTFLS,YTLTFLSRV,FLSRVWHSA,GLLFPGLLY,LFPGLLYTL,VWHSACHGL,LYTLTFLSR,NAHGAGSPL,SQGDWKCGL,GDWKCGLLF,FPGLLYTLT,AMLAGPDHNA,GLLFPGLLYT,LLFPGLLYTL,FLSRVWHSAC,RVWHSACHGL,LLYTLTFLSR,LYTLTFLSRV,YTLTFLSRVW,LSRVWHSACH,CGLLFPGLLY,HNAHGAGSPL,FPGLLYTLTF,MLAGPDHNAH,SQGDWKCGLL,WKCGLLFPGL,SPLAGSQGDW	KIRC
OR51F2	c.200G>C	p.R67P	SIPFCLLYVVAVSGNSMILFVVLCE[p.R67P]PSLHKPMYYFLSMLSATDLSLSLCTL	VLCEPSLHK,PSLHKPMYY,CEPSLHKPM,VVLCEPSLHK,LCEPSLHKPM,EPSLHKPMYY	LUSC
OR51S1	c.476G>A	p.R159Q	ICRPLHYPALLTNGVISKISLAISF[p.R159Q]QCLGLHLPLPFLLAYMPYCLPQVLTH	SLAISFQCL,SFQCLGLHL,ISFQCLGLH,FQCLGLHLPL,ISLAISFQCL,LAISFQCLGL,ISFQCLGLHL	LUSC
OR51V1	c.892C>A	p.P298T	FGKHLSPVAHVLIGNIYILFPPLMN[p.P298T]TIIYSVKTQQIHTRMLRLFSLKRY	ILFPPLMNT,LMNTIIYSV,LFPPLMNTI,MNTIIYSVK,NTIIYSVKT,PPLMNTIIY,FPPLMNTII,ILFPPLMNTI,PLMNTIIYSV,LMNTIIYSVK,LFPPLMNTII,FPPLMNTIIY	LUAD
OR52W1	c.397C>T	p.R133C	FVHALTAMESGVLLAMACDRAAAIG[p.R133C]CPLHYPVLVTKACVGYAALALALKAV	RAAAIGCPL,AAIGCPLHY,CPLHYPVLV,AIGCPLHYPV,RAAAIGCPLH,AAAIGCPLHY,IGCPLHYPVL	CRC
OR5AK2	c.267G>T	p.K89N	QHLAFVDICYTSAITPKMLQSFTEE[p.K89N]NNLMLFQGCVIQFLVYATFATSDCYL	FTEENNLML,TEENNLMLF,FTEENNLMLF,LQSFTEENNL,QSFTEENNLM	UCEC
OR5AS1	c.117G>T	p.M39I	FVGFTDYLPLRVTLFLVFLLVYTLT[p.M39I]IVGNILLIILVNINSSLQIPMYYFLS	FLLVYTLTI,LLVYTLTIV,YTLTIVGNI,TIVGNILLI,LTIVGNILL,FLLVYTLTIV,VFLLVYTLTI,VYTLTIVGNI,YTLTIVGNIL,LTIVGNILLI	LUAD
OR5AU1	c.935G>A	p.R312H	KAFSTCASHLTAICLFFGTTLFMYL[p.R312H]HPRSSYSLTQDRTVAVIYTVVIPVLN	FMYLHPRSS,YLHPRSSYS,TLFMYLHPR,GTTLFMYLH,MYLHPRSSY,HPRSSYSLT,LHPRSSYSL,YLHPRSSYSL,FMYLHPRSSY,TTLFMYLHPR	CRC
OR5B12	c.865A>T	p.S289C	HFMGTDKMASVFYAIVIPMLNPLVY[p.S289C]CLRNKEVKSAFKKTVGKAKASIGFIF	MLNPLVYCL,LVYCLRNKEV,MLNPLVYCLR,CLRNKEVKSA	LUAD
OR5B17	c.488G>A	p.R163H	VCACLAIGCYVIGFLNASIQIGDTF[p.R163H]HLSFCMSNVIHHFFCDKPAVITLTCS	IQIGDTFHL,HLSFCMSNV,DTFHLSFCM,IGDTFHLSF,HLSFCMSNVI,DTFHLSFCMS,QIGDTFHLSF	CRC
OR5B17	c.798G>T	p.M266I	SHLIAIFLFYITVIIMYIRPSSSHS[p.M266I]IDTDKIASVFYTMIIPMLSPIVYTLR	SSHSIDTDK,SIDTDKIASV,YIRPSSSHSI,SSSHSIDTDK,RPSSSHSIDT,IDTDKIASVF	LUAD
OR5D13	c.706C>T	p.R236C	SSLIIILTSYMLIFTTIMKMRSASG[p.R236C]CQKTFSTCASHLTAITIFHGTILFLY	KMRSASGCQ,SASGCQKTF,CQKTFSTCA,KMRSASGCQK,RSASGCQKTF,CQKTFSTCAS	GBM
OR5D14	c.736C>A	p.H246N	VFIFVTVLKIRSVSGRHKAFSTWAS[p.H246N]NLTSITIFHGTILFLYCVPNSKNSRQ	TWASNLTSI,KAFSTWASN,ASNLTSITI,SNLTSITIF,STWASNLTSI,KAFSTWASNL,WASNLTSITI,ASNLTSITIF	LUAD
OR5D16	c.790C>A	p.P264T	VFSTCASHLTAITIFHGTILFLYCV[p.P264T]TNSKNSRHTVKVASVFYTVVIPLLNP	FLYCVTNSK,CVTNSKNSR,LFLYCVTNSK	LUAD
OR5D18	c.812C>A	p.T271K	LTAITIFHGTILFLYCVPNSKNSRH[p.T271K]KVKVASVFYTVVIPMLNPLIYSLRNK	KVKVASVFY,RHKVKVASV,HKVKVASVF,NSKNSRHKVK,KVKVASVFYT,RHKVKVASVF,HKVKVASVFY	LUSC
OR5F1	c.131G>T	p.G44V	DTLELQIILFLFFLVIYTLTVLGNL[p.G44V]VMILLIRIDSQLHTPMYFFLANLSFV	VLGNLVMIL,TLTVLGNLV,TVLGNLVMI,LTVLGNLVM,YTLTVLGNLV,VLGNLVMILL,NLVMILLIRI,TLTVLGNLVM	LUAD
OR5J2	c.106G>T	p.A36S	EFILLGLTDHAELKAVLFVVFLVIY[p.A36S]SITLLRNLGMILLIQITSKLHTPMYF	VVFLVIYSI,FLVIYSITL,LVIYSITLL,VIYSITLLR,YSITLLRNL,FVVFLVIYSI,FLVIYSITLL,LVIYSITLLR,VFLVIYSITL,IYSITLLRNL	LUAD
OR5L1	c.824C>A	p.T275N	VFHGTVLSIYCRPSSGNSGDADKVA[p.T275N]NVFYTVVIPMLNSVIYSLRNKDVKEA	KVANVFYTV,ANVFYTVVI,DADKVANVF,DADKVANVFY,KVANVFYTVV,NVFYTVVIPM,GDADKVANVF,VANVFYTVVI	LUAD
OR5M3	c.265delA	p.T89fs	LSFVDVWFSSNVTPKMLENLLSDKK[p.T89fs]QLLMLVV*	LSDKKQLLM,LLSDKKQLL,KKQLLMLVV,LSDKKQLLML,LLSDKKQLLM	STAD
OR5P2	c.299C>T	p.A100V	PNMLVNFLVERNTVSYLGCAIQLGS[p.A100V]VAFFATVECVLLAAMAYDRFVAICSP	QLGSVAFFA,GSVAFFATV,IQLGSVAFF,AIQLGSVAF,CAIQLGSVA,IQLGSVAFFA,VAFFATVECV,CAIQLGSVAF,AIQLGSVAFF	GBM
OR6C65	c.460_461insT	p.I154fs	TTIMSNKVCNWLVISSWLAGFLIIF[p.I154fs]SPRDYGPPTGFL*	DYGPPTGFL,GFLIIFSPR,LIIFSPRDY,SPRDYGPPT,RDYGPPTGF,WLAGFLIIFS,AGFLIIFSPR,FLIIFSPRDY,RDYGPPTGFL	LUAD
OR6C75	c.280G>T	p.G94W	ISFTSVCIPRFLVTVVTGNRTISYN[p.G94W]WCVAQLFFFIFLGVTEFYLLAAMSYD	RTISYNWCV,SYNWCVAQL,YNWCVAQLF,NWCVAQLFF,SYNWCVAQLF,YNWCVAQLFF,NWCVAQLFFF,RTISYNWCVA,ISYNWCVAQL	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR6K2	c.236C>A	p.P79Q	HLHTPMYTFISALSFLEIWYTTATI[p.P79Q]QKMLSSLLSERSISFNGCLLQMYFFH	TIQKMLSSL,IQKMLSSLL,YTTATIQKM,TTATIQKML,ATIQKMLSSL,TIQKMLSSLL,IWYTTATIQK,WYTTATIQKM,YTTATIQKML,IQKMLSSLLS	LUAD
OR6K6	c.931T>C	p.F311L	YLRFSATYSVFWDTAIAVTFVILAP[p.F311L]LFNPIIYSLKNKDMKEAIGRLFHYQK	VTFVILAPL,ILAPLFNPI,TFVILAPLF,APLFNPIIY,VILAPLFNPI,ILAPLFNPII,AVTFVILAPL,LFNPIIYSLK,VTFVILAPLF,LAPLFNPIIY	TGCT,THCA
OR6N2	c.877C>T	p.R293C	LTLDRTLAIVYSVLTPMVNPIIYSL[p.R293C]CNKEIIKAIKRTIFQKGDKASLAHL	SLCNKEIIK,PIIYSLCNK,IYSLCNKEI,YSLCNKEII,IIYSLCNKEI,YSLCNKEIIK,IYSLCNKEII,CNKEIIKAIK,MVNPIIYSLC	GBM
OR6V1	c.744delC	p.I248fs	VLRIPSASSCQKAFSTCGSHLTLVF[p.I248fs]MATVVPSFCMSGLAKLTLCKSGRSWPW*	LTLVFMATV,TLVFMATVV,FMATVVPSF,FCMSGLAKL,GLAKLTLCK,SFCMSGLAK,GSHLTLVFM,VPSFCMSGL,MSGLAKLTL,TLCKSGRSW,CKSGRSWPW,HLTLVFMATV,LTLVFMATVV,FMATVVPSFC,VVPSFCMSGL,CMSGLAKLTL,PSFCMSGLAK,SGLAKLTLCK,VFMATVVPSF,MATVVPSFCM,LTLCKSGRSW	HNSC
OR7C1	c.311delT	p.F104fs	PKMLLNILTQNKFITYAGCLSQIFF[p.F104fs]SLHLDAWTIYS*	CLSQIFFSL,SQIFFSLHL,SLHLDAWTI,FFSLHLDAW,LHLDAWTIY,FSLHLDAWTI,IFFSLHLDAW,SLHLDAWTIY,LSQIFFSLHL	KIRC
OR7C1	c.535delT	p.C179fs	MGSLLETLTVLRLSFCTEMEIPHFF[p.C179fs]VIYLKS*	MEIPHFFVI,EMEIPHFFV,IPHFFVIYL,MEIPHFFVIY,IPHFFVIYLK,TEMEIPHFFV,EMEIPHFFVI,EIPHFFVIYL	STAD
OR7E24	c.21_22insT	p.L7fs	MSYFPILFFFF[p.L7fs]PQKVSELHRATESHRCLRIPPPGTLRGSRTAAGPRWAVPVHVPGHGAGEPAHHPGCQL*	ILFFFFPQK,LFFFFPQKV,ATESHRCLR,GSRTAAGPR,RTAAGPRWA,TAAGPRWAV,TLRGSRTAA,RATESHRCL,LRIPPPGTL,FPQKVSELH,ILFFFFPQKV,RTAAGPRWAV,PILFFFFPQK,FFFPQKVSEL,RATESHRCLR,CLRIPPPGTL,GTLRGSRTAA,RGSRTAAGPR,ELHRATESHR,GPRWAVPVHV,EPAHHPGCQL,SELHRATESH,HRATESHRCL,GSRTAAGPRW,FPILFFFFPQ	PRAD
OR8D2	c.917G>T	p.R306M	IIPMLNPIIYSLRNKDVKNALKKMT[p.R306M]MGRQSS	ALKKMTMGR,KNALKKMTM,KKMTMGRQS,KMTMGRQSS,NALKKMTMGR,VKNALKKMTM,KKMTMGRQSS	LUAD
OR8H2	c.498G>T	p.L166F	CLALITGPYVIGFIDSFVNVVSMSR[p.L166F]FHFYDSNVIHHFFCDTSPIILALSCTD	VSMSRFHFY,VVSMSRFHF,MSRFHFYDS,RFHFYDSNV,VNVVSMSRF,FHFYDSNVI,VVSMSRFHFY,RFHFYDSNVI,MSRFHFYDSN,FVNVVSMSRF,NVVSMSRFHF,SRFHFYDSNV,FHFYDSNVIH	LUSC
OR8J3	c.479C>T	p.S160L	VVSRRLCLLLVSLTYLYGFSTAIVV[p.S160L]LPCIFSVSYCSSNIINHFYCDIAPLL	VVLPCIFSV,TAIVVLPCI,LPCIFSVSY,AIVVLPCIF,IVVLPCIFSV,VLPCIFSVSY,STAIVVLPCI,YGFSTAIVVL,TAIVVLPCIF	LUSC
OR8K3	c.705G>T	p.K235N	SLLIVLLSYLLILVAILRMNSAGRQ[p.K235N]NAFSTCGAHLTVVIVFYGTLLFMYVQ	NSAGRQNAF,NAFSTCGAH,RQNAFSTCG,RMNSAGRQNA,RQNAFSTCGA,MNSAGRQNAF,NAFSTCGAHL	LUSC
OR8S1	c.296C>T	p.A99V	SSVIVPKMLENLLSQRKTISVEGCL[p.A99V]VQVFFVFVTAGTEACLLSGMAYDRHA	LVQVFFVFV,TISVEGCLV,CLVQVFFVF,VEGCLVQVF,VQVFFVFVT,CLVQVFFVFV,VQVFFVFVTA,KTISVEGCLV,GCLVQVFFVF,EGCLVQVFFV,SVEGCLVQVF,VEGCLVQVFF	CRC
OR9A2	c.865C>T	p.R289W	VEYNKIVSLLVSVLTPFLNPFIFTL[p.R289W]WNDKVKEALRDGMKRCCQLLKD*	FIFTLWNDK,FTLWNDKVK,LNPFIFTLW,FIFTLWNDKV,TLWNDKVKEA,FLNPFIFTLW	LUAD
OR9G9	c.506G>T	p.R169L	VAVSYCGGFINSSIITKKTFSFNFC[p.R169L]LENIIDDFFCDLLPLVELACGEKGGY	KTFSFNFCL,SFNFCLENI,FNFCLENII,LENIIDDFF,FSFNFCLENI,SFNFCLENII,KTFSFNFCLE,KKTFSFNFCL	LUAD
OSBP	c.2163G>C	p.Q721H	FSELALTLNAWESGTAPTDSRLRPD[p.Q721H]HRLMENGRWDEANAEKQRLEEKQRLS	RLRPDHRLM,DSRLRPDHR,RLRPDHRLME,SRLRPDHRLM	CESC
OSBP2	c.1881_1882insC	p.H627fs	ETFELDRLDDMGLRSLCEQVSHHPP[p.H627fs]LSCALRVLQAWLEPLAGDHHLQQVPGKIHLHHAARCHPLRIPGQWESLRVEEEHLNCSQHHRGQALDRPVRGHRDCEP*	VLQAWLEPL,ALRVLQAWL,KIHLHHAAR,HAARCHPLR,AARCHPLRI,HLNCSQHHR,SQHHRGQAL,HHAARCHPL,EQVSHHPPL,CALRVLQAW,LQAWLEPLA,LQQVPGKIH,QQVPGKIHL,GKIHLHHAA,GQWESLRVE,EPLAGDHHL,HPLRIPGQW,RVLQAWLEPL,VLQAWLEPLA,KIHLHHAARC,HHAARCHPLR,CEQVSHHPPL,SHHPPLSCAL,LQAWLEPLAG,LQQVPGKIHL,QQVPGKIHLH,LHHAARCHPL,LRIPGQWESL,WESLRVEEEH,LEPLAGDHHL,HPPLSCALRV,IPGQWESLRV	STAD
OSBPL6	c.1730G>A	p.R577Q	SEDNTSVADNISRQILNGELTGGAF[p.R577Q]QNGRRACLPAPCPDTSNINLWNILRN	FQNGRRACL,LTGGAFQNGR	UCEC
OSTN	c.344G>A	p.R115Q	PLDRLSAGSVDHKGKQRKVVDHPKR[p.R115Q]QFGIPMDRIGRNRLSNSRG	RQFGIPMDR,PKRQFGIPM,RQFGIPMDRI,HPKRQFGIPM,KVVDHPKRQF	CRC

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OTOF	c.1163C>T	p.T388M	DDISSGLKGYVKCDVAVVGKGDNIK[p.T388M]MPHKANETDEDDIEGNLLLPEGVPPE	KGDNIKMPHK	BRCA
OTOF	c.3910G>A	p.E1304K	KLETMVKLDATSEAVVKVDVAEEEK[p.E1304K]KKKKKKKGTAEEPEEEEPDESMLDWW	KVDVAEEEKK	STAD
OTOL1	c.1291G>A	p.V431I	VAQNKKQFKSRETLYGQEIDQASLL[p.V431I]IILKLSAGDQVWLEVSKDWNGVYVSA	QASLLIILK,IDQASLLII,DQASLLIIL,QEIDQASLLI,IDQASLLIIL	CRC
OTOP1	c.310_318delCTGCTGTGG	p.LLW104del	AWAVHAAGVSKSDLLCFLTALMLLQ[p.LLW104del]MLWYVGRSSAHRRLFRLKDTHAGAGWLRGSITLF	MLLQMLWYV,LQMLWYVGR,LMLLQMLWY,LTALMLLQM,ALMLLQMLW,FLTALMLLQM,LMLLQMLWYV,ALMLLQMLWY,LLQMLWYVGR,TALMLLQMLW	ACC
OTUD3	c.830G>T	p.R277I	VQNLEAENYNIESAIIAVLRMNQGK[p.R277I]INNAEENLEPSGRVLKQCGPLWEEGG	RMNQGKINNA,GKINNAEENL	CRC
OTUD4	c.2726C>T	p.T909I	ALASIPPVAEGKAHPPTQILNRERE[p.T909I]IVPVELEPKRTIQSLKEKTEKVKDPK	ILNREREIV,REREIVPVE,LNREREIVPV,TQILNREREI,REREIVPVEL,REIVPVELEP	BLCA,PRAD,THCA
OTUD4	c.458_460delCTG	p.A153del	VADEDNSEISDSEDDSCKSKTAAAA[p.A153del]DVNGFKPLSGNEQLKNNGNSTSLPLSRK	KSKTAAAAD,KSKTAAAADV,TAAAADVNGF	PRAD
OTX2	c.130delC	p.R44fs	TSGMDLLHPSVGYPGPWASCPAATP[p.R44fs]GNSAGRGRRSLGRS*	RGRRSLGRS,SAGRGRRSL,AGRGRRSLGR,CPAATPGNSA,NSAGRGRRSL	STAD
OXR1	c.364G>A	p.E122K	GTIEYTVESRDSLNSIALKFDTTPN[p.E122K]KLVQLNKLFSRAVVTGQVLYVPDPEY	KLVQLNKLF,ALKFDTTPNK,DTTPNKLVQL,LKFDTTPNKL,NKLVQLNKLF	UCEC
P2RX1	c.58delC	p.R20fs	MARRFQEELAAFLFEYDTP[p.R20fs]AWCWCVIRRWALSSD*	FLFEYDTPA,DTPAWCWCV,TPAWCWCVI,WCVIRRWAL,FLFEYDTPAW,AWCWCVIRRW,CWCVIRRWAL,TPAWCWCVIR,DTPAWCWCVI,FEYDTPAWCW	STAD
P2RX7	c.425C>A	p.P142Q	RLCPEYPTRRTLCSSDRGCKKGWMD[p.P142Q]QQSKGIQTGRCVVYEGNQKTCEVSAW	WMDQQSKGI,KGWMDQQSK	LUAD
PABPC1	c.1223A>T	p.Y408F	MQRMASVRAVPNPVINPYQPAPPSG[p.Y408F]FFMAAIPQTQNRAAYYPPSQIAQLRP	YQPAPPSGF,QPAPPSGFF,PYQPAPPSGF,YQPAPPSGFF,QPAPPSGFFM,APPSGFFMAA,PPSGFFMAAI	KIRC
PABPC1	c.280C>T	p.R94C	LDTMNFDVIKGKPVRIMWSQRDPSL[p.R94C]CKSGVGNIFIKNLDKSIDNKALYDTF	SQRDPSLCK,CKSGVGNIF,SLCKSGVGNI,WSQRDPSLCK,LCKSGVGNIF	DLBCL
PABPC1	c.467_468insG	p.E156fs	DENGSKGYGFVHFETQEAAERAIEK[p.E156fs]NEWNAPK*	AERAIEKNEW	KIRC
PABPC1	c.541G>A	p.A181T	EKMNGMLLNDRKVFVGRFKSRKERE[p.A181T]TELGARAKEFTNVYIKNFGEDMDDER	SRKERETEL,KERETELGA,RETELGARA,KSRKERETEL,TELGARAKEF	KIRC
PABPC1	c.761_762insT	p.K254fs	KSKGFGFVSFERHEDAQKAVDEMNG[p.K254fs]NGAQWKTNLCWSSSEKGGTADGT*	NLCWSSSEK,KTNLCWSSS,AQWKTNLCW,DEMNGNGAQ,TNLCWSSSEK,AQWKTNLCWS,DEMNGNGAQW	CLL
PABPC1	c.999delA	p.K333fs	LRKEFSPFGTITSAKVMMEGGRSKG[p.K333fs]LVLYVSPPQKKPLKQLQK*	VLYVSPPQK,RSKGLVLYV,GRSKGLVLY,MMEGGRSKGL,LVLYVSPPQK,VLYVSPPQKK,RSKGLVLYVS,VSPPQKKPLK,GGRSKGLVLY	KIRC
PABPC3	c.975_979delTATGA	p.V325fs	LDDGIDDERLRKAFSPFGTITSAKV[p.V325fs]GRWSQQRVWFCMFLLPRRSH*	RVWFCMFLL,KVGRWSQQR,RWSQQRVWF,QQRVWFCMF,TITSAKVGR,WFCMFLLPR,GRWSQQRVW,SQQRVWFCM,GTITSAKVGR,VWFCMFLLPR,SQQRVWFCMF,KVGRWSQQRV,QQRVWFCMFL,WFCMFLLPRR,VGRWSQQRVW,GRWSQQRVWF,WSQQRVWFCM,CMFLLPRRSH	TGCT
PABPC3	c.997delA	p.K333fs	LRKAFSPFGTITSAKVMMEGGRSKG[p.K333fs]LVLYVSPPQKKPLKQLQK*	VLYVSPPQK,RSKGLVLYV,GRSKGLVLY,MMEGGRSKGL,LVLYVSPPQK,VLYVSPPQKK,RSKGLVLYVS,VSPPQKKPLK,GGRSKGLVLY	BLCA
PACSIN1	c.1075G>A	p.E359K	AVESTSQAGDRGSVSSYDRGQPYAT[p.E359K]KWSDDESGNPFGGSETNGGANPFEDD	RGQPYATKW	HNSC

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PACSIN2	c.993G>C	p.Q331H	ADLNRTLSRREKKKATDGVTLTGIN[p.Q331H]HTGDQSLPSKPSSTLNVPSNPAQSAQ	INHTGDQSL,HTGDQSLPSK	BRCA
PADI2	c.340A>C	p.T114P	SSDKVTVNYYDEEGSIPIDQAGLFL[p.T114P]PAIEISLDVDADRDGVVEKNNPKKAS	GLFLPAIEI,FLPAIEISL,DQAGLFLPA,LFLPAIEISL,DQAGLFLPAI,LPAIEISLDV,IDQAGLFLPA	MM
PAFAH1B1	c.904delA	p.K302fs	VECISWAPESSYSSISEATGSETKK[p.K302fs]VVNLGHSCCLDPETRLLRCGMSVLACAL*	RLLRCGMSV,GMSVLACAL,LLRCGMSVL,SETKKVVNL,RLLRCGMSVL,LLRCGMSVLA,CGMSVLACAL	STAD
PALB2	c.839delA	p.N280fs	DSGSSQHLEHIPPKGSSELTTHDLK[p.N280fs]TLDLLHL*	LKTLDLLHL,SELTTHDLKT	STAD
PALLD	c.2986G>A	p.A996T	DSAHKMLVRENGVHSLIIEPVTSRD[p.A996T]TGIYTCIATNRAGQNSFSLELVVAAK	VTSRDTGIY,RDTGIYTCI,PVTSRDTGIY	KIRC
PALM2-AKAP2	c.3213_3214insGAAGCT	p.1075_1076insEA	KAVSKTSRDGAEQQGPEATVEEAEA[p.1075_1076insEA]EAAAFGSEKPQSMFEPPQVSSPVQEKRDVLP	EAEAEAAAF,VEEAEAEAA,AEAEAAAFG,EEAEAEAAAF,AEAEAAAFGS,VEEAEAEAAA	KIRC
PALM2-AKAP2	c.3354_3355insC	p.G1118fs	VQEKRDVLPKILPAEDRALRERGPP[p.G1118fs]PATASCAAQWPD*	RERGPPPAT,ALRERGPPPA,RERGPPPATA	KIRC
PALM2-AKAP2	c.895G>A	p.A299T	KLEMVHKSRKDHSSGNPGQQAQAPS[p.A299T]TAGPEANLDQPVTMIFMGYQNIEDEE	STAGPEANL,APSTAGPEA,GQQAQAPST,QQAQAPSTA,GQQAQAPSTA,QQAQAPSTAG	BRCA
PAMR1	c.302delG	p.G101fs	CDSCLIHPGCTIFENCKSCRNGSWG[p.G101fs]VPWMTSM*	WGVPWMTSM,RNGSWGVPW,KSCRNGSWGV,CRNGSWGVPW,RNGSWGVPWM,SWGVPWMTSM	STAD
PANK1	c.1199delA	p.K400fs	DSVGFNGKPECYYFENPTNPELCQK[p.K400fs]SRTALITHTLCCWLTWAQVSAF*	TLCCWLTWA,WLTWAQVSA,RTALITHTL,HTLCCWLTW,CQKSRTALI,KSRTALITH,LTWAQVSAF,LCQKSRTAL,LITHTLCCWL,KSRTALITHT,HTLCCWLTWA,ELCQKSRTAL,WLTWAQVSAF,SRTALITHTL,ALITHTLCCW	STAD
PANK2	c.1251delT	p.T417fs	VSILAVYSKDNYKRVTGTSLGGGTF[p.T417fs]LVSAVFLLAVPLLKKLLKWHLVEIAPKWIN*	SLGGGTFLV,FLVSAVFLL,AVFLLAVPL,LLKWHLVEI,LVSAVFLLA,FLLAVPLLK,LLAVPLLKK,TFLVSAVFL,VFLLAVPLL,GTFLVSAVF,VSAVFLLAV,LKWHLVEIA,HLVEIAPKW,FLVSAVFLLA,LVSAVFLLAV,AVFLLAVPLL,LLAVPLLKKL,KLLKWHLVEI,LLKKLLKWHL,LLKWHLVEIA,HLVEIAPKWI,FLLAVPLLKK,VFLLAVPLLK,AVPLLKKLLK,TFLVSAVFLL,GTFLVSAVFL,KWHLVEIAPK,TSLGGGTFLV,SAVFLLAVPL,GGTFLVSAVF,VPLLKKLLKW	PRAD
PANK2	c.377G>C	p.G126A	AAEEARRNPTLGGLLGRQRLLLRMG[p.G126A]AGRLGAPMERHGRASATSVSSAGEQA	LLRMGAGRL,RMGAGRLGA,LLLRMGAGR,GAGRLGAPM,RQRLLLRMGA,RLLLRMGAGR,AGRLGAPMER,MGAGRLGAPM,LRMGAGRLGA	ACC
PANK3	c.779G>T	p.R260I	LEMASKGDSTQADKLVRDIYGGDYE[p.R260I]IFGLPGWAVASSFGNMIYKEKRESVS	IYGGDYEIF,IFGLPGWAV,DIYGGDYEI,EIFGLPGWA,YEIFGLPGW,EIFGLPGWAV,DIYGGDYEIF,RDIYGGDYEI,YEIFGLPGWA	CRC
PAOX	c.319C>T	p.H107Y	QLAAEYGLLGEKELSQENQLVETGG[p.H107Y]YVGLPSVSYASSGASVSLQLVAEMAT	QLVETGGYV,NQLVETGGY,YVGLPSVSY,VETGGYVGL,YVGLPSVSYA,GYVGLPSVSY	CESC
PAPD4	c.675_676insT	p.C225fs	SLNGFGTRSSDGDLCLVVKEEPCFF[p.C225fs]SGKSED*	KEEPCFFSG	STAD
PAPPA2	c.2749C>A	p.P917T	QYVHTASSRRVCDSSGYWTPEEAVG[p.P917T]TPDVDQPCEPSLQAWSPEVHLYHMNM	EEAVGTPDV	LUAD
PAPPA2	c.5049delC	p.I1683fs	NSVEYKCEQGYGIGAVCSPLCVIPP[p.I1683fs]VTP*	SPLCVIPPV,CSPLCVIPPV	STAD
PAPPA2	c.5117C>A	p.P1706H	CVIPPSDPVMLPENITADTLEHWME[p.P1706H]HVKVQSIVCTGRRQWHPDPVLVHCIQ	TLEHWMEHV,MEHVKVQSI,WMEHVKVQSI,TLEHWMEHVK,DTLEHWMEHV,MEHVKVQSIV,LEHWMEHVKV	LUAD
PARD6A	c.252_253insC	p.G84fs	TDAHGDLLPLTNDDSLHRALASGPP[p.G84fs]ATAPTGAEAGRS*	ALASGPPAT,RALASGPPA,ALASGPPATA,RALASGPPAT,HRALASGPPA	KIRC

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PARG	c.1750G>A	p.A584T	KYNVAYSKKWDFTALIDFWDKVLEE[p.A584T]TEAQHLYQSILPDMVKIALCLPNICT	EETEAQHLY,LEETEAQHL,TEAQHLYQS,LEETEAQHLY,TEAQHLYQSI	KIRP,PRAD
PARP15	c.1381delA	p.K461fs	PSLKTVKVVIFQPELLNIFYDSMKK[p.K461fs]ETSLHH*	SMKKETSLH,DSMKKETSL,MKKETSLHH,SMKKETSLHH	STAD
PARP4	c.2541delA	p.K847fs	SSLDSSGFSLHIGLSAAYLPRMWVE[p.K847fs]NIQKKKARLACLSFNPISMSTSLT*	RMWVENIQK,IQKKKARLA,KARLACLSF,LPRMWVENI,NPISMSTSL,NIQKKKARL,KKKARLACL,LACLSFNPI,CLSFNPISM,YLPRMWVENI,RLACLSFNPI,RMWVENIQKK,KARLACLSFN,KKARLACLSF,ACLSFNPISM	STAD
PASD1	c.685_687delGCT	p.A236del	SSQGQRGHTSMKAVYVEPAAAAAAA[p.A236del]ISDDQIDIAEVEQYGPQENVHMFVDSDS	EPAAAAAAAI	GBM
PASK	c.185C>T	p.T62I	PSRSFSSAHRHLSRRNGLSRLCQSR[p.T62I]IALSEDRWSSYCLSSLAAQNICTSKL	RLCQSRIAL,LSRLCQSRI,GLSRLCQSRI,LSRLCQSRIA,SRLCQSRIAL	KIRC
PAX2	c.1183delC	p.P395fs	YSHPQYTAYNEAWRFSNPALLMPPP[p.P395fs]VRPCRCCRCL*	PVRPCRCCR,MPPPVRPCR,RPCRCCRCL,LLMPPPVRPC,LMPPPVRPCR,NPALLMPPPV	STAD
PAX3	c.1271C>T	p.T424M	HGGVPHQPQTDYALSPLTGGLEPTT[p.T424M]MVSASCSQRLDHMKSLDSLPTSQSYC	MVSASCSQR,LEPTTMVSA,MVSASCSQRL,TMVSASCSQR	CRC
PAX3	c.590C>T	p.S197L	LERKEAEESEKKAKHSIDGILSERA[p.S197L]LAPQSDEGSDIDSEPDLPLKRKQRRS	SERALAPQS	BLCA
PAX6	c.1124delC	p.P375fs	QTSSYSYCMLPTSPSVNGRSYDTYTP[p.P375fs]HICRHT*	RSYDTYTPH,SYDTYTPHI,DTYTPHICR,RSYDTYTPHI	STAD
PBLD	c.164C>A	p.P55Q	LDEDMHQKIAREMNLSETAFIRKLH[p.P55Q]QTDNFAQSSCFGLRWFTPA5EVPLCG	KLHQTDNFA,RKLHQTDNF,IRKLHQTDNF,HQTDNFAQSS	LUAD
PBX2	c.208G>A	p.E70K	PGGRGKQDIGDILQQIMTITDQSLD[p.E70K]KAQAKKHALNCHRMKPALFSVLCEIK	TITDQSLDK,QSLDKAQAK,SLDKAQAKK,KAQAKKHAL,MTITDQSLDK,QSLDKAQAKK	BLCA
PBX2	c.785A>T	p.Y262F	LRSRFLDARRKRRNFSKQATEVLNE[p.Y262F]FFYSHLSNPYPSEEAKEELAKKCGIT	QATEVLNEF,TEVLNEFFY,NEFFYSHLS,ATEVLNEFFY,VLNEFFYSHL,KQATEVLNEF,FFYSHLSNPY,NEFFYSHLSN	KIRP,LUSC,TGCT
PBXIP1	c.2186_2188delACC	p.H729del	KKDKHSQSPRAAGPREGHSHSHHHH[p.H729del]RG*	HSHSHHHHR	BLCA
PCBP1	c.305T>A	p.L102Q	DKLEEDINSSMTNSTAASRPPVTLR[p.L102Q]QVVPATQCGSLIGKGGCKIKEIRIST	RPPVTLRQV,RQVVPATQC,RPPVTLRQVV,RQVVPATQCG	CRC
PCCA	c.689G>A	p.R230H	AVRIAREIGYPVMIKASAGGGGKGM[p.R230H]HIAWDDEETRDGFRLSSQEAASSFGD	HIAWDDEETR	STAD
PCDH10	c.1429G>A	p.V477M	QVSDVNDNAPRFSQPVYDVYVTENN[p.V477M]MPGAYIYAVSATDRDEGANAQLAYSI	NMPGAYIYA,TENNMPGAY,NNMPGAYIY,MPGAYIYAV,VTENNMPGAY,YVTENNMPGA,NMPGAYIYAV,YDVYVTENNM,MPGAYIYAVS,TENNMPGAYI	CRC
PCDH10	c.1759C>A	p.R587S	ILIVDQNDNAPAIVAPLPGRNGTPA[p.R587S]SEVLPRSAEPGYLLTRVAAVDADDGE	GTPASEVLPR,RNGTPASEVL	LUAD
PCDH10	c.2956G>T	p.V986L	SDGRQAADYRSNLHVPGMDSVPDTE[p.V986L]LFETPEAQPGAERSFSTFGKEKALHS	TELFETPEA,GMDSVPDTEL,MDSVPDTELF	LUAD
PCDH10	c.354_355insC	p.N118fs	EVFLENPLELFQVEIEVLDINDNPP[p.N118fs]LFPGARPDGGNL*	VLDINDNPPL,LDINDNPPLF	STAD
PCDH10	c.673_674insC	p.P225fs	TAVDGGGGGGVGEGGGGGGGAGLPP[p.P225fs]PAAAHRHGPTHHPSAGLQ*	AAHRHGPTH,GPTHHPSAGL,RHGPTHHPSA	STAD
PCDH11X	c.1457C>T	p.T486M	DNAPVFTQSFVTVSIPENNSPGIQL[p.T486M]MKVSAMDADSGPNAKINYLLGPDAPP	IQLMKVSAM,QLMKVSAMDA	GBM
PCDH11X	c.3029G>T	p.R1010I	SSDPYSVSDCGYPVTTFEVPVSVHT[p.R1010I]IPPMKEVVRSCTPMKESTTMEIWIHP	SVHTIPPMK,EVPVSVHTI,HTIPPMKEV,VSVHTIPPM,VSVHTIPPMK,TIPPMKEVVR,HTIPPMKEVV,FEVPVSVHTI	LUAD

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PCDH15	c.4655G>T	p.R1552I	DDLSAHNPLYKENISQVSTNSDISQ[p.R1552I]ITDFVDPFSPKIQAKSKSLRGPREKI	DISQITDFV,QITDFVDPF,SDISQITDF,SQITDFVDPF	CRC
PCDH15	c.5138G>T	p.C1713F	VELKSEPNVISSPAECSLELSPSRP[p.C1713F]FVLHSSLSRRETPICMLPIETERNIF	ELSPSRPFV,FVLHSSLSR,RPFVLHSSL,LELSPSRPF,FVLHSSLSRR,SLELSPSRPF,LELSPSRPFV	KIRC
PCDH19	c.1588G>A	p.E530K	YVSINPNSGDIYALRSFNHEQTKAF[p.E530K]KFKVLAKDGGLPSLQSNATVRVIILD	QTKAFKFKV,KAFKFKVLA,AFKFKVLAK,TKAFKFKVL,HEQTKAFKF,KAFKFKVLAK,QTKAFKFKVL	UCEC
PCDH19	c.856C>T	p.R286C	NASDPDEGTNGQVVYSFYGYVNDRT[p.R286C]CELFQIDPHSGLVTVTGALDYEEGHV	YVNDRTCEL,YVNDRTCELF	BRCA
PCDHAC2	c.1555G>A	p.A519T	LVERRVGERALSNYVSVHAESGKVY[p.A519T]TLQPLDHEELELLQFQVSARDAGVPP	AESGKVYTL,GKVYTLQPL,TLQPLDHEEL,KVYTLQPLDH,SGKVYTLQPL,HAESGKVYTL	CRC
PCDHAC2	c.2207C>T	p.A736V	ALSTVSFIFLLTIIILSIIKCYRYT[p.A736V]VYGTACCGGFCGVRERSPAELYKQAN	IIKCYRYTV,YTVYGTACC,IKCYRYTVY,YRYTVYGTA,SIIKCYRYTV,VYGTACCGGF,IIKCYRYTVY,CYRYTVYGTA,YRYTVYGTAC	CRC
PCDHAC2	c.2225C>T	p.A742V	TALRCSAAPTEGACGPVKPTLVCSS[p.A742V]VVGSWSYSQQRRQRVCSGEGLPKADL	SSVVGSWSY,KPTLVCSSV,CSSVVGSWSY,KPTLVCSSVV,LVCSSVVGSW	LUAD
PCDHAC2	c.414G>T	p.K138N	PLQVFHVDVEVKDINDNPPVFPATQ[p.K138N]NNLFIAESRPLDSRFPLEGASDADIG	VFPATQNNL,NNLFIAESR,FPATQNNLF,VFPATQNNLF,FPATQNNLFI	UCEC
PCDHAC2	c.467C>T	p.A156V	RFSRQEQRLFILESRMPDSRFPLEG[p.A156V]VSDLDIGANAQLRYRLNPNEYFDLDV	DSRFPLEGV,FPLEGVSDL	CRC
PCDHAC2	c.568G>A	p.E190K	NALLSYKLSSSEFFFLDIQANDELS[p.E190K]KSLSLVLGKSLDREETAEVNLLLVAT	ELSKSLSLV,KSLSLVLGK,LSKSLSLVL,DELSKSLSL,DELSKSLSLV	CRC
PCDHAC2	c.796G>A	p.A266T	AFERTIYKVRLLENAPNGTLVVTVN[p.A266T]TTDLDEGVNKDIAYSFNTDMSADILS	NTTDLDEGV,TTDLDEGVNK	CRC
PCDHAC2	c.811G>A	p.E271K	SYKVVLSENVQNDTRVIQLNASDPD[p.E271K]KGLNGEISYGIKMILPVSEKCMFSIN	QLNASDPDK,KGLNGEISY	CRC
PCDHB1	c.1704C>G	p.N568K	SSQVTVRVVVLDDNDNRPMILYPLQ[p.N568K]KGTLPCNDLVPRSAEAGYLVTKVVAV	ILYPLQKGT,PMILYPLQK,ILYPLQKGTL,RPMILYPLQK,YPLQKGTLPC	LUSC
PCDHB12	c.865C>T	p.R289C	VSAWDLDSGTNSELSYTFSHASEDI[p.R289C]CKTFEINQKSGDITLTAPLDFEAIES	ASEDICKTF,FSHASEDICK,HASEDICKTF,SEDICKTFEI	UCEC
PCDHB13	c.662C>T	p.P221L	VLDKALDREEEAELRLTLTALDGGS[p.P221L]LPRSGTAQVYIEVLDVNDNAPEFEQP	LPRSGTAQV,SLPRSGTAQV,TALDGGSLPR,LPRSGTAQVY	GBM
PCDHB4	c.763_764CC>TT	p.P255F	LIMDINDNAPEFVHTPYGVQVLENS[p.P255F]FLDSPIVRVLARDIDAGNFGSVSYGLF	FLDSPIVRV,SFLDSPIVR,NSFLDSPIV,GVQVLENSF,VQVLENSFL,FLDSPIVRVL,NSFLDSPIVR,YGVQVLENSF,LENSFLDSPI	TGCT
PCDHB5	c.151G>T	p.D51Y	AGSEAVRYSIPEETESGYSVANLAK[p.D51Y]YLGLGVGELATRGARMHYKGNKELLQ	YSVANLAKY,YLGLGVGEL,AKYLGLGVG,NLAKYLGLGV,YLGLGVGELA,KYLGLGVGEL,GYSVANLAKY,YSVANLAKYL	CRC
PCDHB5	c.1945C>T	p.P649S	RTARLLSERDAAKHRLVVLVKDNGE[p.P649S]SPRSATATLHVLLVDGFSQPYLPLPE	SPRSATATL,GESPRSATA,LVKDNGESPR,ESPRSATATL,GESPRSATAT	LUAD
PCDHB8	c.703G>A	p.D235N	RLTLTALDGGSPPRSGTAQVYIEVV[p.D235N]NVNDNAPEFEQPFYRVQISEDSPISF	QVYIEVVNV,EVVNVNDNA,NVNDNAPEF,AQVYIEVVNV,VNVNDNAPEF,IEVVNVNDNA	CRC
PCDHGC5	c.1796G>T	p.G599V	GVELAPRSAERGYLVTKVVAVDRDS[p.G599V]VQNAWLSYRLLKASEPGLFSVGLHTG	SVQNAWLSY,VQNAWLSYR,VVAVDRDSV,VQNAWLSYRL,SVQNAWLSYR,DSVQNAWLSY,VDRDSVQNAW	KIRC
PCDHGC5	c.1984G>A	p.V662M	ALKQSLVVAVQDHGQPPLSATVTLT[p.V662M]MAVADSIPEVLADLGSLEPSDGPYNY	LSATVTLTM,ATVTLTMAV,LTMAVADSI,TVTLTMAVA,MAVADSIPEV,TLTMAVADSI,SATVTLTMAV,PLSATVTLTM	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PCDHGC5	c.1990G>A	p.D664N	RLLVAVRDGGQPPLSATATLHLVFA[p.D664N]NSLQEVLPDITDRPDPSDLQAELQFY	VFANSLQEV,LHLVFANSL,FANSLQEVL,LVFANSLQEV,TLHLVFANSL,VFANSLQEVL	BRCA
PCDHGC5	c.2051C>A	p.P684H	TVTVAVADRIPDILADLGSIKTPID[p.P684H]HEDLDLTLYLVVAVAAVSCVFLAFVI	HEDLDLTLY,IDHEDLDLTL,TPIDHEDLDL,HEDLDLTLYL	LUAD
PCDHGC5	c.208G>A	p.A70T	SVVGNLAKDLGLSVLDVSARKLRVS[p.A70T]TEKLHFSVDAESGDLLVKNRIDREQI	SARKLRVST,RKLRVSTEK,KLRVSTEKL,STEKLHFSV,RVSTEKLHF,KLRVSTEKLH,VSTEKLHFSV,RKLRVSTEKL,LRVSTEKLHF,TEKLHFSVDA	UCEC
PCDHGC5	c.36G>T	p.K12N	MAALQKLPHCR[p.K12N]NLVLLCFLLATLWEARAGQIRYSVRE	KLPHCRNLV,NLVLLCFLL,LPHCRNLVL,QKLPHCRNL,KLPHCRNLVL,LPHCRNLVLL,LQKLPHCRNL,HCRNLVLLCF	LUAD
PCDHGC5	c.866C>T	p.S289L	LTATDPDEGINGKLTYSFRNEEEKI[p.S289L]LETFQLDSNLGEISTLQSLDYEESRF	EEEKILETF,NEEEKILETF,LETFQLDSNL	CRC
PCDHGC5	c.877C>T	p.R293C	DPDEGANGEVTYSFHNVDHRVAQIF[p.R293C]CLDSYTGEISNKEPLDFEEYKMYSME	CLDSYTGEI,AQIFCLDSY,HRVAQIFCL,VAQIFCLDSY,AQIFCLDSYT	SKCM
PCGF3	c.189delC	p.H63fs	SCLVKYLEENNTCPTCRIVIHQSHP[p.H63fs]CSTSVMTEPCKILFTNWYQASKKRK*	ILFTNWYQA,FTNWYQASK,TSVMTEPCK,HQSHPCSTS,QSHPCSTSV,SHPCSTSVM,VMTEPCKIL,MTEPCKILF,CKILFTNWY,KILFTNWYQA,HQSHPCSTSV,ILFTNWYQAS,FTNWYQASKK,STSVMTEPCK,VMTEPCKILF,LFTNWYQASK,QSHPCSTSVM,EPCKILFTNW	STAD
PCLO	c.11836C>A	p.P3946T	PYQTQPTFQAVATMSFTPQVQPTPT[p.P3946T]TQPSYQLPSQMMVIQQKPRQTTLYLE	PTPTTQPSY,TPTTQPSYQL,QPTPTTQPSY	LUAD
PCLO	c.12397C>T	p.R4133C	VKAEEDPMEDPYELKLLKHQIKQEF[p.R4133C]CRGTESLDHLAGLSHYYHADTSYRHF	HQIKQEFCR,QEFCRGTES,QEFCRGTESL	SKCM
PCMTD1	c.812G>T	p.R271M	LARIYIRRTLRNFINDEMQAKGIPQ[p.R271M]MAPPKRKRKRVKQRINTYVFVGNQLI	MQAKGIPQM,GIPQMAPPK,MAPPKRKRK,QMAPPKRKR,MQAKGIPQMA,KGIPQMAPPK,QMAPPKRKRK,MAPPKRKRK,EMQAKGIPQM	LUAD
PCMTD1	c.842T>C	p.V281A	RNFINDEMQAKGIPQRAPPKRKRKR[p.V281A]AKQRINTYVFVGNQLIPQPLDSEEDE	RAKQRINTY,RAKQRINTYV,KRAKQRINTY,AKQRINTYVF	TGCT
PCNXL2	c.404G>A	p.R135Q	GEHITNHRNPSNNRQIHNGKKEEAS[p.R135Q]QNLSTPPLRCSSRGQSITSHHSSGPL	SQNLSTPPL,KKEEASQNL,SQNLSTPPLR,GKKEEASQNL,ASQNLSTPPL,KEEASQNLST	CRC
PCOLCE2	c.1043C>T	p.A348V	ITTITRDGSLHATVSIINIYKEGNL[p.A348V]VIQQAGKNMSARLTVVCKQCPLLRRG	NIYKEGNLV,IYKEGNLVI,LVIQQAGKNM,KEGNLVIQQA	CRC
PCOLCE2	c.260G>A	p.R87H	KITVPEGKVVVLNFRFIDLESDNLC[p.R87H]HYDFVDVYNGHANGQRIGRFCGTFRP	LESDNLCHY,CHYDFVDVY,SDNLCHYDF,ESDNLCHYDF,NLCHYDFVDV,LCHYDFVDVY	CRC
PCP4L1	c.191A>G	p.K64R	DLTAPETEKAALAIQGKFRRFQKRK[p.K64R]RDPSS*	KFRRFQKRKR	TGCT
PDE4B	c.1250C>T	p.S417L	MMTLEDHYHSDVAYHNSLHAADVAQ[p.S417L]LTHVLLSTPALDAVFTDLEILAAIFA	HAADVAQLT,DVAQLTHVL,LHAADVAQL,AQLTHVLLS,SLHAADVAQL,DVAQLTHVLL,LTHVLLSTPA,HAADVAQLTH,ADVAQLTHVL,AQLTHVLLST	CRC
PDGFRA	c.685G>A	p.E229K	NVYALKATSELDLEMEALKTVYKSG[p.E229K]KTIVVTCAVFNNEVVDLQWTYPGEVK	KTIVVTCAV,TVYKSGKTI,YKSGKTIVV,ALKTVYKSGK,KTIVVTCAVF,KTVYKSGKTI,TVYKSGKTIV,YKSGKTIVVT	GBM
PDGFRB	c.1949C>T	p.S650L	SQATMKVAVKMLKSTARSSEKQALM[p.S650L]LELKIMSHLGPHLNVVNLLGACTKGG	KQALMLELK,EKQALMLEL,ALMLELKIM,LELKIMSHL,MLELKIMSHL,RSSEKQALML,SEKQALMLEL,KQALMLELKI,LMLELKIMSH	GBM
PDIA6	c.168T>G	p.N56K	PCSPTSPAHSLSRKSPIMYPSTTMA[p.N56K]KAPGLVSCTFFLAVNGLYSSSDDVIE	TMAKAPGLV,MYPSTTMAK,TTMAKAPGL,YPSTTMAKA,TTMAKAPGLV,IMYPSTTMAK,MYPSTTMAKA,KAPGLVSCTF	TGCT
PDILT	c.1498G>A	p.E500K	LYKGEHTLKGFSDFLESHIKTKIED[p.E500K]KDELLSVEQNEVIEEEVLAEEKEVPM	HIKTKIEDK,IEDKDELLSV	CESC
PDPR	c.2377G>T	p.G793W	TMFILDDHDSDLDLWPWWGEPIYRN[p.G793W]WQYVGKTTSSAYSYSLERHVCLGFVH	EPIYRNWQY,WQYVGKTTS,WWGEPIYRNW,IYRNWQYVGK,EPIYRNWQYV,WQYVGKTTSS	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PDS5A	c.3927G>C	p.L1309F	KNDDLNKPINKGRKRAAVGQESPGG[p.L1309F]FEAGNAKAPKLQDLAKKAAPAERQID	QESPGGFEA,GQESPGGFEA	TGCT
PDYN	c.571G>T	p.G191W	EDPKEQVKRYGGFLRKYPKRSSEVA[p.G191W]WEGDGDSMGHEDLYKRYGGFLRRIRP	YPKRSSEVAW,VAWEGDGDSM	LUAD
PDZD2	c.1693C>A	p.R565S	RKHSLPQLLDSSSASQEYHIVKKST[p.R565S]SSLSTTQVESPWRLIRPSVISIIGLY	IVKKSTSSL,TSSLSTTQV,KKSTSSLST,HIVKKSTSSL,STSSLSTTQV,IVKKSTSSLS,KKSTSSLSTT	LUAD
PDZD2	c.302_303insG	p.R101fs	DTETVGLSFGNIPVFGDYGEKRRGG[p.R101fs]QEEENPPGSCAGCGLHLGDRAEEEQPSREEWEGPTAG*	REEWEGPTA,EEQPSREEW,EEWEGPTAG,EENPPGSCA	STAD
PELI2	c.589delG	p.G197fs	AKWKNPDGHMDGLTTNGVLVMHPRG[p.G197fs]ASPRSPSPGSGARSLSVEMCTPCEKPGRPSNEESWWKVRPTSCRTAPSLTCVGPLSSGEQQMGFFILQLRST*	RTAPSLTCV,QMGFFILQL,VLVMHPRGA,MGFFILQLR,GARSLSVEM,KVRPTSCRT,SPGSGARSL,RPTSCRTAP,VMHPRGASP,SSGEQQMGF,GEQQMGFFI,EQQMGFFIL,RPSNEESWW,QQMGFFILQL,VMHPRGASPR,SVEMCTPCEK,QMGFFILQLR,RSPSPGSGAR,KVRPTSCRTA,WWKVRPTSCR,HPRGASPRSP,RPTSCRTAPS,APSLTCVGPL,GPLSSGEQQM,SGARSLSVEM,LSSGEQQMGF,GEQQMGFFIL,EESWWKVRPT	STAD
PEX1	c.1108delA	p.I370fs	QSKTKQNVLSPEKEKQMSEPLDQKK[p.I370fs]LGQIIMKKMRRPVCYK*	KLGQIIMKK,KMRRPVCYK,IMKKMRRPV,QIIMKKMRR,MKKMRRPVC,QKKLGQIIM,KKMRRPVCY,IIMKKMRRPV,KKMRRPVCYK,IMKKMRRPVC,DQKKLGQIIM,KLGQIIMKKM,MKKMRRPVCY	BLCA,PRAD
PFKM	c.352C>A	p.R118S	TSGGDAQGMNAAVRAVVRVGIFTGA[p.R118S]SVFFVHEGYQGLVDGGDHIKEATWES	FTGASVFFV,SVFFVHEGY,IFTGASVFF,GIFTGASVF,VGIFTGASV,RVGIFTGASV,ASVFFVHEGY,IFTGASVFFV,VGIFTGASVF,GIFTGASVFF	LUAD
PFKP	c.1779delG	p.M593fs	SGTKRRVFIIETMGGYCGYLANMGG[p.M593fs]SRPELMPHTFSKSPSTSGICSPTWST*	ELMPHTFSK,GSRPELMPH,HTFSKSPST,YLANMGGSR,STSGICSPT,RPELMPHTF,NMGGSRPEL,SKSPSTSGI,TSGICSPTW,MPHTFSKSPS,ANMGGSRPEL,NMGGSRPELM,SRPELMPHTF,FSKSPSTSGI,STSGICSPTW	STAD
PGAM1	c.719G>A	p.R240H	PIVYELDKNLKPIKPMQFLGDEETV[p.R240H]HKAMEAVAAQGKAKK*	TVHKAMEAV,ETVHKAMEA,HKAMEAVAA,DEETVHKAM,ETVHKAMEAV,EETVHKAMEA	CRC
PGAP1	c.1694T>G	p.F565C	QAPSSTEISLKLHIAQPENNTHVAL[p.F565C]CKMYTSSDCRYEVTVKTSFSQILGQV	THVALCKMY,NTHVALCKMY	OV
PGM5	c.1277_1278insC	p.G426fs	VWLSIIAARKQSVEEIVRDHWAKFG[p.G426fs]PPLLLQV*	HWAKFGPPL,AKFGPPLLL,HWAKFGPPLL,KFGPPLLLQV	KIRC
PGM5	c.292A>G	p.I98V	RTAIEIVVQMAAANGIGRLIIGQNG[p.I98V]VLSTPAVSCIIRKIKAAGGIILTASH	RLIIGQNGV,VLSTPAVSCI,RLIIGQNGVL,GQNGVLSTPA	STAD
PGPEP1L	c.490_491insA	p.R164fs	KGCAALIHVPPLSRGLPASLLGRAL[p.R164fs]KSHHPGNAGRGGKAQAQSPVRRKLNHGPSSQRELTGGLLL*	SQRELTGGL,ASLLGRALK,RALKSHHPG,KSHHPGNAG,KAQAQSPVR,QAQSPVRRK,GKAQAQSPV,AQSPVRRKL,RKLNHGPSS,RELTGGLLL,ALKSHHPGNA,KLNHGPSSQR,KSHHPGNAGR,KAQAQSPVRR,AQAQSPVRRK,SQRELTGGLL	KIRC
PHACTR1	c.752_753insG	p.V251fs	LPCLPVKLSPPLPPKKVMICMPVGG[p.V251fs]ARPLTGVLHSPEEWPAGCGPAPPHCPALPDPAPAAVRQPRPAPPLHHRLPPHAPLGLQNDRRAQQNAGHDHAEAGKL*	ALPDPAPAA,AVRQPRPAP,RQPRPAPPL,MICMPVGGA,MPVGGARPL,GARPLTGVL,GPAPPHCPA,LPDPAPAAV,LPPHAPLGL,HRLPPHAPL,AQQNAGHDH,WPAGCGPAP,VMICMPVGGA,VLHSPEEWPA,ALPDPAPAAV,RLPPHAPLGL,CMPVGGARPL,MICMPVGGAR,GARPLTGVLH,AVRQPRPAPP,AGHDHAEAGK,MPVGGARPLT,GPAPPHCPAL,CPALPDPAPA,RPAPPLHHRL,HHRLPPHAPL,EEWPAGCGPA,VRQPRPAPPL,RQPRPAPPLH,AQQNAGHDHA,WPAGCGPAPP	LAML
PHACTR1	c.753delG	p.V251fs	LPCLPVKLSPPLPPKKVMICMPVGG[p.V251fs]QTSHWCPTQPRRVASRVWPSTTTLSCPPRSSTSCSTAATASTSPPPPAPSPCTPRAAE*	RVWPSTTTL,TTTLSCPPR,RVASRVWPS,ASRVWPSTT,RSSTSCSTA,HWCPTQPRR,TQPRRVASR,CPTQPRRVA,QPRRVASRV,WPSTTTLSC,GQTSHWCPT,SRVWPSTTT,MPVGGQTSH,TSHWCPTQPR,STTTLSCPPR,RVASRVWPST,ASRVWPSTTT,RSSTSCSTAA,STSCSTAATA,PTQPRRVASR,CPTQPRRVAS,QPRRVASRVW,APSPCTPRAA,MPVGGQTSHW,SRVWPSTTTL	STAD
PHACTR2	c.711_712insA	p.S237fs	APVPPPKPASRNTTREAAGSSHSKK[p.S237fs]NNWL*	5SHSKKNNWL	STAD

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PHACTR4	c.1061delC	p.S354fs	DEREKSTCSMGSELLPMISPRSPSP[p.S354fs]HCLLIYLQSLHAPLHSLLRLFKLCQKLSFHHP*	CLLIYLQSL,YLQSLHAPL,SLHAPLHSL,RLFKLCQKL,LIYLQSLHA,RSPSPHCLL,LHSLLRLFK,HAPLHSLLR,SPSPHCLLI,SPHCLLIYL,APLHSLLRL,LQSLHAPLH,LHAPLHSLL,FKLCQKLSF,LLIYLQSLHA,SLHAPLHSLL,PLHSLLRLFK,LLRLFKLCQK,RSPSPHCLLI,IYLQSLHAPL,LFKLCQKLSF,SPSPHCLLIY,SPRSPSPHCL,APLHSLLRLF,YLQSLHAPLH,QSLHAPLHSL	STAD
PHC3	c.104_106delCCA	p.T35del	STAMDTEPNPGTSSVSTTTSSTTTT[p.T35del]ITTSSSRMQQPQISVYSGSDRHAVQVIQ	TTSSTTTTI,TTTSSTTTTI	GBM
PHGDH	c.517_518GG>TT	p.G173L	LGILGLGRIGREVATRMQSFGMKTI[p.G173L]LYDPIISPEVSASFGVQQLPLEEIWPL	KTILYDPII,SFGMKTILY,QSFGMKTIL,MKTILYDPI,GMKTILYDPI,QSFGMKTILY,LYDPIISPEV,MQSFGMKTIL,MKTILYDPII	SKCM
PHIP	c.5043C>G	p.I1681M	KKRGRKPKKLQYAKPEDLEQNNVHP[p.I1681M]MRDEVLPSSTCNFLSETNNVKEDLLQ	EQNNVHPMR,NVHPMRDEV,LEQNNVHPM,HPMRDEVLPS	LUSC
PHOSPHO1	c.95_97delCCT	p.S32del	PWPANQPLPGGLLPRPLSLAPSSSS[p.S32del]CCSPPCSQDGRMAAQGAPRFLLTFDFDE	SLAPSSSSC,SLAPSSSSCC	PRAD
PI15	c.64G>T	p.V22F	MIAISAVSSALLFSLLCEAST[p.V22F]FVLLNSTDSSPPTNNFTDIEAALKAQ	LLCEASTFV,SLLCEASTF,CEASTFVLL,SLLCEASTFV,LLCEASTFVL,FSLLCEASTF	LUAD
PIAS2	c.1556C>T	p.S519L	SETQSSPTKGVLMYQPSSVRVPSVT[p.S519L]LVDPAAIPPSLTDYSVPFHHTPISSM	SVRVPSVTL,SVRVPSVTLV,SSVRVPSVTL	CRC
PIAS3	c.1378G>A	p.D460N	GGDPSENKKKVEVIDLTIESSSDEE[p.D460N]NLPPTKKHCSVTSAAIPALPGSKGVL	IESSSDEENL	CESC
PIAS3	c.348delC	p.H116fs	LAPIPPTLLAPGTLLGPKREVDMHP[p.H116fs]LCPSLCTLMSP*	KREVDMHPL,REVDMHPLC,DMHPLCPSL,HPLCPSLCTL,VDMHPLCPSL,REVDMHPLCP	STAD
PIGM	c.674G>T	p.R225L	NDKSLRQFRYTFQACLYELLKRLCN[p.R225L]LAVLLFVAVAGLTFFALSFGFYYEYG	RLCNLAVLL,NLAVLLFVA,LLKRLCNLA,LAVLLFVAV,ELLKRLCNL,LKRLCNLAV,KRLCNLAVL,LCNLAVLLF,NLAVLLFVAV,LLKRLCNLAV,RLCNLAVLLF,YELLKRLCNL,LKRLCNLAVL,KRLCNLAVLL	LUAD
PIGO	c.2361delC	p.P787fs	VTVLVKAGAGAPRTRTVLTPFSGPP[p.P787fs]LLKLTWIMWSLKSTDTCRRSSGAG*	KLTWIMWSL,WIMWSLKST,LTWIMWSLK,SLKSTDTCR,TPFSGPPLL,LLKLTWIMW,VLTPFSGPPL,KLTWIMWSLK,SLKSTDTCRR,LKLTWIMWSL	STAD
PIGR	c.548T>G	p.V183G	NAQKRKSLYKQIGLYPVLVIDSSGY[p.V183G]GNPNYTGRIRLDIQGTGQLLFSVVIN	SSGYGNPNY,DSSGYGNPNY	TGCT
PIGT	c.1037delC	p.A346fs	TAMINNSRNLNIQLKWKRPPENEAP[p.A346fs]QCPSCMPSGT*	NEAPQCPSCM	STAD
PIK3C2B	c.4419C>G	p.F1473L	EELNGYIWHLIHAPPEVAECDLVYT[p.F1473L]LFHPLPRDEKAMGTSPAPKSSDGTWA	LVYTLFHPL,YTLFHPLPR,AECDLVYTL,DLVYTLFHPL,LFHPLPRDEK,VYTLFHPLPR,AECDLVYTLF	KIRC

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PIK3C2B	c.859delC	p.R287fs	PLDFSKDTSGKPVARSKTMPPQVPP[p.R287fs]APMPPAMATERMRRLARTAGFLQPRWAPGPTLLPMAMSCLRSQKREMRRLLHFATCWISFDLALTSKTTSSLAMSGVLSPLAQSTSGMRST*	TMPPQVPPA,LLHFATCWI,AMSGVLSPL,RLARTAGFL,FLQPRWAPG,LLPMAMSCL,EMRRLLHFA,WISFDLALT,VLSPLAQST,AMATERMRR,AMSCLRSQK,RTAGFLQPR,RWAPGPTLL,REMRRLLHF,HFATCWISF,CWISFDLAL,RMRRLARTA,RSQKREMRR,TSKTTSSLA,LPMAMSCLR,MSCLRSQKR,LTSKTTSSL,TSSLAMSGV,PPQVPPAPM,VPPAPMPPA,PPAPMPPAM,APMPPAMAT,QPRWAPGPT,APGPTLLPM,GPTLLPMAM,MATERMRRL,CLRSQKREM,RRLARTAGF,PRWAPGPTL,SQKREMRRL,QKREMRRLL,RLLHFATCW,SKTTSSLAM,SSLAMSGVL,LAMSGVLSP,TLLPMAMSCL,RLLHFATCWI,LAMSGVLSPL,AMSGVLSPLA,KTMPPQVPPA,AMATERMRRL,ALTSKTTSSL,TTSSLAMSGV,MAMSCLRSQK,ISFDLALTSK,ATERMRRLAR,RMRRLARTAG,CLRSQKREMR,RSQKREMRRL,SQKREMRRLL,TSKTTSSLAM,RTAGFLQPRW,LLPMAMSCLR,AMSCLRSQKR,QVPPAPMPPA,FATCWISFDL,LTSKTTSSLA,MPPQVPPAPM,VPPAPMPPAM,MPPAMATERM,QPRWAPGPTL,SPLAQSTSGM,MRRLARTAGF,EMRRLLHFAT,RRLARTAGFL,WAPGPTLLPM,KREMRRLLHF,REMRRLLHFA,RRLLHFATCW,LHFATCWISF,AQSTSGMRST,LPMAMSCLRS	GBM
PIK3CA	c.1035T>A	p.N345K	GETSTKSLWVINSALRIKILCATYV[p.N345K]KVNIRDIDKIYVRTGIYHGGEPLCDN	ILCATYVKV,KILCATYVK,KVNIRDIDK,ATYVKVNIR,KILCATYVKV,TYVKVNIRDI,CATYVKVNIR	BRCA,CRC,STAD,UCEC
PIK3CA	c.1049A>G	p.D350G	KSLWVINSALRIKILCATYVNVNIR[p.D350G]GIDKIYVRTGIYHGGEPLCDNVNTQR	YVNVNIRGI,NVNIRGIDK,NIRGIDKIY,TYVNVNIRGI,VNIRGIDKIY	CRC
PIK3CA	c.113G>A	p.R38H	IHLMPPRILVECLLPNGMIVTLECL[p.R38H]HEATLITIKHELFKEARKYPLHQLLQ	VTLECLHEA,LECLHEATL,CLHEATLITI,HEATLITIKH,LECLHEATLI	UCEC
PIK3CA	c.115G>A	p.E39K	HLMPPRILVECLLPNGMIVTLECLR[p.E39K]KATLITIKHELFKEARKYPLHQLLQD	IVTLECLRK,LRKATLITI,LECLRKATL,CLRKATLITI,MIVTLECLRK,RKATLITIKH,LECLRKATLI	UCEC
PIK3CA	c.1258T>C	p.C420R	DLPRAARLCLSICSVKGRKGAKEEH[p.C420R]RPLAWGNINLFDYTDTLVSGKMALNL	KEEHRPLAW,GAKEEHRPLA,RPLAWGNINL,AKEEHRPLAW	BRCA,UCEC
PIK3CA	c.1338_1364delGCCAGTACCTCATGGATTAGAAGATTT	p.PVPHGLEDL447del	LAWGNINLFDYTDTLVSGKMALNLW[p.PVPHGLEDL447del]LNPIGVTGSNPNKETPCLELEFDWFSSVVKFPDMSVIEEHANWSVSREAGFS	ALNLWLNPI,NLWLNPIGV,GKMALNLWL,MALNLWLNPI	BRCA
PIK3CA	c.1357G>A	p.E453K	NLFDYTDTLVSGKMALNLWPVPHGL[p.E453K]KDLLNPIGVTGSNPNKETPCLELEFD	GLKDLLNPI,LWPVPHGLK,VPHGLKDLL,NLWPVPHGLK,WPVPHGLKDL,HGLKDLLNPI	BRCA
PIK3CA	c.1364_1365insG	p.L455fs	DYTDTLVSGKMALNLWPVPHGLEDL[p.L455fs]AEPYWCYWIKSK*	GLEDLAEPY,DLAEPYWCY,AEPYWCYWI,LAEPYWCYW,HGLEDLAEPY	BRCA
PIK3CA	c.1624G>A	p.E542K	LARDNELRENDKEQLKAISTRDPLS[p.E542K]KITEQEKDFLWSHRHYCVTIPEILPK	ISTRDPLSK,STRDPLSKI,LSKITEQEK,AISTRDPLSK,SKITEQEKDF	BLCA,BRCA,CESC,CRC,HNSC,LUAD,LUSC,STAD,UCEC
PIK3CA	c.1633G>A	p.E545K	DNELRENDKEQLKAISTRDPLSEIT[p.E545K]KQEKDFLWSHRHYCVTIPEILPKLL	SEITKQEKDF,KQEKDFLWSH	BLCA,BRCA,CESC,CRC,GBM,HNSC,KIRC,LUAD,LUSC,STAD,TGCT,UCEC,UCS
PIK3CA	c.1634A>C	p.E545A	DNELRENDKEQLKAISTRDPLSEIT[p.E545A]AQEKDFLWSHRHYCVTIPEILPKLL	TAQEKDFLW,SEITAQEKDF,AQEKDFLWSH,ITAQEKDFLW	BRCA,CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PIK3CA	c.1634A>G	p.E545G	DNELRENDKEQLKAISTRDPLSEITⅠp.E545G]GQEKDFLWSHRHYCVTIPEILPKLLL	SEITGQEKDF,GQEKDFLWSH	CRC
PIK3CA	c.1636C>A	p.Q546K	NELRENDKEQLKAISTRDPLSEITE[p.Q546K]KEKDFLWSHRHYCVTIPEILPKLLLS	KEKDFLWSH,TEKEKDFLW,SEITEKEKDF	BRCA,CRC,UCEC
PIK3CA	c.1637A>C	p.Q546P	NELRENDKEQLKAISTRDPLSEITE[p.Q546P]PEKDFLWSHRHYCVTIPEILPKLLLS	EITEPEKDFL,SEITEPEKDF,EPEKDFLWSH	UCEC
PIK3CA	c.1637A>G	p.QS46R	NELRENDKEQLKAISTRDPLSEITE[p.Q546R]REKDFLWSHRHYCVTIPEILPKLLLS	REKDFLWSH,TEREKDFLW,SEITEREKDF	BRCA,UCEC
PIK3CA	c.1A>G	p.M1V	[p.M1V]VPPRPSSGELWGIHLMPPRILVECLL	VPPRPSSGEL	GBM
PIK3CA	c.2176G>A	p.E726K	HLNRQVEAMEKLINLTDILKQEKKD[p.E726K]KTQKVQMKFLVEQMRRPDFMDALQGF	KTQKVQMKF,KDKTQKVQMK,KTQKVQMKFL,KKDKTQKVQM	BRCA,CESC,LUSC
PIK3CA	c.263G>A	p.R88Q	QDESSYIFVSVTQEAEREEFFDETR[p.R88Q]QLCDLRLFQPFLKVIEPVGNREEKIL	RQLCDLRLF,ETRQLCDLR,EEFFDETRQL	BRCA,CRC,GBM,STAD,UCEC
PIK3CA	c.278G>A	p.R93Q	YIFVSVTQEAEREEFFDETRRLCDL[p.R93Q]QLFQPFLKVIEPVGNREEKILNREIG	QLFQPFLKV,LQLFQPFLK,RRLCDLQLF,CDLQLFQPF,LQLFQPFLKV,QLFQPFLKVI,DLQLFQPFLK,TRRLCDLQLF,LCDLQLFQPF,CDLQLFQPFL	UCEC
PIK3CA	c.3012G>A	p.M1004I	RFQEMCYKAYLAIRQHANLFINLFS[p.M1004I]IMLGSGMPELQSFDDIAYIRKTLALD	NLFINLFSI,FINLFSIML,LFINLFSIM,FSIMLGSGM,IMLGSGMPEL,NLFINLFSIM,LFINLFSIML,LFSIMLGSGM	BRCA
PIK3CA	c.3127A>G	p.M1043V	DIAYIRKTLALDKTEQEALEYFMKQ[p.M1043V]VNDAHHGGWTTKMDWIFHTIKQHALN	ALEYFMKQV,FMKQVNDAH,MKQVNDAHH,EALEYFMKQV,FMKQVNDAHH	GBM,HNSC,UCEC
PIK3CA	c.3129G>A	p.M1043I	DIAYIRKTLALDKTEQEALEYFMKQ[p.M1043I]INDAHHGGWTTKMDWIFHTIKQHALN	FMKQINDAH,KQINDAHHG,EALEYFMKQI,FMKQINDAHH,KQINDAHHGG	BRCA,UCEC
PIK3CA	c.3130A>T	p.N1044Y	IAYIRKTLALDKTEQEALEYFMKQM[p.N1044Y]YDAHHGGWTTKMDWIFHTIKQHALN*	MYDAHHGGW,FMKQMYDAH,LEYFMKQMY,MKQMYDAHH,KQMYDAHHG,ALEYFMKQMY,FMKQMYDAHH,QMYDAHHGGW,KQMYDAHHGG	BRCA
PIK3CA	c.3132T>A	p.N1044K	IAYIRKTLALDKTEQEALEYFMKQM[p.N1044K]KDAHHGGWTTKMDWIFHTIKQHALN*	FMKQMKDAH,KQMKDAHHG,MKDAHHGGW,ALEYFMKQMK,FMKQMKDAHH,KQMKDAHHGG,QMKDAHHGGW	KIRC
PIK3CA	c.3140A>G	p.H1047R	IRKTLALDKTEQEALEYFMKQMNDA[p.H1047R]RHGGWTTKMDWIFHTIKQHALN*	FMKQMNDAR,KQMNDARHG,RHGGWTTKM,YFMKQMNDAR,FMKQMNDARH,KQMNDARHGG,QMNDARHGGW,ARHGGWTTKM	BRCA,CRC,GBM,HNSC,LIHC,LUSC,STAD,UCEC,UCS
PIK3CA	c.3140A>T	p.H1047L	IRKTLALDKTEQEALEYFMKQMNDA[p.H1047L]LHGGWTTKMDWIFHTIKQHALN*	FMKQMNDAL,ALHGGWTTK,KQMNDALHG,LHGGWTTKM,ALHGGWTTKM,YFMKQMNDAL,DALHGGWTTK,FMKQMNDALH,KQMNDALHGG,QMNDALHGGW	BRCA,HNSC,UCEC
PIK3CA	c.317G>T	p.G106V	EFFDETRRLCDLRLFQPFLKVIEPV[p.G106V]VNREEKILNREIGFAIGMPVCEFDMV	FLKVIEPVV,KVIEPVVNR	UCS
PIK3CA	c.323G>A	p.R108H	FDETRRLCDLRLFQPFLKVIEPVGN[p.R108H]HEEKILNREIGFAIGMPVCEFDMVKD	HEEKILNREI	UCEC
PIK3CA	c.325_327delGAA	p.E110del	ETRRLCDLRLFQPFLKVIEPVGNRE[p.E110del]KILNREIGFAIGMPVCEFDMVKDPEVQD	REKILNREI	BRCA,UCEC
PIK3CA	c.331A>G	p.K111E	TRRLCDLRLFQPFLKVIEPVGNREE[p.K111E]EILNREIGFAIGMPVCEFDMVKDPEV	REEEILNREI,EEILNREIGF	UCEC
PIK3CA	c.331_333delAAG	p.K111del	TRRLCDLRLFQPFLKVIEPVGNREE[p.K111del]ILNREIGFAIGMPVCEFDMVKDPEVQDF	REEILNREI,EEILNREIGF	BRCA

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PIK3CD	c.1141T>C	p.C381R	CFALYAVIEKAKKARSTKKKSKKAD[p.C381R]RPIAWANLMLFDYKDQLKTGERCLYM	KSKKADRPI,RPIAWANLM,KKADRPIAW,KSKKADRPIA,RPIAWANLML,KKSKKADRPI,SKKADRPIAW,ADRPIAWANL	TGCT
PIK3CG	c.493G>A	p.V165I	RHPPSEESQAFQRQLTALIGYDVTD[p.V165I]ISNVHDDELEFTRRGLVTPRMAEVAS	LIGYDVTDI,ALIGYDVTDI	LUAD
PIK3R1	c.1126G>A	p.G376R	ADGTFLVRDASTKMHGDYTLTLRKG[p.G376R]RNNKLIKIFHRDGKYGFSDPLTFSSV	TLRKGRNNK,KGRNNKLIK,YTLTLRKGR,RNNKLIKIF,LTLRKGRNNK,TLRKGRNNKL,KGRNNKLIKI,GRNNKLIKIF	GBM
PIK3R1	c.1137A>T	p.K379N	TFLVRDASTKMHGDYTLTLRKGGNN[p.K379N]NLIKIFHRDGKYGFSDPLTFSSVVEL	KGGNNNLIK,NNLIKIFHR,RKGGNNNLI,GNNNLIKIF,TLRKGGNNNL,NNNLIKIFHR,GGNNNLIKIF	GBM
PIK3R1	c.1697_1708delTTAAACCAGACC	p.KPDL567del	RRRLEEDLKKQAAEYREIDKRMNSI[p.KPDL567del]IQLRKTRDQYLMWLTQKGVRQKKLNEWLGNENTEDQY	RMNSIIQLR,MNSIIQLRK,SIIQLRKTR,KRMNSIIQL,RMNSIIQLRK,NSIIQLRKTR	BRCA
PIK3R5	c.1112T>G	p.L371R	LLSTSSLASHDSTLSLASSQASGPA[p.L371R]RSRHLLTSFVSGLSDGMDSGYVEDSE	SSQASGPAR,RSRHLLTSF,GPARSRHLL,ASSQASGPAR,RSRHLLTSFV,ARSRHLLTSF	KIRC
PILRA	c.872_873insC	p.S291fs	VYASLALSSSTSPRAPPSHRPLKSP[p.S291fs]PERDPVLCLKGLTNGQPSQD*	SPPERDPVL	LUAD
PIM1	c.490C>T	p.L164F	LQEELARSFFWQVLEAVRHCHNCGV[p.L164F]FHRDIKDENILIDLNRGELKLIDFGS	RHCHNCGVF,HCHNCGVFHR,VRHCHNCGVF	DLBCL
PIM1	c.550C>T	p.L184F	HNCGVLHRDIKDENILIDLNRGELK[p.L184F]FIDFGSGALLKDTVYTDFDGTRVYSP	FIDFGSGAL,RGELKFIDF,FIDFGSGALL,IDLNRGELKF,LKFIDFGSGA,KFIDFGSGAL,GELKFIDFGS	DLBCL
PIP4K2A	c.656G>A	p.R219K	IVTRNVFSHRLSVYRKYDLKGSTVA[p.R219K]KEASDKEKAKELPTLKDNDFINEGQK	TVAKEASDK,KEASDKEKA,STVAKEASDK,VAKEASDKEK	KIRP
PIP4K2C	c.611G>A	p.R204H	NTLLPQFLGMYRVSVDNEDSYMLVM[p.R204H]HNMFSHRLPVHRKYDLKGSLVSREAS	VMHNMFSHR,LVMHNMFSH,SYMLVMHNM,YMLVMHNMF,MHNMFSHRL,VMHNMFSHRL,LVMHNMFSHR,SYMLVMHNMF,DSYMLVMHNM,HNMFSHRLPV,MLVMHNMFSH	CRC
PITPNM1	c.884delC	p.P295fs	PPGKPSTEARSAASNTGTPDGPEAP[p.P295fs]QAQMPPPMPALGSSGPHPPVPPTHPNMEGLCLPRACLSGACRTLPETLRTAPRKSSLMPTKASRTVRRSSPRR*	AQMPPPMPA,QMPPPMPAL,CLSGACRTL,TLPETLRTA,RTVRRSSPR,ETLRTAPRK,RTAPRKSSL,RKSSLMPTK,KSSLMPTKA,SLMPTKASR,ASRTVRRSS,TVRRSSPRR,NMEGLCLPR,GPEAPQAQM,HPNMEGLCL,LPRACLSGA,MPTKASRTV,PQAQMPPPM,MEGLCLPRA,AQMPPPMPAL,CLPRACLSGA,SLMPTKASRT,LMPTKASRTV,RTVRRSSPRR,SSLMPTKASR,RTLPETLRTA,RTAPRKSSLM,PTKASRTVRR,APQAQMPPPM,MPALGSSGPH,LPRACLSGAC,APRKSSLMPT,LRTAPRKSSL,RKSSLMPTKA	STAD
PIWIL1	c.2095G>A	p.V699M	GLKVCLQAALRAWNSCNEYMPSRII[p.V699M]MYRDGVGDGQLKTLVNYEVPQFLDCL	RIIMYRDGV,EYMPSRIIM,YMPSRIIMY,MPSRIIMYR,YMPSRIIMYR,NEYMPSRIIM	HNSC
PKD1	c.2813C>T	p.T938M	VENSASRANLSLRVTAEEPICGLRA[p.T938M]MPSPEARVLQGVLVRYSPVVEAGSDM	AMPSPEARV,RAMPSPEAR,EPICGLRAM,MPSPEARVL,GLRAMPSPEA,RAMPSPEARV,AMPSPEARVL,EEPICGLRAM	TGCT
PKD2	c.1457A>T	p.Y486F	KLIRYVTTFDFFLAACEIIFCFFIF[p.Y486F]FYVVEEILEIRIHKLHYFRSFWNCLD	FCFFIFFYV,IIFCFFIFF,CFFIFFYVV,IFFYVVEEI,FFYVVEEIL,IFCFFIFFY,FCFFIFFYVV,FIFFYVVEEI,IIFCFFIFFY,IFCFFIFFYV,IFFYVVEEIL,FYVVEEILEI,EIIFCFFIFF	CLL
PKHD1L1	c.5568C>A	p.F1856L	PPVASLSPTSGSIGGGTTLVITGNG[p.F1856L]LYPGNTTVTIGDEPCQIISINPNEVY	LVITGNGLY,GLYPGNTTV,TLVITGNGL,GLYPGNTTVT,LYPGNTTVTI,TLVITGNGLY,TTLVITGNGL	CRC
PKN2	c.226delA	p.K76fs	KREIRKELKIKEGAENLRKVTTDKK[p.K76fs]VWLM*	TTDKKVWLM,RKVTTDKKVW	STAD
PLA2G15	c.689delG	p.W230fs	FLQRQPQAWKDKYIRAFVSLGAPWG[p.W230fs]AWPRPCASWLQETTTGSQSSGP*	WLQETTTGS,AWPRPCASW,GAPWGAWPR,WPRPCASWL,SLGAPWGAW,FVSLGAPWGA,LGAPWGAWPR,VSLGAPWGAW,GAWPRPCASW	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PLA2G1B	c.157_158insTG	p.L53fs	KMIKCVIPGSDPFLEYNNYGCYCGL[p.L53fs]WGAQAPPWMNWTSAARHMTTAMTRPRSWTAVNFCWTTRTPTPIHTRALARQSPVAAKTKSVRPSFATATATLPSAFQKLHITRHTRTWTPRSIVRVEYHLSKASPLSASSHTVLSNKAPC*	ALARQSPVA,SVRPSFATA,TLPSAFQKL,PLSASSHTV,ATLPSAFQK,SSHTVLSNK,MTTAMTRPR,AVNFCWTTR,NYGCYCGLW,LWGAQAPPW,SWTAVNFCW,SFATATATL,AARHMTTAM,RHMTTAMTR,MTRPRSWTA,RSWTAVNFC,TTRTPTPIH,RTPTPIHTR,HTRALARQS,RALARQSPV,LARQSPVAA,KTKSVRPSF,KLHITRHTR,ITRHTRTWT,HTRTWTPRS,RTWTPRSIV,RSIVRVEYH,RVEYHLSKA,LSKASPLSA,WMNWTSAAR,AFQKLHITR,TWTPRSIVR,WTSAARHMT,WTAVNFCWT,WTTRTPTPI,WTPRSIVRV,RPRSWTAVN,TPIHTRALA,RPSFATATA,YHLSKASPL,ATATLPSAF,AQAPPWMNW,TAMTRPRSW,RQSPVAAKT,FQKLHITRH,HITRHTRTW,SKASPLSAS,LSASSHTVL,VEYHLSKAS,AMTRPRSWTA,MTRPRSWTAV,ALARQSPVAA,ATATATLPSA,HLSKASPLSA,RTWTPRSIVR,IVRVEYHLSK,ASSHTVLSNK,TAVNFCWTTR,TATLPSAFQK,SAFQKLHITR,RSWTAVNFCW,CWTTRTPTPI,AARHMTTAMT,TTRTPTPIHT,RTPTPIHTRA,HTRALARQSP,RALARQSPVA,LARQSPVAAK,RQSPVAAKTK,KTKSVRPSFA,KSVRPSFATA,SVRPSFATAT,KLHITRHTRT,ITRHTRTWTP,HTRTWTPRSI,RSIVRVEYHL,SSHTVLSNKA,PWMNWTSAAR,HMTTAMTRPR,TPIHTRALAR,TSAARHMTTA,WTAVNFCWTT,APPWMNWTSA,SAARHMTTAM,RPRSWTAVNF,TPTPIHTRAL,SPVAAKTKSV,RPSFATATAT,LPSAFQKLHI,SPLSASSHTV,MNWTSAARHM,TATATLPSAF,GLWGAQAPPW,WMNWTSAARH,AKTKSVRPSF,PSFATATATL,FQKLHITRHT,LHITRHTRTW,KASPLSASSH,TPRSIVRVEY	STAD
PLA2G3	c.602G>A	p.R201Q	GPDLCCREHDRCPQNISPLQYNYGI[p.R201Q]QNYRFHTISHCDCDTRFQQCLQNQHD	IQNYRFHTI,NYGIQNYRF,QYNYGIQNY,YNYGIQNYR,LQYNYGIQN,YNYGIQNYRF,LQYNYGIQNY,QYNYGIQNYR,IQNYRFHTIS,QNYRFHTISH	UCEC
PLAG1	c.551delA	p.K184fs	FESTGVLLEHLKSHAGKSSGGVKEK[p.K184fs]STSANIVIAGSTPERMSGDTWWCTLEERTSSVSIVHRDLGERIT*	RMSGDTWWC,TLEERTSSV,VIAGSTPER,RTSSVSIVH,TSSVSIVHR,GVKEKSTSA,KSTSANIVI,TWWCTLEER,IVHRDLGER,STSANIVIA,KEKSTSANI,EERTSSVSI,RMSGDTWWCT,CTLEERTSSV,IVIAGSTPER,RTSSVSIVHR,KSTSANIVIA,DTWWCTLEER,SIVHRDLGER,KEKSTSANIV,MSGDTWWCTL,LEERTSSVSI,EERTSSVSIV,TPERMSGDTW	STAD
PLAGL2	c.30delC	p.P10fs	MTTFFTSVPP[p.P10fs]GFKMQSRRRKWAGN*	FTSVPPGFK,FFTSVPPGF,TSVPPGFKM,KMQSRRRKW,FFTSVPPGFK,TFFTSVPPGF,GFKMQSRRRK,KMQSRRRKWA,FTSVPPGFKM,FKMQSRRRKW	STAD
PLAU	c.602_603insG	p.R201fs	IIGGEFTTIENQPWFAAIYRRHRGG[p.R201fs]LCHLRVWRQPHQPLLGDQRHTLLH*	LLGDQRHTL,VWRQPHQPL,HLRVWRQPH,GLCHLRVWR,RHRGGLCHL,WRQPHQPLL,LLGDQRHTLL,VWRQPHQPLL,AIYRRHRGGL,RHRGGLCHLR,HLRVWRQPHQ,RVWRQPHQPL,RRHRGGLCHL,RGGLCHLRVW	STAD
PLCD3	c.1495delG	p.E499fs	KGRVLVKGKKLPAARSEDGRALSDR[p.E499fs]RRRRRMTRRKKRRWRLQRRGGWPSRSPRSCRPWLCTATPPA*	WLCTATPPA,RALSDRRRR,RRRRRRMTR,RRRRRMTRR,RRRRMTRRK,RRRMTRRKK,RMTRRKKRR,KKRRWRLQR,KRRWRLQRR,RWRLQRRGG,GGWPSRSPR,WPSRSPRSC,SPRSCRPWL,RRKKRRWRL,LQRRGGWPS,RSPRSCRPW,RALSDRRRRR,ALSDRRRRRR,RRRRRRMTRR,RRRRRMTRRK,RRRRMTRRKK,MTRRKKRRWR,RKKRRWRLQR,KKRRWRLQRR,RWRLQRRGGW,LQRRGGWPSR,RGGWPSRSPR,RSPRSCRPWL,RSCRPWLCTA,RPWLCTATPP,TRRKKRRWRL,RMTRRKKRRW,SRSPRSCRPW	CLL
PLCE1	c.1315G>T	p.G439C	NTVGSLLHFLTKLPASETAHGRISV[p.G439C]CPCLKQCVRDTVCEYRATLQRTSISQ	RISVCPCLK,GRISVCPCL,HGRISVCPCL	LUSC
PLCE1	c.1690G>T	p.G564C	LMEQEQTIYRRVLPVDYLCFLTRDL[p.G564C]CTPECQSSLPCLKASISASILTTQNG	CTPECQSSL	LUAD
PLCL1	c.1692G>T	p.M564I	VKGKKLPSDPDVLEGEVTDEDEEAE[p.M564I]ISRRMSVDYNGEQKQIRLCRELSDLV	ISRRMSVDY,AEISRRMSV,EEAEISRRM,EISRRMSVDY,DEEAEISRRM	LUAD
PLEC	c.4157G>A	p.R1386Q	QDARRRQEQIQAMPLADSQAVREQL[p.R1386Q]QQEQALLEEIERHGEKVEECQRFAKQ	EQLQQEQAL,REQLQQEQA,REQLQQEQAL,EQLQQEQALL,QQEQALLEEI	ACC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PLEKHA6	c.329G>T	p.R110L	VDRCLFYYKDEKEESILGSIPLLSF[p.R110L]LVAAVQPSDNISRKHTFKAEHAGVRT	SIPLLSFLV,LLSFLVAAV,FLVAAVQPS,IPLLSFLVA,GSIPLLSFL,GSIPLLSFLV,PLLSFLVAAV,IPLLSFLVAA	LUAD
PLEKHA6	c.982delG	p.V328fs	TNPDKIAQRKSSMNQLQQWVNLRRG[p.V328fs]YPRLKTFGVPLGSILCLAGSLSTMAPTPPSTPMIISTTRQECGRRASVPCRPMIGSARPGPWRTSAMPSAMGVALPTSCESGRSPPATGGRMPPSGSQAPPGSQSIMMSWMPPLAPCAACPCSPAPTLCPAHPARAPTAVPAFTPLSAHPVPVLSGCHLAVRTSMLTLLPM*	RLKTFGVPL,CLAGSLSTM,SAMPSAMGV,IMMSWMPPL,MMSWMPPLA,WMPPLAPCA,FTPLSAHPV,PLSAHPVPV,VLSGCHLAV,NLRRGYPRL,TMAPTPPST,AMPSAMGVA,RMPPSGSQA,HLAVRTSML,RGYPRLKTF,RAPTAVPAF,LRRGYPRLK,STMAPTPPS,RASVPCRPM,SARPGPWRT,RTSAMPSAM,AVRTSMLTL,QWVNLRRGY,VNLRRGYPR,TPMIISTTR,STTRQECGR,TLCPAHPAR,CAACPCSPA,TAVPAFTPL,YPRLKTFGV,APTPPSTPM,RPGPWRTSA,MPSAMGVAL,SPPATGGRM,APPGSQSIM,MPPLAPCAA,CPCSPAPTL,SPAPTLCPA,HPARAPTAV,VPAFTPLSA,VPVLSGCHL,SQSIMMSWM,TSMLTLLPM,FGVPLGSIL,RQECGRRAS,IGSARPGPW,WRTSAMPSA,SAMGVALPT,CESGRSPPA,SQAPPGSQS,GSQSIMMSW,MSWMPPLAP,ARAPTAVPA,LSAHPVPVL,CHLAVRTSM,VRTSMLTLL,VPLGSILCL,QECGRRASV,TPPSTPMII,RTSMLTLLPM,CLAGSLSTMA,AMPSAMGVAL,SIMMSWMPPL,IMMSWMPPLA,WMPPLAPCAA,KTFGVPLGSI,SQAPPGSQSI,TLCPAHPARA,HLAVRTSMLT,AVRTSMLTLL,NLRRGYPRLK,WVNLRRGYPR,STPMIISTTR,RGYPRLKTFG,RLKTFGVPLG,STMAPTPPST,CGRRASVPCR,RASVPCRPMI,SARPGPWRTS,PWRTSAMPSA,RTSAMPSAMG,SWMPPLAPCA,QQWVNLRRGY,PTLCPAHPAR,VLSGCHLAVR,MAPTPPSTPM,TSAMPSAMGV,YPRLKTFGVP,APTPPSTPMI,RPMIGSARPG,RPGPWRTSAM,APPGSQSIMM,APTLCPAHPA,CPAHPARAPT,TPLSAHPVPV,RRGYPRLKTF,LCLAGSLSTM,RQECGRRASV,RRASVPCRPM,MIGSARPGPW,WRTSAMPSAM,SAMPSAMGVA,RMPPSGSQAP,MMSWMPPLAP,ARAPTAVPAF,GCHLAVRTSM,CHLAVRTSML,LAVRTSMLTL,MPSAMGVALP,MPPLAPCAAC,SPAPTLCPAH,VPAFTPLSAH,HPVPVLSGCH,CESGRSPPAT,VPLGSILCLA,VPVLSGCHLA	CRC,STAD
PLEKHB1	c.436T>C	p.S146P	TALLEANSTPAPAGATVPPRSRRVC[p.S146P]PKVRCVTRSWSPCKVERRIWVRVYSP	RSRRVCPKV,RVCPKVRCV,CPKVRCVTR,RSRRVCPKVR	CLL
PLEKHG4B	c.1150G>A	p.E384K	AIIFLQNSFCSLNTHRTPRTAQEVA[p.E384K]KLIDQHETMMKLVLEDPLLVSLRLEG	KLIDQHETM,RTAQEVAKL,KLIDQHETMM,AKLIDQHETM	CRC
PLEKHM1	c.2684C>T	p.A895V	RIIHNWDLTKRPICRQALKFLTQIR[p.A895V]VQPLINLQMVNASLYEHVERMHLIGR	TQIRVQPLI,LTQIRVQPL,LKFLTQIRV,IRVQPLINL,VQPLINLQM,FLTQIRVQPL,ALKFLTQIRV,QIRVQPLINL,RVQPLINLQM	TGCT
PLEKHM2	c.1376C>T	p.S459L	DQSFRTGSPGDAPERPPLCDFSEGL[p.S459L]LAPMDFYRFTVESPSTVTSGGGHHDP	LLAPMDFYR,LAPMDFYRF,GLLAPMDFY,FSEGLLAPM,LLAPMDFYRF,GLLAPMDFYR,SEGLLAPMDF,DFSEGLLAPM	BLCA
PLEKHO1	c.761delC	p.T254fs	QPSADRASSLSRPWEKTDKGATYTP[p.T254fs]RHPRS*	ATYTPRHPR,ATYTPRHPRS,GATYTPRHPR	STAD
PLEKHO2	c.1051G>C	p.E351Q	GEMQASGPPAPGTVQVSVNGMDDSP[p.E351Q]QPAKPSQAEGTPGTPPKDATTSTALP	GMDDSPQPA,GMDDSPQPAK,SPQPAKPSQA	CESC
PLIN5	c.916C>T	p.R306W	LETLVLSRSLTQELQGTVEALESSV[p.R306W]WGLPAGAQEKVAEVRRSVDALQTAFA	ALESSVWGL,ESSVWGLPA,SVWGLPAGA,VEALESSVW,EALESSVWGL,SSVWGLPAGA,LESSVWGLPA	ACC
PLK1	c.698A>G	p.D233G	KKTLCGTPNYIAPEVLSKKGHSFEV[p.D233G]GVWSIGCIMYTLLVGKPPFETSCLKE	SFEVGVWSI,KGHSFEVGV,GVWSIGCIM,FEVGVWSIG,GVWSIGCIMY,HSFEVGVWSI,EVGVWSIGCI,KGHSFEVGVW,VGVWSIGCIM,FEVGVWSIGC	CRC
PLOD3	c.888_889insC	p.P296fs	GWTPEGGCGFCNQDRRTLPGGQPPP[p.P296fs]PGVSGRVCGTAYSVSAPLPAAAATPGLSPRQGHPFPAQQRGLP*	RVCGTAYSV,SVSAPLPAA,SGRVCGTAY,AATPGLSPR,TAYSVSAPL,YSVSAPLPA,APLPAAAAT,LPAAAATPG,LSPRQGHPF,RQGHPFPAQ,VSGRVCGTAY,GTAYSVSAPL,SVSAPLPAAA,AAATPGLSPR,YSVSAPLPAA,LPAAAATPGL,SPRQGHPFPA,HPFPAQQRGL,GLSPRQGHPF,GRVCGTAYSV	STAD

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PLOD3	c.889delC	p.R297fs	GWTPEGGCGFCNQDRRTLPGGQPPP[p.R297fs]GCFWPCLWNSLLRFCPASCSGCYSWTIPPTGSPFSCTTTRSSMNPTSLTPGRSSRTTSQL*	FWPCLWNSL,CLWNSLLRF,NSLLRFCPA,TTRSSMNPT,RSSMNPTSL,RSSRTTSQL,SPFSCTTTR,SLTPGRSSR,TIPPTGSPF,CPASCSGCY,ASCSGCYSW,SCTTTRSSM,SMNPTSLTP,WPCLWNSLL,CFWPCLWNSL,FWPCLWNSLL,WTIPPTGSPF,TTRSSMNPTS,RSSMNPTSLT,TSLTPGRSSR,MNPTSLTPGR,FSCTTTRSSM,TRSSMNPTSL,SMNPTSLTPG,GRSSRTTSQL	CRC,STAD
PLSCR3	c.229G>A	p.E77K	FPSPGPVALGSAAPFLPLPGVPSGL[p.E77K]KFLVQIDQILIHQKAERVETFLGWET	KFLVQIDQI,VPSGLKFLV,GVPSGLKFLV,KFLVQIDQIL,LPGVPSGLKF,LKFLVQIDQI	CRC
PLXNA1	c.3046delC	p.P1016fs	LTPPGQSPGSAPIIININRAQLTNP[p.P1016fs]R*	INRAQLTNPR	STAD
PLXNA1	c.3883G>A	p.E1295K	ALECKEAFAELQTDIHELTNDLDGA[p.E1295K]SIPFLDYRTYAMRVLFPGIEDHPVLK	ASIPFLDYR,GASIPFLDY,DLDGASIPF,GASIPFLDYR,SIPFLDYRTY,LTNDLDGASI,NDLDGASIPF	UCEC
PLXNA2	c.1392_1393insCC	p.P464fs	YNGYSVVFVGTKSGKLKKIRADGPP[p.P464fs]PMVGSSTRWSLCSRTEAPSSGTWPSPLISATCTSCLRDRSPGSPWSHVSSIRLVGSA*	STRWSLCSR,KIRADGPPP,SATCTSCLR,WPSPLISAT,SPWSHVSSI,IRADGPPPM,PMVGSSTRW,VGSSTRWSL,TEAPSSGTW,ISATCTSCL,RDRSPGSPW,WSHVSSIRL,SPGSPWSHV,LISATCTSCL,SSTRWSLCSR,ISATCTSCLR,KIRADGPPPM,STRWSLCSRT,RWSLCSRTEA,MVGSSTRWSL,RTEAPSSGTW,WPSPLISATC,PPMVGSSTRW	STAD
PLXNA3	c.172C>T	p.P58S	LTHLAVHRVTGEVFVGAVNRVFKLA[p.P58S]SNLTELRAHVTGPVEDNARCYPPPSM	KLASNLTEL,RVFKLASNL,LASNLTELR,KLASNLTELR,RVFKLASNLT,FKLASNLTEL	HNSC
PLXNC1	c.1385C>T	p.S462L	IYIYLTAGKEVRRIRVANCNKHKSC[p.S462L]LECLTATDPHCGWCHSLQRCTFQGDC	NKHKSCLECL	CRC
PLXNC1	c.2455C>T	p.R819C	NINVSEYCVATYCGFLAPSLKSSKV[p.R819C]CTNVTVKLRVQDTYLDCGTLQYREDP	KVCTNVTVK,CTNVTVKLR,KSSKVCTNV,SKVCTNVTV,SSKVCTNVTV	CRC
PLXND1	c.1100G>T	p.R367L	GLQCAGGAGRGDLYSRLVSVFPARE[p.R367L]LLFAVFERPQGSPAARAAPAALCAFR	VFPARELLF,SVFPARELL,ELLFAVFER,ARELLFAVF,FPARELLFA,RELLFAVFE,SVFPARELLF,FPARELLFAV,PARELLFAVF	TGCT
PMEPA1	c.624delC	p.P208fs	RAPPNRTIFDSDLMDSARLGGPCPP[p.P208fs]AVTRASAPRATAAAGAWRGRRPPTARSSATTRGPPSSTSRAVGRPPCWRGPGSTTHTSRP*	RLGGPCPPA,AVTRASAPR,ATAAAGAWR,SSTSRAVGR,AVGRPPCWR,VTRASAPRA,RASAPRATA,AWRGRRPPT,RGRRPPTAR,TARSSATTR,AAGAWRGRR,SAPRATAAA,APRATAAAG,RPPTARSSA,RPPCWRGPG,RATAAAGAW,RAVGRPPCW,RLGGPCPPAV,VTRASAPRAT,RASAPRATAA,ASAPRATAAA,RATAAAGAWR,AWRGRRPPTA,RGRRPPTARS,TSRAVGRPPC,RAVGRPPCWR,TAAAGAWRGR,AAAGAWRGRR,CPPAVTRASA,APRATAAAGA,RPPTARSSAT,GPPSSTSRAV,ARLGGPCPPA	STAD
PMS2	c.1952A>G	p.K651R	AKRIKQLHHEAQQSEGEQNYRKFRA[p.K651R]RICPGENQAAEDELRKEISKTMFAEM	NYRKFRARI,KFRARICPG,RARICPGEN,QNYRKFRAR,KFRARICPGE,RARICPGENQ,EQNYRKFRAR,RKFRARICPG	TGCT
PNKP	c.520G>T	p.G174W	NLEKLLVFTAAGVKPQGKVAGFDLD[p.G174W]WTLITTRSGKVFPTGPSDWRILYPEI	AGFDLDWTL,WTLITTRSGK,DLDWTLITTR,GKVAGFDLDW	LUAD
PNLIP	c.110C>T	p.T37M	GAVAGKEVCYERLGCFSDDSPWSGI[p.T37M]MERPLHILPWSPKDVNTRFLLYTNEN	GIMERPLHI,SPWSGIMER,IMERPLHIL,GIMERPLHIL,DSPWSGIMER,MERPLHILPW	MM
PNPLA4	c.668T>C	p.L223P	LDLYVNIAKQDIMLSLANLVRLNQA[p.L223P]PFPPSKRKMESLYQCGFDDTVKFLLK	NQAPFPPSK,LVRLNQAPF,LNQAPFPPSK,NQAPFPPSKR,APFPPSKRKM,NLVRLNQAPF,RLNQAPFPPS	TGCT

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PNPLA7	c.3597delC	p.P1199fs	LAYVCCVRQLEVVKSSDYCEYLRPP[p.P1199fs]STATAPWTSASSTRSAKWATSTGARCLTSGAAAACWRRCSATSRGRARSPRVRSSPVPTPPSRTLPKLCLALSPPSPPWWMTNLTTRRSTRRSCWTSPGMHTQTSRAPQPSRAQTWRTSPHCGIDTPVWLSQNCLRAPLTRTGRGLC*	YLRPPSTAT,CLTSGAAAA,TLPKLCLAL,GMHTQTSRA,WLSQNCLRA,SQNCLRAPL,SASSTRSAK,STRSAKWAT,KWATSTGAR,GARCLTSGA,AACWRRCSA,RGRARSPRV,RARSPRVRS,RVRSSPVPT,RTLPKLCLA,TTRRSTRRS,STRRSCWTS,RSCWTSPGM,TSRAPQPSR,LTRTGRGLC,SATSRGRAR,WWMTNLTTR,WMTNLTTRR,NLTTRRSTR,LTTRRSTRR,VWLSQNCLR,RAPLTRTGR,TATAPWTSA,ATAPWTSAS,APWTSASST,SPRVRSSPV,VPTPPSRTL,SPPWWMTNL,APQPSRAQT,RSAKWATST,AKWATSTGA,ALSPPSPPW,AQTWRTSPH,PPSTATAPW,CEYLRPPST,YLRPPSTATA,TSASSTRSAK,RTLPKLCLAL,STATAPWTSA,STRSAKWATS,SAKWATSTGA,GARCLTSGAA,AAACWRRCSA,CWRRCSATSR,TSRGRARSPR,RGRARSPRVR,RARSPRVRSS,RSPRVRSSPV,RVRSSPVPTP,RSSPVPTPPS,TTRRSTRRSC,STRRSCWTSP,TSRAPQPSRA,RAQTWRTSPH,TWRTSPHCGI,CSATSRGRAR,WWMTNLTTRR,TNLTTRRSTR,NLTTRRSTRR,QTSRAPQPSR,PVWLSQNCLR,WTSASSTRSA,RPPSTATAPW,TPPSRTLPKL,APQPSRAQTW,SPHCGIDTPV,TPVWLSQNCL,APLTRTGRGL,CEYLRPPSTA,SASSTRSAKW,WATSTGARCL,LALSPPSPPW,ALSPPSPPWW,RRSCWTSPGM,AQTWRTSPHC,LSQNCLRAPL,SQNCLRAPLT,LTSGAAAACW	STAD
PNRC1	c.217C>T	p.R73C	PRALPPTLFLPHFLGGDGPCLTPQP[p.R73C]CAPAALPNRSLAVAGGTPRAAPKKRR	LTPQPCAPA,TPQPCAPAA,CLTPQPCAPA,TPQPCAPAAL	CESC
PODN	c.903delC	p.I301fs	RHVPKHLPPALYKLHLKNNKLEKIP[p.I301fs]RGPSAS*	LEKIPRGPSA	STAD
PODNL1	c.449C>T	p.A150V	QLQHLCVAHNKLSVAPQFLPRSLRV[p.A150V]VDLAANQVMEIFPLTFGEKPALRSVY	FLPRSLRVV,RSLRVVDLA,VDLAANQVM,RVVDLAANQV,RSLRVVDLAA,LPRSLRVVDL	GBM
PODXL	c.486_487insC	p.S162fs	TATAKPNTTSSQNGAEDTTNSGGKS[p.S162fs]QPQCDHRPHIH*	QPQCDHRPHI,SQPQCDHRPH	GBM
POGZ	c.223G>T	p.G75W	SAPVPIAAHASVAGHLSTSTTVSSS[p.G75W]WAQNSDSTKKTLVTLIANNNAGNPLV	TSTTVSSSW,STSTTVSSSW	LUAD
POLA1	c.1809G>T	p.E603D	PFQSHFCVVSKPKDCIFPYAFKEVI[p.E603D]DKKNVKVEVAATERTLLGFFLAKVHK	YAFKEVIDK,AFKEVIDKK,YAFKEVIDKK,EVIDKKNVKV	CRC
POLE	c.1231G>T	p.V411L	EIGFQKDSQGEYKAPQCIHMDCLRW[p.V411L]LKRDSYLPVGSHNLKAAAKAKLGYDP	HMDCLRWLK,RWLKRDSYL,IHMDCLRWL,LRWLKRDSY,LKRDSYLPV,WLKRDSYLPV,IHMDCLRWLK,CLRWLKRDSY,HMDCLRWLKR,LRWLKRDSYL	CRC,UCEC
POLE	c.1376C>T	p.S459F	YDPVELDPEDMCRMATEQPQTLATY[p.S459F]FVSDAVATYYLYMKYVHPFIFALCTI	FVSDAVATY,ATYFVSDAV,QPQTLATYF,FVSDAVATYY,TLATYFVSDA,ATYFVSDAVA,YFVSDAVATY,LATYFVSDAV,EQPQTLATYF,QPQTLATYFV	CRC
POLE	c.1718G>T	p.R573L	ESGVFRSDIPCRFRMNPAAFDFLLQ[p.R573L]LVEKTLRHALEEEEKVPVEQVTNFEE	FLLQLVEKT,DFLLQLVEK,AAFDFLLQL,AAFDFLLQLV,FLLQLVEKTL,QLVEKTLRHA,LQLVEKTLRH	LUAD
POLE	c.857C>G	p.P286R	DDLVERPDPVVLAFDIETTKLPLKF[p.P286R]RDAETDQIMMISYMIDGQGYLITNRE	TTKLPLKFR,RDAETDQIM,KFRDAETDQI,ETTKLPLKFR,RDAETDQIMM	UCEC
POLM	c.290delC	p.P97fs	EETSAEEAVSWQERRMAAAPPGCTP[p.P97fs]QLCWT*	APPGCTPQL	STAD
POLQ	c.2579G>A	p.R860Q	NAVPFKSARKAVDEEEEAVEERRNM[p.R860Q]QTIWVTGRKGLTEREAAALIVEEARM	QTIWVTGRK,MQTIWVTGR,RNMQTIWVT,MQTIWVTGRK,NMQTIWVTGR,RNMQTIWVTG,EERRNMQTIW	CRC
POLR1C	c.994A>C	p.K332Q	IFSVESTGVLPPDVLVSEAIKVLMG[p.K332Q]QCRRFLDELDAVQMD*	KVLMGQCRR,VLMGQCRRF,LMGQCRRFL,VLMGQCRRFL,AIKVLMGQCR,KVLMGQCRRF,GQCRRFLDEL	KIRC
POLR3B	c.1114C>T	p.L372F	GDNKVDDRDYYGNKRLELAGQLLSL[p.L372F]FFEDLFKKFNSEMKKIADQVIPKQRA	LLSLFFEDL,SLFFEDLFK,LFFEDLFKK,LSLFFEDLF,FFEDLFKKF,LAGQLLSLF,AGQLLSLFF,QLLSLFFEDL,LSLFFEDLFK,SLFFEDLFKK,LFFEDLFKKF,ELAGQLLSLF,LAGQLLSLFF,LLSLFFEDLF	BLCA

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POM121L12	c.691C>A	p.P231T	GRRNLQPRPSAFKPLSKNGAVASFV[p.P231T]TRPGPLKPSLGPWSLSFCDDAWPSVL	FVTRPGPLK,GAVASFVTR,SFVTRPGPL,SFVTRPGPLK,ASFVTRPGPL,NGAVASFVTR	LUAD
POM121L12	c.725C>A	p.P242H	FKPLSKNGAVASFVPRPGPLKPSLG[p.P242H]HWSLSFCDDAWPSVLVQPAPSAIWDF	SLGHWSLSF,KPSLGHWSL,PSLGHWSLSF,LKPSLGHWSL,GPLKPSLGHW	LUAD
PON1	c.917G>A	p.R306Q	WVGCHPNGMKIFFYDSENPPASEVL[p.R306Q]QIQNILTEEPKVTQVYAENGTVLQGS	SEVLQIQNI,LQIQNILTE,PPASEVLQI,SEVLQIQNIL,NPPASEVLQI	UCEC
POP1	c.2248delA	p.K750fs	VASSPNGKESDLRRSEVPCAPMPKK[p.K750fs]LISHLMKWAHP*	LISHLMKWA,KLISHLMKW,KKLISHLMK,APMPKKLIS,MPKKLISHL,ISHLMKWAH,KLISHLMKWA,APMPKKLISH,MPKKLISHLM,KKLISHLMKW	STAD
POSTN	c.1522C>T	p.R508C	GAIHIFREIIKPAEKSLHEKLKQDK[p.R508C]CFSTFLSLLEAADLKELLTQPGDWTL	KQDKCFSTF,CFSTFLSLL,KCFSTFLSL,KQDKCFSTFL,LKQDKCFSTF,KCFSTFLSLL	CRC
POTEC	c.1519A>G	p.K507E	EEQNTGISQDEILTNKQKQIEVAEK[p.K507E]EMNSELSLSHKKEEDLLRENSMLQEE	AEKEMNSEL,KEMNSELSL,KEMNSELSLS,AEKEMNSELS	GBM,PRAD
POTEE	c.496G>A	p.V166M	DKLHRAAWWGKVPRKDLIVMLRDTD[p.V166M]MNKKDKQKRTALHLASANGNSEVVKL	MLRDTDMNKK	GBM
POTEE	c.862G>A	p.V288M	ADIESKNKHGLTPLLLGVHEQKQQV[p.V288M]MKFLIKKKANLNALDRYGRTALILAV	QVMKFLIKK,VMKFLIKKK,KQQVMKFLI,QQVMKFLIK,VHEQKQQVM,EQKQQVMKF,QVMKFLIKK,KQQVMKFLIK,QQVMKFLIKK,GVHEQKQQVM,HEQKQQVMKF	LUAD
POTEE	c.908G>T	p.R303I	LGVHEQKQQVVKFLIKKKANLNALD[p.R303I]IYGRTALILAVCCGSASIVSLLLEQN	IYGRTALIL,DIYGRTALI,KANLNALDI,ANLNALDIY,LDIYGRTAL,ALDIYGRTAL,IYGRTALILA,KANLNALDIY,NLNALDIYGR,KKANLNALDI	UCEC
POTEF	c.2022G>T	p.K674N	STLREEIAMLRLELDTMKHQSQLRE[p.K674N]NKYLEDIESVKKRNDNLLKALQLNEL	SQLRENKYL,RENKYLEDI,KHQSQLRENK,HQSQLRENKY,NKYLEDIESV	UCEC
POTEF	c.334A>G	p.S112G	DDSAMKTLRNKMGKWCCHCFPCCRG[p.S112G]GSKSKVGAWGDYDDSAFMEPRYHVRG	CCRGGSKSK	TGCT
POTEG	c.151G>A	p.D51N	KWCRHCFPWCRGSGKSNVGTSGDHD[p.D51N]NSAMKTLRSKMGKWCRHCFPWCRGSS	DNSAMKTLR,NSAMKTLRSK	SKCM
POTEG	c.407G>A	p.R136H	GSGKSKVGPWGDYDDSAFMEPRYHV[p.R136H]HREDLDKLIHRAAWWGKVPRKDLIVML	HVHREDLDK,FMEPRYHVH,FMEPRYHVHR	GBM
POU2F2	c.715A>G	p.T239A	RIKLGFTQGDVGLAMGKLYGNDFSQ[p.T239A]ATISRFEALNLSFKNMCKLKPLLEKW	ATISRFEAL,DFSQATISR,FSQATISRF,KLYGNDFSQA,SQATISRFEA,DFSQATISRF,YGNDFSQATI	DLBCL
POU2F2	c.715A>T	p.T239S	RIKLGFTQGDVGLAMGKLYGNDFSQ[p.T239S]STISRFEALNLSFKNMCKLKPLLEKW	STISRFEAL,FSQSTISRF,DFSQSTISR,DFSQSTISRF,YGNDFSQSTI,SQSTISRFEA	DLBCL
POU3F3	c.961G>T	p.D321Y	GGGGGAGPGLNSHDPHSDEDTPTSD[p.D321Y]YLEQFAKQFKQRRIKLGFTQADVGLA	YLEQFAKQF,DEDTPTSDY,TSDYLEQFAK,DYLEQFAKQF,TPTSDYLEQF	LUAD
PPARGC1B	c.403delC	p.P135fs	AFPALDGGDALSCTSASPAPSSAPP[p.P135fs]ALPRRSPRPQPLRWTSSHCCRSSSWPHPTQHQALTPRRKGPPGARQASDLKVNGLVLRRTAPKTRRLP*	KVNGLVLRR,LVLRRTAPK,SSAPPALPR,RSPRPQPLR,SSHCCRSSS,HQALTPRRK,GARQASDLK,RTAPKTRRL,PALPRRSPR,TQHQALTPR,APSSAPPAL,RPQPLRWTS,WPHPTQHQA,RRSPRPQPL,SHCCRSSSW,SPRPQPLRW,ASDLKVNGLV,GLVLRRTAPK,SSAPPALPRR,VLRRTAPKTR,RTAPKTRRLP,DLKVNGLVLR,SPAPSSAPPA,SPRPQPLRWT,RPQPLRWTSS,WPHPTQHQAL,TPRRKGPPGA,SSHCCRSSSW,SDLKVNGLVL	STAD
PPIL4	c.1146T>A	p.S382R	PKQDTKYDLILDEQAEDSKSSHSHT[p.S382R]RKKHKKKTHHCSEEKEDEDYMPIKNT	KSSHSHTRK,SSHSHTRKK,HSHTRKKHK,HTRKKHKKK,KSSHSHTRKK,HSHTRKKHKK,DSKSSHSHTR	CLL

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PPL	c.1362delC	p.P454fs	GESWELMDSAGNKLIAPAVCFVIPP[p.P454fs]QTLRPWLWLTAWAASTGACGRRQLGANARCSSGMRC*	TLRPWLWLT,WLWLTAWAA,WLTAWAAST,FVIPPQTLR,CFVIPPQTL,PQTLRPWLW,NARCSSGMR,TAWAASTGA,RPWLWLTAW,RQLGANARC,ANARCSSGM,IPPQTLRPW,TLRPWLWLTA,LTAWAASTGA,CGRRQLGANA,CFVIPPQTLR,WAASTGACGR,IPPQTLRPWL,RPWLWLTAWA,RQLGANARCS,GANARCSSGM	STAD
PPL	c.976C>T	p.H326Y	DWKEYLNLLICEESHLKYMEDYHQF[p.H326Y]YEDVKDAQELLRKVDSDLNQKYGPDF	YMEDYHQFY,KYMEDYHQFY,HQFYEDVKDA,YEDVKDAQEL	BLCA
PPM1E	c.931C>T	p.R311W	IHLHVNLVRQEMFPHDPAEALCRAF[p.R311W]WVTDERFVQKAARESLRCGTTGVVTF	RAFWVTDER,AFWVTDERF,EALCRAFWV,AEALCRAFW,WVTDERFVQK,RAFWVTDERF,AEALCRAFWV	KIRC
PPM1H	c.678delC	p.P226fs	NSRTLTRAASLRGGVGAPGSPSTPP[p.P226fs]HASLPRRRFPMSAWSSERLKVHSRKWTYR*	SLPRRRFPM,SAWSSERLK,ASLPRRRFP,RLKVHSRKW,KVHSRKWTY,PMSAWSSER,MSAWSSERL,FPMSAWSSE,LPRRRFPMS,HASLPRRRF,RRRFPMSAW,MSAWSSERLK,KVHSRKWTYR,STPPHASLPR,ASLPRRRFPM,SERLKVHSRK,RLKVHSRKWT,FPMSAWSSER,SPSTPPHASL,LPRRRFPMSA,RRFPMSAWSS,LKVHSRKWTY	STAD
PPP1R12C	c.1116delC	p.P372fs	LSSREKISLQDLSKERRPGGAGGPP[p.P372fs]SRTRMRGKKVPPNHPLQNPEPSMASPPRRTPALRVPCSLKRPPSPGALAS*	ALRVPCSLK,PSRTRMRGK,RTRMRGKKV,RMRGKKVPP,RGKKVPPNH,ASPPRRTPA,SLKRPPSPG,SPPRRTPAL,RPPSPGALA,KKVPPNHPL,LQNPEPSMA,SLKRPPSPGA,PSRTRMRGKK,RTRMRGKKVP,RMRGKKVPPN,MASPPRRTPA,ALRVPCSLKR,RPGGAGGPPS,HPLQNPEPSM,TPALRVPCSL,LKRPPSPGAL,GKKVPPNHPL,LQNPEPSMAS	STAD
PPP2R1A	c.536C>G	p.P179R	CYPRVSSAVKAELRQYFRNLCSDDT[p.P179R]RMVRRAAASKLGEFAKVLELDNVKSE	TRMVRRAAA,RMVRRAAAS,NLCSDDTRMV,RMVRRAAASK,RNLCSDDTRM	UCEC,UCS
PPP2R1A	c.547C>T	p.R183W	VSSAVKAELRQYFRNLCSDDTPMVR[p.R183W]WAAASKLGEFAKVLELDNVKSEIIPM	MVRWAAASK,DTPMVRWAA,TPMVRWAAA,VRWAAASKL,CSDDTPMVRW,MVRWAAASKL,DTPMVRWAAA,TPMVRWAAAS,WAAASKLGEF	CRC,UCS
PPP2R1A	c.656C>T	p.S219L	KVLELDNVKSEIIPMFSNLASDEQD[p.S219L]LVRLLAVEACVNIAQLLPQEDLEALV	DEQDLVRLL,NLASDEQDLV,DEQDLVRLLA	UCS
PPP2R1A	c.767C>T	p.S256F	IAQLLPQEDLEALVMPTLRQAAEDK[p.S256F]FWRVRYMVADKFTELQKAVGPEITKT	KFWRVRYMV,FWRVRYMVA,QAAEDKFWR,RQAAEDKFW,DKFWRVRYM,KFWRVRYMVA,QAAEDKFWRV,TLRQAAEDKF,AEDKFWRVRY	UCEC
PPP2R2B	c.977C>T	p.P326L	SKGTIRLCDMRASALCDRHTKFFEE[p.P326L]LEDPSNRSFFSEIISSISDVKFSHSG	RHTKFFEEL,LEDPSNRSF,ELEDPSNRSF,LEDPSNRSFF	CRC
PPP2R3B	c.1165delA	p.T389fs	RKVQKEGKISYADFVWFLISEEDKK[p.T389fs]HRPASSTGSAAWTWTGTAPCPCSSSSTSTRSSAEGWTAWPSRPCPSRTASARCWTWSSRGLKGRSRCRT*	WTWSSRGLK,CSSSSTSTR,STGSAAWTW,SSTSTRSSA,RTASARCWT,SARCWTWSS,EGWTAWPSR,WTWTGTAPC,WTAWPSRPC,RPASSTGSA,RPCPSRTAS,SSAEGWTAW,KKHRPASST,ASSTGSAAW,RSSAEGWTA,AEGWTAWPS,TASARCWTW,RTASARCWTW,SSSTSTRSSA,SARCWTWSSR,CWTWSSRGLK,SSRGLKGRSR,RGLKGRSRCR,TWSSRGLKGR,SAAWTWTGTA,RPASSTGSAA,RPCPSRTASA,SSTGSAAWTW,RSSAEGWTAW,RCWTWSSRGL,SEEDKKHRPA	STAD
PPP2R3B	c.930C>A	p.F310L	ELRRSSFLQNVALLEEEADINQLTE[p.F310L]LFSYEHFYVIYCKFWELDTDHDLLID	LTELFSYEH,NQLTELFSY,ELFSYEHFY,ADINQLTEL,TELFSYEHF,ELFSYEHFYV,LFSYEHFYVI,INQLTELFSY,ADINQLTELF,LTELFSYEHF,TELFSYEHFY	UCEC
PPP2R5C	c.776C>A	p.S259Y	GFALPLKEEHKIFLLKVLLPLHKVK[p.S259Y]YLSVYHPQLAYCVVQFLEKDSTLTEP	YLSVYHPQL,KYLSVYHPQ,KVKYLSVYH,LPLHKVKYL,LHKVKYLSV,HKVKYLSVY,YLSVYHPQLA,LLPLHKVKYL,KYLSVYHPQL,KVKYLSVYHP,VLLPLHKVKY,LHKVKYLSVY,HKVKYLSVYH	CRC
PPP4R1	c.1791G>C	p.L597F	DSVPLISDAVENMDSTLHYIHSDSD[p.L597F]FSNNSSFSPDEERRTKVQDVVPQALL	HYIHSDSDF,SDFSNNSSF,LHYIHSDSDF	CESC
PPP6C	c.901C>T	p.R301C	LVHEGYKFMFDEKLVTVWSAPNYCY[p.R301C]CCGNIASIMVFKDVNTREPKLFRAVP	CYCCGNIASI,YCCGNIASIM	SKCM

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PPT2	c.794G>T	p.R265L	WQSSFFGFYDANETVLEMEEQLVYL[p.R265L]LDSFGLKTLLARGAIVRCPMAGISHT	YLLDSFGLK,VYLLDSFGL,QLVYLLDSF,MEEQLVYLL,LVYLLDSFGL,YLLDSFGLKT,LLDSFGLKTL,EQLVYLLDSF	LUAD
PRAM1	c.802G>A	p.A268T	QPEFSEAAQTPLWKPQSSEPKRDSS[p.A268T]TFPKKASQPPLSDFPKKPPQPELGDL	RDSSTFPKK,EPKRDSSTF,SEPKRDSSTF	UCEC
PRAMEF11	c.251G>C	p.C84S	KLQVLDLQDVCENFWMVWSEAMAHG[p.C84S]SFLNAKRNKTPVQDCPRMRERQPLTV	MAHGSFLNA,SFLNAKRNK,HGSFLNAKR,EAMAHGSFL,SEAMAHGSF,AMAHGSFLNA,MAHGSFLNAK,GSFLNAKRNK,WSEAMAHGSF,SEAMAHGSFL	SKCM
PRAMEF11	c.311G>A	p.R104Q	AMAHGCFLNAKRNKTPVQDCPRMRE[p.R104Q]QQPLTVFVELWLKNRTLDEYLTCLLL	RMREQQPLT,EQQPLTVFV,REQQPLTVF,RMREQQPLTV,CPRMREQQPL,MREQQPLTVF,REQQPLTVFV	CLL
PRAMEF4	c.743G>A	p.R248H	LTQFTPYLGHMRNLQKLILSHMDVS[p.R248H]HYVSPEQKKEIVTQFTTQFLKLRCLQ	LSHMDVSHY,SHMDVSHYV,VSHYVSPEQK,ILSHMDVSHY,LSHMDVSHYV	CRC
PRAMEF8	c.1342A>G	p.I448V	ALCWGRFAELGAELMKTPRDLRQPK[p.I448V]VIVFCTVPCPRCGIRASYDLEPSHCL	LRQPKVIVF,TPRDLRQPKV,DLRQPKVIVF,QPKVIVFCTV	TGCT
PRAMEF8	c.956G>A	p.R319H	LEMVVMTDCLLSESDLKHLSWCPSI[p.R319H]HQLKELDLRGVTLTHFSPEPLTGLLE	SWCPSIHQL,HLSWCPSIH,SWCPSIHQLK,CPSIHQLKEL,LSWCPSIHQL	PRAD
PRB1	c.820delC	p.R274fs	KPQGPPPPGKPQGPPAQGGSKSQSA[p.R274fs]DLLQESHKDHPNKKATILKVPHLQQEAIPSSLRHLLLDSPRDHHALLKGADLPDLPSDSLPSHLGFNDRK*	HPNKKATIL,VPHLQQEAI,IPSSLRHLL,SPRDHHALL,LPDLPSDSL,DSLPSHLGF,SKSQSADLL,LQQEAIPSS,QQEAIPSSL,LPSDSLPSH,LQQEAIPSSL,AIPSSLRHLL,LLKGADLPDL,SADLLQESHK,SPRDHHALLK,EAIPSSLRHL,IPSSLRHLLL,LPSDSLPSHL,KKATILKVPH,LKVPHLQQEA,SDSLPSHLGF	HNSC
PRDM1	c.1763C>G	p.S588C	PYPLKKQNGKIKYECNVCAKTFGQL[p.S588C]CNLKVHLRVHSGERPFKCQTCNKGFT	KTFGQLCNL,GQLCNLKVH,KTFGQLCNLK,QLCNLKVHLR,AKTFGQLCNL,GQLCNLKVHL	MM
PRDM16	c.3107C>T	p.P1036L	HLCNRCFGQQTNLDRHLKKHEHENA[p.P1036L]LVSQHPGVLTNHLGTSASSPTSESDN	ALVSQHPGV,KKHEHENAL,HEHENALVS,HENALVSQH,ALVSQHPGVL,LKKHEHENAL,KKHEHENALV	LUAD
PRDM16	c.811G>C	p.E271Q	RRHKKYTCGSVGAALYEGLAEELKP[p.E271Q]QGLGGGSGQAHECKDCERMFPNKYSL	AEELKPQGL	BLCA
PRDM4	c.2404T>A	p.*802K	DSVGTEDCRINSAVYSADESLSAHK[p.*802K]KKEKKQAILDENANGKIHITSYLL*	KIHITSYLL,SAHKKKEKK,NGKIHITSY,GKIHITSYL,ILDENANGKI,SLSAHKKKEK,AILDENANGK,ANGKIHITSY,NGKIHITSYL,GKIHITSYLL	CLL
PRDM7	c.1159A>C	p.M387L	GQELGIRSSIEPAESLGQAVNCWSG[p.M387L]LGMSMARNWASSGAASGRKSSWQGEN	SGLGMSMAR,QAVNCWSGL,VNCWSGLGM,CWSGLGMSM,LGMSMARNW,GQAVNCWSGL,AVNCWSGLGM,NCWSGLGMSM	PRAD
PRELP	c.601G>T	p.D201Y	LRLSQNHISRIPPGVFSKLENLLLL[p.D201Y]YLQHNRLSDGVFKPDTFHGLKNLMQL	KLENLLLLY,LLYLQHNRL,LLLYLQHNR,LENLLLLYL,KLENLLLYL,LLLYLQHNRL,SKLENLLLLY,LLLLYLQHNR	LUAD
PREP	c.1407C>A	p.F469L	SKDGTKIPMFIVHKKGIKLDGSHPA[p.F469L]LLYGYGGFNISITPNYSVSRLIFVRH	KLDGSHPAL,SHPALLYGY,ALLYGYGGF,KLDGSHPALL,LLYGYGGFNI,GSHPALLYGY,LDGSHPALLY,IKLDGSHPAL	CESC
PREX1	c.2191G>A	p.V731I	AKEIIKIPDQPDTLCFQIRGAAPPY[p.V731I]IYAVGRGSEAMAAGLCAGQCILKVNG	AAPPYIYAV,RGAAPPYIY,GAAPPYIYAV,QIRGAAPPYI,RGAAPPYIYA,IRGAAPPYIY	CRC
PREX1	c.3736G>A	p.E1246K	CLEHLFNQVDSINALLKGPVMSRAF[p.E1246K]KETKHFPMNHSLQEFKQKEECTIRGR	MSRAFKETK,FKETKHFPM,RAFKETKHF,VMSRAFKETK,KGPVMSRAFK,MSRAFKETKH,AFKETKHFPM,SRAFKETKHF	UCEC
PREX2	c.1088G>A	p.R363Q	WFVCMAKTPEEKHEWFEAILKERER[p.R363Q]QKGLKLGMEQDTWVMISEQGEKLYKM	ILKERERQK,RQKGLKLGM,KERERQKGL,RERQKGLKL,AILKERERQK,KERERQKGLK	BRCA
PREX2	c.1686_1687insT	p.R562fs	CDNGFMHHVLEKSEFKDEPLLFRFF[p.R562fs]FG*	EPLLFRFFF,DEPLLFRFFF	STAD
PRG4	c.2023A>C	p.N675H	PTTPEEPTPTTPEEPAPTTPKAAAP[p.N675H]HTPKEPAPTTPKEPAPTTPKEPAPTT	KAAAPHTPK,APHTPKEPA	CLL

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PRIC285	c.3865G>C	p.E1289Q	LFWVQIVLWRQGFYYPLGIVREVLP[p.E1289Q]QASTWEQGLRILGLEYSLRVPPSDQA	IVREVLPQA,REVLPQAST,EVLPQASTW,GIVREVLPQA,QASTWEQGLR,REVLPQASTW	BLCA
PRKAA2	c.1220G>A	p.R407Q	CPLDALNTTKPKSLAVKKAKWHLGI[p.R407Q]QSQSKPYDIMAEVYRAMKQLDFEWKV	GIQSQSKPY,KAKWHLGIQS,LGIQSQSKPY,IQSQSKPYDI	CRC
PRKAB1	c.311C>A	p.P104H	PTVFRWTGGGKEVYLSGSFNNWSKL[p.P104H]HLTRSHNNFVAILDLPEGEHQYKFFV	NWSKLHLTR,HLTRSHNNF,FNNWSKLHL,SKLHLTRSH,HLTRSHNNFV,SFNNWSKLHL,NNWSKLHLTR,LHLTRSHNNF	CLL
PRKAR2B	c.926C>T	p.S309L	ERLKVVDVIGTKVYNDGEQIIAQGD[p.S309L]LADSFFIVESGEVKITMKRKGKSEVE	DLADSFFIV,AQGDLADSF,GDLADSFFI,AQGDLADSFF,IAQGDLADSF,GEQIIAQGDL,GDLADSFFIV	CRC
PRKCD	c.1294delG	p.G432fs	FLTHLICTFQTKDHLFFVMEFLNGG[p.G432fs]T*	FVMEFLNGGT	GBM
PRKCE	c.470_471insG	p.Q157fs	SSGEAPKDNEERVFRERMRPRKRQG[p.Q157fs]GRQAQGPSGQRPQVHGHLSSAAHLLLPLQRLHLGCHRKAGIPVSSLHLRGPQAVPRAHNHKVCWVKEAGDPRPGGLPAVQRQHAPQVRYPQLQGPYLLRSLWVPALGTLAAGFAV*	HLSSAAHLL,YLLRSLWVP,GTLAAGFAV,QVHGHLSSA,SLHLRGPQA,LLRSLWVPA,RLHLGCHRK,AVPRAHNHK,PYLLRSLWV,LWVPALGTL,RPRKRQGGR,HNHKVCWVK,VQRQHAPQV,RQHAPQVRY,RSLWVPALG,RYPQLQGPY,WVKEAGDPR,QLQGPYLLR,SAAHLLLPL,GPSGQRPQV,RPQVHGHLS,VPRAHNHKV,DPRPGGLPA,APQVRYPQL,YPQLQGPYL,VPALGTLAA,ALGTLAAGF,RKRQGGRQA,GQRPQVHGH,HGHLSSAAH,GHLSSAAHL,LSSAAHLLL,LQRLHLGCH,CHRKAGIPV,KAGIPVSSL,LHLRGPQAV,RAHNHKVCW,PQLQGPYLL,GPYLLRSLW,LRSLWVPAL,HLSSAAHLL,LLLPLQRLHL,SLHLRGPQAV,YLLRSLWVPA,LLRSLWVPAL,SLWVPALGTL,ALGTLAAGFA,AAHLLLPLQR,RYPQLQGPYL,RMRPRKRQGG,LQRLHLGCHR,RLHLGCHRKA,SSLHLRGPQA,HLRGPQAVPR,QAVPRAHNHK,RAHNHKVCWV,VQRQHAPQVR,VRYPQLQGPY,SSAAHLLLPL,RPQVHGHLSS,VPRAHNHKVC,DPRPGGLPAV,YPQLQGPYLL,GPYLLRSLWV,HLGCHRKAGI,GQRPQVHGHL,HGHLSSAAHL,GHLSSAAHLL,RKAGIPVSSL,AGIPVSSLHL,RQHAPQVRYP,LQGPYLLRSL,VPALGTLAAG	KIRC
PRKCG	c.1033C>T	p.R345C	SSSPIPSPSPSPTDPKRCFFGASPG[p.R345C]CLHISDFSFLMVLGKGSFGKVMLAER	CLHISDFSF,CLHISDFSFL,SPGCLHISDF,GCLHISDFSF	STAD
PRKCI	c.1438C>T	p.R480C	IVGSSDNPDQNTEDYLFQVILEKQI[p.R480C]CIPRSLSVKAASVLKSFLNKDPKERL	KQICIPRSL,CIPRSLSVK,KQICIPRSLS,LEKQICIPRS	CRC
PRKCQ	c.971C>T	p.A324V	GMNVHHRCQTKVANLCGINQKLMAE[p.A324V]VLAMIESTQQARCLRDTEQIFREGPV	KLMAEVLAM,LMAEVLAMI,NQKLMAEVL,AEVLAMIES,GINQKLMAEV,KLMAEVLAMI,QKLMAEVLAM,AEVLAMIEST	UCEC
PRKDC	c.10702C>G	p.Q3568E	DTSTGHKNKEFVARIKSKLDQGGVI[p.Q3568E]EDFINALDQLSNPELLFKDWSNDVRA	GVIEDFINA,GVIEDFINAL	CESC
PRKRA	c.366G>T	p.K122N	NILKANASICFAVPDPLMPDPSKQP[p.K122N]NNQLNPIGSLQELAIHHGWRLPEYTL	QPNNQLNPI,KQPNNQLNPI	CRC
PRMT8	c.84delC	p.S28fs	SSRCLLLRRKMAENAAESTEVNSPP[p.S28fs]PSPPSPSSLLSPCNASIMCPLNPAAQDGARCPSC*	LLSPCNASI,SIMCPLNPA,IMCPLNPAA,SPPSPSSLL,LSPCNASIM,SLLSPCNASI,SIMCPLNPAA,LLSPCNASIM,PPSPPSPSSL	STAD
PRMT8	c.91T>C	p.S31P	SSRCLLLRRKMAENAAESTEVNSPP[p.S31P]PQPPQPVVPAKPVQCVHHVSTQPSCP	SPPPQPPQPV	BLCA
PRODH	c.1579C>G	p.L527V	TVRFALRRMEELGLHPADHRVYFGQ[p.L527V]VLGMCDQISFPLGQAGYPVYKYVPYG	VYFGQVLGM,RVYFGQVLG,HRVYFGQVL,RVYFGQVLGM,VLGMCDQISF,GQVLGMCDQI	TGCT
PROKR2	c.889G>A	p.V297I	KTVLVLMCILTAYVLCWAPFYGFTI[p.V297I]IRDFFPTVFVKEKHYLTAFYVVECIA	IIRDFFPTV,GFTIIRDFF,TIIRDFFPT,APFYGFTII,YGFTIIRDF,IRDFFPTVF,TIIRDFFPTV,FYGFTIIRDF,YGFTIIRDFF,APFYGFTIIR,FTIIRDFFPT,IIRDFFPTVF	GBM

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PROX1	c.1774delT	p.F592fs	SPYSGSAMQEGLSPNHLKKAKLMFF[p.F592fs]IPVIPAPIC*	KLMFFIPVI,FIPVIPAPI,KAKLMFFIP,MFFIPVIPA,KKAKLMFFI,AKLMFFIPV,LMFFIPVIPA,FFIPVIPAPI,KAKLMFFIPV,AKLMFFIPVI	STAD
PROX1	c.674T>A	p.V225D	PRESYRENKRKQKLPQQQQQSFQQL[p.V225D]DSARKEQKREERRQLKQQLEDMQKQL	SFQQLDSAR,QSFQQLDSAR	KIRC
PRPF31	c.865C>T	p.R289W	STSVLPHTGYIYHSDIVQSLPPDLR[p.R289W]WKAARLVAAKCTLAARVDSFHESTEG	RWKAARLVA,DLRWKAARL,WKAARLVAA,LRWKAARLV,LPPDLRWKA,SLPPDLRWKA,QSLPPDLRWK,RWKAARLVAA,DLRWKAARLV,VQSLPPDLRW,LRWKAARLVA,LPPDLRWKAA	TGCT
PRPF6	c.2288G>T	p.R763L	KCPHSTPLWLLLSRLEEKIGQLTRA[p.R763L]LAILEKSRLKNPKNPGLWLESVRLEY	QLTRALAIL,KIGQLTRAL,GQLTRALAI,ALAILEKSRL,LTRALAILEK,KIGQLTRALA,RALAILEKSR,EKIGQLTRAL,GQLTRALAIL	LUAD
PRRC2C	c.5647C>A	p.P1883T	SASIPILASALASTSAPTPAPAASS[p.P1883T]TAAPVITAPTIPASAPTASVPLAPAS	AASSTAAPV,STAAPVITA,TPAPAASST,APAASSTAA,ASSTAAPVI,TAAPVITAPT,TPAPAASSTA,APAASSTAAP,AASSTAAPVI	KIRC
PRRX1	c.587C>T	p.A196V	DVTAVEQPIVPRPAPRPTDYLSWGT[p.A196V]VSPYSAMATYSATCANNSPAQGINMA	LSWGTVSPY,YLSWGTVSP,TVSPYSAMA,GTVSPYSAM,TDYLSWGTV,PTDYLSWGTV,YLSWGTVSPY,VSPYSAMATY,WGTVSPYSAM	BRCA
PRSS1	c.319G>A	p.D107N	EGNEQFINAAKIIRHPQYDRKTLNN[p.D107N]NIMLIKLSSRAVINARVSTISLPTAP	TLNNNIMLI,KTLNNNIML,RKTLNNNIM,KTLNNNIMLI,TLNNNIMLIK,NIMLIKLSSR,RKTLNNNIML	HNSC
PRSS36	c.2038delC	p.L680fs	LPQGHQVSRLVISIRLPQHLGLRPP[p.L680fs]WPSWS*	GLRPPWPSW,QHLGLRPPW,PQHLGLRPPW,LGLRPPWPSW	STAD
PRSSS7	c.115G>C	p.E39Q	TVATALMLPVKPPAGSWGAQIIGGH[p.E39Q]QVTPHSRPYMASVRFGGQHHCGGFLL	AQIIGGHQV,QVTPHSRPY,HQVTPHSRPY,AQIIGGHQVT	LUSC
PSD2	c.766delG	p.G256fs	NVLSRLSLMAMPNGFHEDGPQGPGG[p.G256fs]MRMMMRRTRTSC*	GGMRMMMRR,GMRMMMRRT,RMMMRRTRT,MMMRRTRTS,MMRRTRTSC,GPGGMRMMM,PQGPGGMRM,MMMRRTRTSC,GMRMMMRRTR,RMMMRRTRTS,GPQGPGGMRM,PQGPGGMRMM	STAD
PSD3	c.1687A>C	p.T563P	PEIAFWGSNAGVKTTRLEAHSEMGS[p.T563P]PEILEKETPENLSNGTSSNVEAAKRL	MGSPEILEK,SEMGSPEIL,EMGSPEILEK,AHSEMGSPEI	KIRC
PSG8	c.1189C>T	p.R397C	FQLSGQKLFIPQITTKHSGLYACSV[p.R397C]CNSATGKESSKSMTVKVSGKRIPVSL	SVCNSATGK,GLYACSVCNS,CSVCNSATGK	CRC
PSG8	c.958C>T	p.R320C	LILPSVTRNETGPYQCEIRDQYGGI[p.R320C]CSYPVTLNVLYGPDLPRIYPSFTYYR	DQYGGICSY,CSYPVTLNV,QYGGICSYPV,RDQYGGICSY,GGICSYPVTL,CSYPVTLNVL	CRC
PSG9	c.1210G>A	p.E404K	LFIPQITRNHSGLYACSVHNSATGK[p.E404K]KISKSMTVKVSGPCHGDLTESQS*	KISKSMTVK,SATGKKISK,KKISKSMTV,KISKSMTVKV,SVHN5ATGKK	SKCM
PSMD11	c.14C>T	p.A5V	MAAA[p.A5V]VVVEFQRAQSLLSTDREASIDILHSI	MAAAVVVEF,AAAVVVEFQR	TGCT
PSMD12	c.602G>A	p.R201Q	SMEKKERVEFILEQMRLCLAVKDYI[p.R201Q]QTQIISKKINTKFFQEENTEKLKLKY	YIQTQIISK,IQTQIISKK,KDYIQTQII,AVKDYIQTQI,YIQTQIISKK,IQTQIISKKI	CRC
PSME3	c.691C>T	p.R231W	IAKYPHVEDYRRTVTEIDEKEYISL[p.R231W]WLIISELRNQYVTLHDMILKNIEKIK	SLWLIISEL,KEYISLWLI,EYISLWLII,DEKEYISLW,SLWLIISELR,KEYISLWLII,ISLWLIISEL,DEKEYISLWL	CESC
PSME4	c.1483A>G	p.N495D	GGRWFPEGPTHMLPLLMRALPGVDP[p.N495D]DDFSKCMITFQFIATFSTLVPLVDCS	GVDPDDFSK,LPGVDPDDF,DDFSKCMITF,DPDDFSKCMI	TGCT
PSPH	c.433G>A	p.V145I	IRELVSRLQERNVQVFLISGGFRSI[p.V145I]IEHVASKLNIPATNVFANRLKFYFNG	SIIEHVASK,ISGGFRSII,SIIEHVASKL,LISGGFRSII,RSIIEHVASK,GFRSIIEHVA,IEHVASKLNI	GBM
PTCH1	c.2066C>A	p.P689H	LRTEYDPHTHVYYTTAEPRSEISVQ[p.P689H]HVTVTQDTLSCQSPESTSSTRDLLSQ	EISVQHVTV,SEISVQHVT,SEISVQHVTV,VQHVTVTQDT	KIRC

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PTCH1	c.3921delC	p.P1307fs	RQQPHLDSGSLPPGRQGQQPRRDPP[p.P1307fs]EKACGHPPTDRAETLLKFLLKGILALAIGPAGALAGPVLTTLGTQRPLPWAAPCPATASPSPL*	FLLKGILAL,LLKGILALA,ILALAIGPA,ALAIGPAGA,LLKFLLKGI,AIGPAGALA,ALAGPVLTT,ETLLKFLLK,KFLLKGILA,TQRPLPWAA,WAAPCPATA,LAIGPAGAL,RPLPWAAPC,LPWAAPCPA,LKFLLKGIL,LKGILALAI,AGALAGPVL,LAGPVLTTL,LGTQRPLPW,AETLLKFLL,TLLKFLLKGI,FLLKGILALA,LLKGILALAI,ALAIGPAGAL,ALAGPVLTTL,KFLLKGILAL,HPPTDRAETL,GPAGALAGPV,CPATASPSPL,LLKFLLKGIL,TDRAETLLKF,LKFLLKGILA,TQRPLPWAAP,LPWAAPCPAT	STAD
PTCHD3	c.1764delT	p.F588fs	KKFCCFPFGSVPDEHGTDIHPISLF[p.F588fs]LETILAPFSQGVSPSIL*	SLFLETILA,FLETILAPF,ILAPFSQGV,DIHPISLFL,ISLFLETIL,FSQGVSPSI,SQGVSPSIL,HPISLFLET,LETILAPFS,TILAPFSQGV,LFLETILAPF,HPISLFLETI,FSQGVSPSIL	STAD
PTEN	c.388C>G	p.R130G	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130G]GTGVMICAYLLHRGKFLKAQEALDFY	GTGVMICAY,GGTGVMICAY,KAGKGGTGVM	UCEC
PTEN	c.389G>A	p.R130Q	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130Q]QTGVMICAYLLHRGKFLKAQEALDFY	QTGVMICAY,GKGQTGVMI,GQTGVMICAY,KAGKGQTGVM	CESC,CRC,UCEC
PTEN	c.389G>C	p.R130P	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130P]PTGVMICAYLLHRGKFLKAQEALDFY	PTGVMICAY,GKGPTGVMI,GPTGVMICAY,KAGKGPTGVM	UCEC
PTEN	c.389G>T	p.R130L	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130L]LTGVMICAYLLHRGKFLKAQEALDFY	LTGVMICAY,GLTGVMICA,KAGKGLTGV,GKGLTGVMI,GLTGVMICAY,KAGKGLTGVM	UCEC
PTEN	c.407G>A	p.C136Y	WLSEDDNHVAAIHCKAGKGRTGVMI[p.C136Y]YAYLLHRGKFLKAQEALDFYGEVRTR	GVMIYAYLL,VMIYAYLLH,RTGVMIYAY,KGRTGVMIY,VMIYAYLLHR,GVMIYAYLLH,KGRTGVMIYA,RTGVMIYAYL,GKGRTGVMIY,GRTGVMIYAY	GBM
PTEN	c.509G>A	p.S170N	FLKAQEALDFYGEVRTRDKKGVTIP[p.S170N]NQRRYVYYYSYLLKNHLDYRPVALLF	VTIPNQRRY,NQRRYVYYY,IPNQRRYVY,GVTIPNQRRY,TIPNQRRYVY,VTIPNQRRYV,IPNQRRYVYY	GBM
PTEN	c.518G>A	p.R173H	AQEALDFYGEVRTRDKKGVTIPSQR[p.R173H]HYVYYYSYLLKNHLDYRPVALLFHKM	TIPSQRHYV,HYVYYYSYL,SQRHYVYYY,RHYVYYYSY,VTIPSQRHY,IPSQRHYVY,PSQRHYVYY,PSQRHYVYYY,VTIPSQRHYV,RHYVYYYSYL,HYVYYYSYLL,SQRHYVYYYS,GVTIPSQRHY,TIPSQRHYVY,QRHYVYYYSY,IPSQRHYVYY	GBM
PTEN	c.701G>T	p.R234L	GTCNPQFVVCQLKVKIYSSNSGPTR[p.R234L]LEDKFMYFEFPQPLPVCGDIKVEFFH	RLEDKFMYF,YSSNSGPTRL,TRLEDKFMYF,LEDKFMYFEF	LUAD
PTEN	c.795delA	p.L265fs	EFPQPLPVCGDIKVEFFHKQNKMLK[p.L265fs]RTKCFTFG*	KMLKRTKCF,MLKRTKCFT,LKRTKCFTF,MLKRTKCFTF,KQNKMLKRTK,KMLKRTKCFT,NKMLKRTKCF	STAD
PTEN	c.830C>T	p.T277I	DIKVEFFHKQNKMLKKDKMFHFWVN[p.T277I]IFFIPGPEETSEKVENGSLCDQEIDS	KMFHFWVNI,MFHFWVNIF,FHFWVNIFF,HFWVNIFFI,KMFHFWVNIF,MFHFWVNIFF,FHFWVNIFFI	GBM
PTGR1	c.119A>C	p.E40A	GYPTNSDFELKTAELPPLKNGEVLL[p.E40A]AALFLTVDPYMRVAAKRLKEGDTMMG	VLLAALFLT,LLAALFLTV,EVLLAALFL,GEVLLAALF,VLLAALFLTV,AALFLTVDPY,LKNGEVLLAA,GEVLLAALFL	TGCT
PTH2	c.64C>G	p.L22V	METRQVSRSPRVRLLLLLLLL[p.L22V]VVVPWGVRTASGVALPPVGVLSLRPP	LLLLLLVVV,LLVVVPWGV,LVVVPWGVR,LLLLVVVPW,RLLLLLLLV,LLLLLLLVVV,LLLVVVPWGV,LLVVVPWGVR,LLLLLVVVPW	PRAD
PTPDC1	c.1288C>T	p.R430W	AVAADFDNRGMIFSNEQQFDPLWKR[p.R430W]WNVECLQPLTHLKRRLSYSDSDLKRA	WKRWNVECL,WNVECLQPL,LWKRWNVECL,RWNVECLQPL,QQFDPLWKRW	CRC
PTPN11	c.1508G>T	p.G503V	IIREKGVDCDIDVPKTIQMVRSQRS[p.G503V]VMVQTEAQYRFIYMAVQHYIETLQRR	QMVRSQRSV,MVRSQRSVM,RSVMVQTEA,VMVQTEAQY,SQRSVMVQT,IQMVRSQRSV,SVMVQTEAQY,MVRSQRSVMV,QMVRSQRSVM	LUAD
PTPN11	c.226G>A	p.E76K	VTHIKIQNTGDYYDLYGGEKFATLA[p.E76K]KLVQYYMEHHGQLKEKNGDVIELKYP	KLVQYYMEH,ATLAKLVQY,LAKLVQYYM,TLAKLVQYY,EKFATLAKL,TLAKLVQYYM,ATLAKLVQYY,FATLAKLVQY,GEKFATLAKL,KLVQYYMEHH	MM
PTPN12	c.2294G>A	p.R765Q	PPTFSDKREQISENPTEATDIGFGN[p.R765Q]QCGKPKGPRDPPSEWT*	IGFGNQCGK	CRC
PTPN13	c.2660C>T	p.S887L	SYQHKFQLQMRARQSNQDAQDIERA[p.S887L]LFRSLNLQAESVRGFNMGRAISTGSL	RALFRSLNL,LFRSLNLQA,AQDIERALF,IERALFRSL,ALFRSLNLQA	CRC

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PTPN13	c.6199G>A	p.E2067K	YIQEDDIYDDSQEAEVIQSLLDVVD[p.E2067K]KEAQNLLNENNAAGYSCGPGTLKMNG	QSLLDVVDK,SLLDVVDKEA	LUAD
PTPN14	c.2147_2149delAGG	p.E716del	QYHHKKTFSDATMLIHSSESEEEEE[p.E716del]APESVPQIPMLREKMEYSAQLQAALARI	SESEEEEEA	GBM
PTPN14	c.856G>A	p.E286K	THNKSTILVELINKEETALFHTDDI[p.E286K]KNAKYISRLFATRHKFYKQNKICTEQ	ALFHTDDIK,HTDDIKNAK,KNAKYISRL,HTDDIKNAKY,TALFHTDDIK,DIKNAKYISR,IKNAKYISRL,KNAKYISRLF	MM
PTPN18	c.1113_1118delGACGGG	p.TG378del	TYAVVQKRGAPAGAGSGTQTGTGTG[p.TG378del]ARSAEEAPLYSKVTPRAQRPGAHAEDARGTL	QTGTGTGAR	UCS
PTPN4	c.957delT	p.N319fs	NLWKACVEHHTFFRLDRPLPPQKNF[p.N319fs]LHIILH*	QKNFLHIIL,RPLPPQKNFL,LPPQKNFLHI	STAD
PTPRB	c.2178A>T	p.Q726H	SLTPGRLYTVTITTRSGKYENHSFS[p.Q726H]HERTVPDKVQGVSVSNSARSDYLRVS	HSFSHERTV,ENHSFSHER,FSHERTVPDK,GKYENHSFSH	TGCT
PTPRB	c.4678G>A	p.D1560N	ENPNSNSKSFNIKLGAEMESLGGKC[p.D1560N]NPTQQKFCDGPLKPHTAYRISIRAFT	KCNPTQQKF,GGKCNPTQQK,GKCNPTQQKF	SKCM
PTPRC	c.2685A>C	p.Q895H	GLEAENKVDVYGYVVKLRRQRCLMV[p.Q895H]HVEAQYILIHQALVEYNQFGETEVNL	RQRCLMVHV,LMVHVEAQY,MVHVEAQYI,VHVEAQYIL,LMVHVEAQYI,RQRCLMVHVE,CLMVHVEAQY,MVHVEAQYIL	STAD
PTPRF	c.3521G>A	p.R1174Q	PRWSTPEELELDELLEAIEQGGEEQ[p.R1174Q]QRRRRQAERLKPYVAAQLDVLPETFT	EQQRRRRQA,QQRRRRQAER	PRAD
PTPRJ	c.1000G>T	p.G334W	HDESLVGPVDPSSGQQSRDTEVLLV[p.G334W]WLEPGTRYNATVYSQAANGTEGQPQA	LVWLEPGTR,RDTEVLLVW,VWLEPGTRY,VLLVWLEPGT,WLEPGTRYNA,LVWLEPGTRY,RDTEVLLVWL	LUAD
PTPRT	c.2783G>T	p.R928L	SWDTAKEDENRNKNRYGNIISYDHS[p.R928L]LVRLLVLDGDPHSDYINANYIDGYHR	IISYDHSLV,NIISYDHSL,ISYDHSLVR,SYDHSLVRL,HSLVRLLVL,YDHSLVRLL,NIISYDHSLV,IISYDHSLVR,SYDHSLVRLL,ISYDHSLVRL,YDHSLVRLLV	LUAD
PTPRT	c.3224delC	p.P1075fs	WPDHGVPCYATGLLGFVRQVKFLNP[p.P1075fs]RKLGP*	RQVKFLNPR,QVKFLNPRK,VKFLNPRKL,RQVKFLNPRK	STAD
PTPRU	c.1675C>T	p.P559S	VNVPGPRRTISKLRNETYHVFSNLH[p.P559S]SGTTYLFSVRARTGKGFGQAALTEIT	NLHSGTTYL,LHSGTTYLF,SNLHSGTTY,FSNLHSGTTY,NLHSGTTYLF,SGTTYLFSVR,HVFSNLHSGT,HSGTTYLFSV,SNLHSGTTYL	LUAD
PTPRU	c.4300G>A	p.D1434N	FFAAKTLRNYKPNMVETMDQYHFCY[p.D1434N]NVALEYLEGLESR*	CYNVALEYL,FCYNVALEY,DQYHFCYNV,YHFCYNVAL,QYHFCYNVAL,HFCYNVALEY,NVALEYLEGL,DQYHFCYNVA,MDQYHFCYNV	CRC
PUF60	c.1187C>T	p.S396L	VMAAQAPGVITGVTPARPPIPVTIP[p.S396L]LVGVVNPILASPPTLGLLEPKKEKEE	VTIPLVGVV,PLVGVVNPI,PPIPVTIPL,RPPIPVTIPL,IPLVGVVNPI,PPIPVTIPLV,IPVTIPLVGV	BLCA
PVRL4	c.1072G>A	p.A358T	LDPQEDSGKQVDLVSASVVVVGVIA[p.A358T]TLLFCLLVVVVVLMSRYHRRKAQQMT	VIATLLFCL,ATLLFCLLV,TLLFCLLVV,VVVGVIATL,VGVIATLLF,GVIATLLFCL,VIATLLFCLL,ATLLFCLLVV,TLLFCLLVVV,VVVGVIATLL,VVGVIATLLF	UCEC
PWWP2B	c.251delC	p.S84fs	PVNDSHGRAPEEGDAEVMQLGSSSP[p.S84fs]LLPAGFSPPRPPAPSHPRPSCRRCPPEACPRTLPTSKAPPSLTRCGSGTRTSCGCPSRRPGPSSARGGVCPATATRGASSSAPSACGRARCSVRSARAR*	MQLGSSSPL,QLGSSSPLL,RTSCGCPSR,GVCPATATR,SSAPSACGR,GFSPPRPPA,LTRCGSGTR,SARGGVCPA,ATRGASSSA,CGRARCSVR,RARCSVRSA,TSCGCPSRR,APSHPRPSC,HPRPSCRRC,RPSCRRCPP,GPSSARGGV,CPATATRGA,LPAGFSPPR,VMQLGSSSPL,MQLGSSSPLL,TSKAPPSLTR,RTSCGCPSRR,SSSAPSACGR,AGFSPPRPPA,RTLPTSKAPP,GTRTSCGCPS,PSRRPGPSSA,RGASSSAPSA,RARCSVRSAR,SSSPLLPAGF,LLPAGFSPPR,RPSCRRCPPE,CPRTLPTSKA,LPTSKAPPSL,CPATATRGAS	STAD
PXDNL	c.3935C>T	p.T1312M	IPKVDLRVWQDCCADCRSRGQFRAV[p.T1312M]MQESQKKRSAQYSYPVDKDMELSHLR	RAVMQESQK,AVMQESQKK,SRGQFRAVM,RSRGQFRAVM,RAVMQESQKK,GQFRAVMQES	CRC
PXDNL	c.4366C>A	p.P1456T	CPPAPCPSPELVKGTCCPVCRDRGM[p.P1456T]TSDSPEKR*	GMTSDSPEK,MTSDSPEKR,RGMTSDSPEK	LUAD

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PYGO2	c.448delC	p.Q150fs	GPQPLRRQPPPFPPNPMGPAFNMPP[p.Q150fs]RVLATHPQAT*	NMPPRVLAT,VLATHPQAT,RVLATHPQA,MPPRVLATH,AFNMPPRVLA,RVLATHPQAT,MGPAFNMPPR,GPAFNMPPRV	STAD
PYHIN1	c.443G>C	p.G148A	NRLTAKGAEETLGPQKRKKPSEEET[p.G148A]ATKRSKMSKEQTRPSCSAGASTSTAM	ATKRSKMSK,TATKRSKMSK	LUSC
QRSL1	c.677C>T	p.S226L	AHCGLVGFKPSYGLVSRHGLIPLVN[p.S226L]LMDVPGILTRCVDDAAIVLGALAGPD	GLIPLVNLM,NLMDVPGIL,IPLVNLMDV,NLMDVPGILT,LVNLMDVPGI	CRC
QSOX1	c.1202G>T	p.R401L	DDRKEGAVLAKKVNWIGCQGSEPHF[p.R401L]LGFPCSLWVLFHFLTVQAARQNVDHS	HFLGFPCSL,CQGSEPHFL,GSEPHFLGF,EPHFLGFPC,FLGFPCSLWV,HFLGFPCSLW,QGSEPHFLGF,LGFPCSLWVL,SEPHFLGFPC	LUAD
QSOX2	c.2048G>T	p.R683L	SLDMSLCVVLYVASSLFLMVMYFFF[p.R683L]LVRSRRWKVKHHHPAV*	LMVMYFFFL,MVMYFFFLV,VMYFFFLVR,FLVRSRRWK,FFLVRSRRW,LVRSRRWKV,YFFFLVRSR,FFFLVRSRR,FLMVMYFFFL,LMVMYFFFLV,FLVRSRRWKV,MVMYFFFLVR,FFFLVRSRRW,MYFFFLVRSR,FFLVRSRRWK,LVRSRRWKVK,YFFFLVRSRR	LUAD
R3HDM2	c.1763G>A	p.S588N	MPNQQQAAYQGMIGVQQPQNQGLLS[p.S588N]NQRSSMGGQMQGLVVQYTPLPSYQVP	LLSNQRSSM,NQRSSMGGQM,GLLSNQRSSM	CLL
R3HDM2	c.1774A>G	p.S592G	QQAAYQGMIGVQQPQNQGLLSSQRS[p.S592G]GMGGQMQGLVVQYTPLPSYQVPVGSD	GMGGQMQGL,LLSSQRSGM,QRSGMGGQM,GMGGQMQGLV,SQRSGMGGQM,GLLSSQRSGM	CLL
R3HDM2	c.616C>T	p.R206W	EFINDNNNQFKKFPQMTSYHRMLLH[p.R206W]WVAAYFGMDHNVDQTGKAVIINKTSN	RMLLHWVAA,MLLHWVAAY,SYHRMLLHW,HWVAAYFGM,LLHWVAAYF,HRMLLHWVA,MLLHWVAAYF,RMLLHWVAAY,SYHRMLLHWV,YHRMLLHWVA,TSYHRMLLHW,HRMLLHWVAA,LHWVAAYFGM	CLL
RAB11FIP4	c.1787C>T	p.S596L	SLYEAKNLFAAQTKAQSLAAEIDTA[p.S596L]LRDELMEALKEQEEINFRLRQYMDKI	ALRDELMEA,LAAEIDTAL,SLAAEIDTAL,ALRDELMEAL,LAAEIDTALR	BLCA
RAB11FIP5	c.509G>A	p.R170H	WYKLHSKPGKKEKERGEIEVTIQFT[p.R170H]HNNLSASMFDLSMKDKPRSPFSKIRD	IEVTIQFTH,IQFTHNNLS,THNNLSASM,HNNLSASMF,IQFTHNNLSA,FTHNNLSASM,VTIQFTHNNL,THNNLSASMF	GBM
RAB13	c.500G>T	p.R167L	EHGIRFFETSAKSSMNVDEAFSSLA[p.R167L]LDILLKSGGRRSGNGNKPPSTDLKTC	SLALDILLK,DEAFSSLAL,FSSLALDIL,SSLALDILLK,EAFSSLALDI,VDEAFSSLAL	LUAD
RAB7L1	c.235C>T	p.R79W	YEIVRLQLWDIAGQERFTSMTRLYY[p.R79W]WDASACVIMFDVTNATTFSNSQRWKQ	RLYYWDASA,TSMTRLYYW,YYWDASACV,MTRLYYWDA,WDASACVIM,SMTRLYYWDA,RLYYWDASAC,FTSMTRLYYW,LYYWDASACV,YYWDASACVI,MTRLYYWDAS,YWDASACVIM,WDASACVIMF	CRC
RAB8A	c.58G>T	p.G20W	MAKTYDYLFKLLLIGDSGV[p.G20W]WKTCVLFRFSEDAFNSTFISTIGIDF	LIGDSGVWK,GVWKTCVLF,VWKTCVLFR,LLIGDSGVW,WKTCVLFRF,GVWKTCVLFR,SGVWKTCVLF,VWKTCVLFRF,LLLIGDSGVW	LUAD
RABGAP1	c.2782_2783insA	p.K928fs	LEEESAQLKEMCRRELDKAESEIKK[p.K928fs]KQFYHW*	SEIKKKQFY,IKKKQFYHW,AESEIKKKQF	STAD
RABGAP1	c.2782delA	p.K928fs	LEEESAQLKEMCRRELDKAESEIKK[p.K928fs]TVLSLVTISRFVLS*	SLVTISRFV,KTVLSLVTI,VLSLVTISR,EIKKTVLSL,LSLVTISRF,KKTVLSLVT,AESEIKKTV,SLVTISRFVL,TVLSLVTISR,EIKKTVLSLV,VLSLVTISRF,AESEIKKTVL,SEIKKTVLSL,KKTVLSLVTI	STAD
RABGEF1	c.619A>G	p.N207D	PASADDFLPTLIYIVLKGNPPRLQS[p.N207D]DIQYITRFCNPSRLMTGEDGYYFTNL	RLQSDIQYI,LQSDIQYIT,SDIQYITRF,QSDIQYITRF	TGCT
RAC1	c.101C>G	p.P34R	VGDGAVGKTCLLISYTTNAFPGEYI[p.P34R]RTVFDNYSANVMVDGKPVNLGLWDTA	RTVFDNYSA,YIRTVFDNY,NAFPGEYIR,FPGEYIRTV,FPGEYIRTVF	TGCT
RAC1	c.476C>T	p.A159V	LTPITYPQGLAMAKEIGAVKYLECS[p.A159V]VLTQRGLKTVFDEAIRAVLCPPPVKK	AVKYLECSV,SVLTQRGLK,KYLECSVLT,VKYLECSVL,VLTQRGLKTV,CSVLTQRGLK,AVKYLECSVL	HNSC
RAC1	c.85C>T	p.P29S	IKCVVVGDGAVGKTCLLISYTTNAF[p.P29S]SGEYIPTVFDNYSANVMVDGKPVNLG	TTNAFSGEY,FSGEYIPTV,SGEYIPTVF,YTTNAFSGEY,TTNAFSGEYI,FSGEYIPTVF	SKCM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
RAD50	c.205G>T	p.D69Y	THECLKYICTGDFPPGTKGNTFVH[p.D69Y]YPKVAQETDVRAQIRLQFRDVNGELI	GNTFVHYPK,NTFVHYPKV,TKGNTFVHY,KGNTFVHYPK,GTKGNTFVHY,NTFVHYPKVA,YPKVAQETDV	LUAD
RAD51AP2	c.946delA	p.T316fs	RDFTNIYWSQNRPDVKKQKLQNDKK[p.T316fs]L*	KQKLQNDKKL	STAD
RAD51C	c.499G>A	p.D167N	VQIPECFGGVAGEAVFIDTEGSFMV[p.D167N]NRVVDLATACIQHLQLIAEKHKGEEH	FMVNRVVDL,MVNRVVDLA,EGSFMVNRV,FMVNRVVDLA,SFMVNRVVDL,DTEGSFMVNR,TEGSFMVNRV	BLCA
RAD51C	c.670T>C	p.Y224H	FTLDNILSHIYYFRCRDYTELLAQV[p.Y224H]HLLPDFLSEHSKVRLVIVDGIAFPFR	ELLAQVHLL,AQVHLLPDF,TELLAQVHL,AQVHLLPDFL,LAQVHLLPDF,HLLPDFLSEH,TELLAQVHLL	BLCA
RAF1	c.770C>T	p.S257L	YSTPHAFTFNTSSPSSEGSLSQRQR[p.S257L]LTSTPNVHMVSTTLPVDSRMIEDAIR	RQRLTSTPN,LTSTPNVHM,SQRQRLTST,RLTSTPNVH,LTSTPNVHMV,RQRLTSTPNV,RLTSTPNVHM,SQRQRLTSTP	CRC
RALGAPA1	c.1192C>T	p.R398C	LTEREPSSSSLCSIDEEHLTDIEIV[p.R398C]CRVFSSKRSNVNFVTEIFRQAFLLPI	IVCRVFSSK,LTDIEIVCRV,EIVCRVFSSK,IVCRVFSSKR,HLTDIEIVCR,TDIEIVCRVF,IEIVCRVFSS	CRC
RALGAPB	c.1136delC	p.T379fs	RSDSAPPTPVNRLSMPQSAAVSTTP[p.T379fs]HITGGTGLLL*	TTPHITGGT,SAAVSTTPH,AAVSTTPHI,TPHITGGTGL,SAAVSTTPHI	STAD
RALGPS1	c.1142G>A	p.R381Q	SKSATFPSEKARHLLDDSVLESRSP[p.R381Q]QRGLALTSSSAVTNGLSLGSSESSEF	RSPQRGLAL,SVLESRSPQR,LESRSPQRGL,SRSPQRGLAL	BLCA
RANBP17	c.2700G>T	p.M900I	HSDLLQYRKLSQSYYPLLECLTQDH[p.M900I]ISFIINLEPPVLMYVLTSISEGLTTL	LTQDHISFI,CLTQDHISF,TQDHISFII,CLTQDHISFI,LLECLTQDHI,LTQDHISFII,QDHISFIINL	TGCT
RANBP2	c.3691C>T	p.R1231C	VESKEWKERGIGNVKILRHKTSGKI[p.R1231C]CLLMRREQVLKICANHYISPDMKLTP	KTSGKICLL,CLLMRREQV,SGKICLLMR,HKTSGKICL,TSGKICLLMR,KTSGKICLLM,SGKICLLMRR,CLLMRREQVL,RHKTSGKICL,HKTSGKICLL	CRC
RANBP3	c.1157T>G	p.L386W	EATPEKESLAESAAAYTKATARKCL[p.L386W]WEKVEVITGEEAESNVLQMQCKLFVF	CLWEKVEVI,TARKCLWEK,KATARKCLW,ATARKCLWEK	KIRC
RANBP6	c.2743C>T	p.R915W	QWGLCIFDDIIEHCSPTSFKYVEYF[p.R915W]WWPMLLNMRDNNPEVRQAAAYGLGVM	YVEYFWWPM,SFKYVEYFW,KYVEYFWWP,EYFWWPMLL,FWWPMLLNM,FKYVEYFWW,VEYFWWPML,YVEYFWWPML,SFKYVEYFWW,KYVEYFWWPM,VEYFWWPMLL,YFWWPMLLNM,FWWPMLLNMR,TSFKYVEYFW	CESC
RANBP6	c.2950A>C	p.I984L	LVKVIKCANSKTKKNVIATENCISA[p.I984L]LGKILKFKPNCVNVDEVLPHWLSWLP	ISALGKILK,ALGKILKFK,SALGKILKF,TENCISALG,CISALGKILK,SALGKILKFK,IATENCISAL,ISALGKILKF	LUSC
RAPGEFL1	c.1067G>T	p.R356L	LPGKFKNLFRKFENLTDPCRNHKSY[p.R356L]LEVISKMKPPVIPFVPLILKDLTFLH	KSYLEVISK,SYLEVISKM,RNHKSYLEV,KSYLEVISKM,SYLEVISKMK,RNHKSYLEVI	LUAD
RARS2	c.16C>T	p.R6C	MACGF[p.R6C]CRAIACQLSRVLNLPPENLITSISAV	MACGFCRAI	BLCA
RASAL3	c.245G>A	p.R82H	VSTQPAPRSIFRRVLSAPPKESRTS[p.R82H]HLRLSKALWGRHKNPPPEPDPEPEQE	RTSHLRLSK,TSHLRLSKA,SHLRLSKAL,HLRLSKALW,RTSHLRLSKA,HLRLSKALWG,KESRTSHLRL,SHLRLSKALW	GBM
RASGEF1C	c.562G>A	p.A188T	LAALRQGPEGLVGADKPISYRTKPP[p.A188T]TSIHRELLGVCSDPYTLAQQLTHVEL	SYRTKPPTS,RTKPPTSIH,YRTKPPTSI,SYRTKPPTSI,RTKPPTSIHR,TSIHRELLGV,KPPTSIHREL	KIRC
RASIP1	c.1801C>T	p.R601C	ATLLALCVQHSARELELGHLPRLLG[p.R601C]CLARLIKEAVWEKIKEIGDRQPENHP	RLLGCLARL,HLPRLLGCL,LLGCLARLI,CLARLIKEA,LPRLLGCLA,RLLGCLARLI,CLARLIKEAV,HLPRLLGCLA,LLGCLARLIK	ACC
RB1	c.948_951delTCTT	p.N316fs	FKNFIPFMNSLGLVTSNGLPEVENL[p.N316fs]NDTKKFILKIKI*	KKFILKIKI,DTKKFILKIK,VENLNDTKKF	GBM
RBBP4	c.988G>A	p.E330K	NLKLKLHSFESHKDEIFQVQWSPHN[p.E330K]KTILASSGTDRRLNVWDLSKIGEQS	QVQWSPHNK,SPHNKTILA,VQWSPHNKT,FQVQWSPHNK,SPHNKTILAS,VQWSPHNKTI	LAML
RBBP7	c.820G>A	p.E274K	QKLMIWDTRSNTTSKPSHLVDAHTA[p.E274K]KVNCLSFNPYSEFILATGSADKTVAL	LVDAHTAKV,HLVDAHTAK,HTAKVNCLS,TAKVNCLSF,HLVDAHTAKV,KVNCLSFNPY,HTAKVNCLSF	CRC
RBBP7	c.937G>A	p.E313K	LATGSADKTVALWDLRNLKLKLHTF[p.E313K]KSHKDEIFQVHWSPHNETILASSGTD	KLHTFKSHK,KLKLHTFKS,LKLHTFKSH,FKSHKDEIF,NLKLKLHTFK,KLKLHTFKSH,KSHKDEIFQV,HTFKSHKDEI	CRC

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RBFOX2	c.1018G>A	p.A340T	NTYIPLISLPLVPGFPYPTAATTAA[p.A340T]TFRGAHLRGRGRTVYGAVRAVPPTAI	ATFRGAHLR,AATTAATFR,TTAATFRGA,TAATTAATF,TAATTAATFR,TFRGAHLRGR,AATFRGAHLR,YPTAATTAAT,PTAATTAATF	CRC
RBL2	c.379G>A	p.E127K	VSKGTVEGNYVSLTRILKCSEQSLI[p.E127K]KFFNKMKKWEDMANLPPHFRERTERL	SLIKFFNKM,QSLIKFFNK,LIKFFNKMK,KFFNKMKKW,CSEQSLIKF,SEQSLIKFF,SLIKFFNKMK,LIKFFNKMKK,EQSLIKFFNK,KCSEQSLIKF,IKFFNKMKKW	UCEC
RBM14	c.856_876delGCTGCTGCTGCAGCAGCAGCC	p.AAAAAAAAA286del	LTSTSLDPYDRHLLPTSGAAATAAA[p.AAAAAAAA286del]VTAASTSYYGRDRSPLRRATAPVPTVGEGYGYGHESELSQASAAAR	GAAATAAAV,ATAAAVTAA,TAAAVTAAS,SGAAATAAAV,TAAAVTAAST	PAAD
RBM19	c.1168G>T	p.G390W	FREKNVPTTKGAPKNTTKSWQGRIL[p.G390W]WENEEEEDLAESGRLFVRNLPYTSTE	KSWQGRILW,WENEEEEDL,TKSWQGRILW	LUAD
RBM26	c.1930C>G	p.P644A	TTSPKPLVQQPILPVVKQSVKERLG[p.P644A]AVPSSTIEPAEAQSASSDLPQNVTKL	SVKERLGAV,KERLGAVPS,LGAVPSSTI,RLGAVPSSTI,KERLGAVPSS	BLCA
RBM39	c.1058C>T	p.T353I	ERTDASSASSFLDSDELERTGIDLG[p.T353I]ITGRLQLMARLAEGTGLQIPPAAQQA	LGITGRLQL,ITGRLQLMAR,LERTGIDLGI,LGITGRLQLM	UCEC
RBM47	c.1485_1505delGGCCGCAGCCGCCGCAGCCGC	p.495_502AAAAAAA>A	HTVEHMISPIAVQPDPASAAAAAAA[p.495_502AAAAAAAA>A]VIPTVSTPPPFQGRPITPVYTVAPNVQRIPTAGIYGASYVPFAAPA	ASAAAAAAAV,SAAAAAAAVI	PAAD
RBM6	c.2024T>G	p.V675G	RQDGESKTIMLKRIYRSTPPEVIVE[p.V675G]GLEPYVRLTTANVRIIKNRTGPMGHT	VIVEGLEPY,VIVEGLEPYV,EVIVEGLEPY	MM
RBM6	c.287_288insG	p.R96fs	SYGARDGPHGDYRGGEGPGHDFRGG[p.R96fs]RFFVF*	FRGGRFFVF,HDFRGGRFF,DFRGGRFFVF,HDFRGGRFFV	STAD
RCL1	c.335C>A	p.P112Q	HDCSVLRGIGYYLESLLCLAPFMKH[p.P112Q]QLKIVLRGVTNDQVDPSVDVLKATAL	FMKHQLKIV,QLKIVLRGV,PFMKHQLKI,APFMKHQLK,MKHQLKIVL,CLAPFMKHQL,HQLKIVLRGV,FMKHQLKIVL,LAPFMKHQLK,APFMKHQLKI	LUAD
RDH8	c.593C>T	p.A198V	LLQFNIFISLVEPGPVVTEFEGKLL[p.A198V]VQVSMAEFPGTDPETLHYFRDLYLPA	KLLVQVSMA,LVQVSMAEF,TEFEGKLLV,GKLLVQVSM,FEGKLLVQV,VTEFEGKLLV,LLVQVSMAEF,VQVSMAEFPG,TEFEGKLLVQ,FEGKLLVQVS	GBM
REG1B	c.170G>T	p.W57L	PRISCPEGTNAYRSYCYYFNEDPET[p.W57L]LVDADLYCQNMNSGNLVSVLTQAEGA	ETLVDADLY,YFNEDPETL,YYFNEDPETL	LUAD
REG1B	c.201G>T	p.M67I	AYRSYCYYFNEDPETWVDADLYCQN[p.M67I]INSGNLVSVLTQAEGAFVASLIKESS	CQNINSGNL,NINSGNLVSV,CQNINSGNLV,INSGNLVSVL	LUSC
REG3A	c.449C>T	p.S150L	SDVMNYFAWERNPSTISSPGHCASL[p.S150L]LRSTAFLRWKDYNCNVRLPYVCKFTD	SLLRSTAFL,LLRSTAFLR,SPGHCASLL,ASLLRSTAF,LRSTAFLRW,SLLRSTAFLR,ASLLRSTAFL,CASLLRSTAF,LLRSTAFLRW	LUAD
REG4	c.329G>T	p.G110V	GYQRSQPIWIGLHDPQKRQQWQWID[p.G110V]VAMYLYRSWSGKSMGGNKHCAEMSSN	WIDVAMYLY,QWIDVAMYL,WQWIDVAMY,RQQWQWIDV,QQWQWIDVA,QWQWIDVAM,VAMYLYRSW,WQWIDVAMYL,WIDVAMYLYR,QWQWIDVAMY,QWIDVAMYLY,QQWQWIDVAM,RQQWQWIDVA	LUAD
REN	c.45_47delGCT	p.15_16LL>L	MDGWRRMPRWGLLLL[p.15_16LL>L]WGSCTFGLPTDTTTFKRIFLKRMPSIRE	MPRWGLLLLW	GBM
RERE	c.528G>C	p.K176N	PACSLPVASQPPQHLSEAGRGPVGS[p.K176N]NRDHLLMNVKWYYRQSEVPDSVYQHL	GSNRDHLLM,AGRGPVGSNR,GPVGSNRDHL	BLCA
REV3L	c.88G>T	p.A30S	RIVTADYYMASPLQGLDTCQSPLTQ[p.A30S]SPVKKVPVVRVFGATPAGQKTCLHLH	SPVKKVPVV,CQSPLTQSP,CQSPLTQSPV,TQSPVKKVPV	TGCT
RFC3	c.245T>A	p.I82N	RELYGVGVEKLRIEHQTITTPSKKK[p.I82N]NEISTIASNYHLEVNPSDAGNSDRVV	TPSKKKNEI,KKKNEISTI,KKNEISTIA,NEISTIASNY,SKKKNEISTI	TGCT
RFC3	c.888G>T	p.K296N	LLEVRGRLYELLTHCIPPEIIMKAC[p.K296N]NEESRSCDIF*	IMKACNEESR,NEESRSCDIF	TGCT

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RGMB	c.187A>C	p.S63R	AWTGMGLRAAPSSAAAAAAEVEQRR[p.S63R]RPGLCPPPLELLLLLLFSLGLLHAGD	RPGLCPPPL,VEQRRRPGL,RRPGLCPPPL	ACC
RGS6	c.1097G>T	p.W366L	LKDQVGRDQFLRFLESEFSSENLRF[p.W366L]LLAVQDLKKQPLQDVAKRVEEIWQEF	FLLAVQDLK,LLAVQDLKK,RFLLAVQDL,FSSENLRFL,SENLRFLLA,FLLAVQDLKK,RFLLAVQDLK,FSSENLRFLL,SENLRFLLAV,LRFLLAVQDL	LUSC
RGS7	c.130C>T	p.R44C	PNMLVYRKMEDVIARMQDEKNGIPI[p.R44C]CTVKSFLSKIPSVFSGSDIVQWLIKN	CTVKSFLSK,IPICTVKSF,KNGIPICTVK,CTVKSFLSKI,IPICTVKSFL	SKCM
RGS9BP	c.286G>T	p.A96S	ERAEFERLWVAFSGCLDLLEADMRR[p.A96S]SLELGAAFPLHAPRRPLVRTGVAGAS	RSLELGAAF,LEADMRRSL,ADMRRSLEL,SLELGAAFPL,RRSLELGAAF	ACC
RGSL1	c.664G>A	p.V222I	HTKMTMAKEEACHGLMQEYETRLYS[p.V222I]ICYTHIGGLPLNMSIKKCHHFQKRYS	RLYSICYTH,EYETRLYSI,LYSICYTHI,ETRLYSICY,YETRLYSIC,RLYSICYTHI,SICYTHIGGL,QEYETRLYSI,YETRLYSICY	BRCA
RHBDD3	c.101_102insG	p.G34fs	SPALPLASSVLMLLMSTLWLVGAGP[p.G34fs]RPGPGPGAVAGPLAGAPAADPCPGPHGPARPAPEPAAPAHCGLAAGVPPGHAEIPACLSPARPGFWAAGSAAGRPWAVQCSRQLWIHACPPGHAGWGGTPP*	AVAGPLAGA,GLAAGVPPG,EIPACLSPA,SAAGRPWAV,CSRQLWIHA,WAAGSAAGR,RPWAVQCSR,GPRPGPGPG,RPGPGPGAV,GPGAVAGPL,GPLAGAPAA,GPHGPARPA,APAHCGLAA,SPARPGFWA,CLSPARPGF,AEIPACLSP,GFWAAGSAA,AGSAAGRPW,WAVQCSRQL,VQCSRQLWI,RQLWIHACP,WIHACPPGHA,TLWLVGAGPR,EIPACLSPAR,FWAAGSAAGR,EPAAPAHCGL,GPRPGPGPGA,RPGPGPGAVA,GPARPAPEPA,RPAPEPAAPA,SPARPGFWAA,RPGFWAAGSA,AEIPACLSPA,ACLSPARPGF,AAGSAAGRPW,WAVQCSRQLW,RQLWIHACPP,HACPPGHAGW	KICH
RHEB	c.103T>A	p.Y35N	AILGYRSVGKSSLTIQFVEGQFVDS[p.Y35N]NDPTIENTFTKLITVNGQEYHLQLVD	FVDSNDPTI,GQFVDSNDPT,SNDPTIENTF	KIRC
RHOA	c.118G>C	p.E40Q	ACGKTCLLIVFSKDQFPEVYVPTVF[p.E40Q]QNYVADIEVDGKQVELALWDTAGQED	VFQNYVADI,YVPTVFQNY,VPTVFQNYV,YVPTVFQNYV,FQNYVADIEV,VYVPTVFQNY,TVFQNYVADI,VPTVFQNYVA	HNSC
RHOA	c.125A>G	p.Y42C	GKTCLLIVFSKDQFPEVYVPTVFEN[p.Y42C]CVADIEVDGKQVELALWDTAGQEDYD	VPTVFENCV,YVPTVFENCV,TVFENCVADI,CVADIEVDGK,VYVPTVFENC,FENCVADIEV	STAD
RHOBTB1	c.1391C>T	p.T464M	VLEMFDLRMMVENIMNKEAFMNQEI[p.T464M]MKAFHVRKANRIKECLSKGTFSDVTF	FMNQEIMKA,IMKAFHVRK,AFMNQEIMK,EIMKAFHVR,MNQEIMKAF,MKAFHVRKA,EAFMNQEIM,QEIMKAFHV,FMNQEIMKAF,IMKAFHVRKA,EAFMNQEIMK,EIMKAFHVRK,KEAFMNQEIM	CRC
RHPN2	c.217G>A	p.V73M	LKAVRMRTGAENLLKVATNSKVREQ[p.V73M]MRLELSFVNSDLQMLKEELEGLNISV	QMRLELSFV,KVREQMRLE,NSKVREQMR,EQMRLELSF,SKVREQMRL,VREQMRLEL,REQMRLELS,EQMRLELSFV,KVREQMRLEL,REQMRLELSF	TGCT
RILPL1	c.1074C>A	p.S358R	RIPQPPPIAHPRTSPQPESGIKRLF[p.S358R]RFFSRDKKRLANTQRNVHIQESFGQW	SGIKRLFRF,GIKRLFRFF,KRLFRFFSR,LFRFFSRDK,ESGIKRLFR,RFFSRDKKR,RLFRFFSRDK,SGIKRLFRFF,GIKRLFRFFS,IKRLFRFFSR,LFRFFSRDKK	KICH
RIMBP2	c.2489G>A	p.R830H	FPRGSAGPQRSRPVTVPSIDDYGRD[p.R830H]HLSPDFYEESETDPGAEELPARIFVA	RDHLSPDFY,YGRDHLSPDF	GBM
RIMBP3	c.1187_1189delCGG	p.A396del	HELIKLNWLLAKALWVLARRCYTLQ[p.A396del]ENKQLRRAGCPYQADEKVKRLKVKRAEL	RCYTLQENK,TLQENKQLR,QENKQLRRA,YTLQENKQLR	KIRC
RIMBP3	c.3461A>G	p.Q1154R	YADGLKVCEVADATAGSTLLEFSQL[p.Q1154R]RVPLTWQKVSVRTMSLCGESLDSVPA	LLEFSQLRV,TLLEFSQLR,SQLRVPLTW,LEFSQLRVP,TLLEFSQLRV,QLRVPLTWQK,STLLEFSQLR,FSQLRVPLTW,LEFSQLRVPL	TGCT
RIMS2	c.1203delA	p.V401fs	LGLKVVGGKMTESGRLCAFITKVKK[p.V401fs]EV*	FITKVKKEV	STAD
RIMS2	c.164G>T	p.R55L	EREEYSQYATSDTAMPRSPSDYADR[p.R55L]LSQHEPQFYEDSDHLSYRDSNRRSHR	LSQHEPQFY,SPSDYADRL,RLSQHEPQF,RLSQHEPQFY	LUAD
RIMS2	c.1796G>A	p.R599Q	KRRTKTVKKTLEPKWNQTFIYSPVH[p.R599Q]QREFRERMLEITLWDQARVREEESEF	FIYSPVHQR,HQREFRERM,IYSPVHQREF,TFIYSPVHQR,YSPVHQREFR,HQREFRERML	CRC

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RIN3	c.1345C>G	p.L449V	DTPRESTEQGQDTEVKASDPHSMPE[p.L449V]VPRTAKQPPVPPPRKKRISRQLASTL	SMPEVPRTA,SMPEVPRTAK,HSMPEVPRTA,VPRTAKQPPV	KIRC
RIN3	c.2123C>T	p.S708L	LYKCVLKPLKEAINSCLHQIHSKDG[p.S708L]LLQQLKENQLVILATTTTDLGVTTSV	HQIHSKDGL,SKDGLLQQL,HQIHSKDGLL	CRC
RING1	c.511delG	p.G171fs	QAMHRAQRVRRPIPGSDQTTTMSGG[p.G171fs]KESPGREKGMEKM*	QTTTMSGGK,GGKESPGREK,KESPGREKGM	STAD
RINL	c.1205C>T	p.P402L	RRRQTALRAGAGPPGAQGPGPEGQS[p.P402L]LAPALRSRIHERLAHLHAACAPRRKV	SLAPALRSR,GPGPEGQSL,PEGQSLAPA,SLAPALRSRI,EGQSLAPALR,PEGQSLAPAL	ACC
RINT1	c.321delA	p.L107fs	SKMQLEEQVLTISSEIPKRIRSALK[p.L107fs]MQKNQSNFLISFWSRKLISSAPLTAIC*	MQKNQSNFL,KLISSAPLT,FLISFWSRK,KMQKNQSNF,RIRSALKMQ,ISFWSRKLI,WSRKLISSA,NFLISFWSR,NQSNFLISF,KRIRSALKM,QKNQSNFLI,RKLISSAPL,ISSAPLTAI,KMQKNQSNFL,FLISFWSRKL,KLISSAPLTA,LISSAPLTAI,MQKNQSNFLI,RIRSALKMQK,SNFLISFWSR,KNQSNFLISF,NFLISFWSRK,SRKLISSAPL,LKMQKNQSNF,NQSNFLISFW	STAD
RIT1	c.270G>T	p.M90I	DDEPANLDILDTAGQAEFTAMRDQY[p.M90I]IRAGEGFIICYSITDRRSFHEVREFK	FTAMRDQYI,AMRDQYIRA,YIRAGEGFI,QYIRAGEGF,TAMRDQYIR,IRAGEGFII,YIRAGEGFII,QYIRAGEGFI,AMRDQYIRAG,FTAMRDQYIR,DQYIRAGEGF	LUAD
RIT2	c.254G>T	p.R85L	QVRIDNEPAYLDILDTAGQAEFTAM[p.R85L]LEQYMRGGEGFIICYSVTDRQSFQEA	GQAEFTAML,TAMLEQYMR,FTAMLEQYM,AEFTAMLEQ,FTAMLEQYMR,AEFTAMLEQY	LUAD
RLBP1	c.215C>T	p.A72V	KAKDELNEREETREEAVRELQEMVQ[p.A72V]VQAASGEELAVAVAERVQEKDSGFFL	RELQEMVQV,QEMVQVQAA,VQAASGEEL,LQEMVQVQAA,VQAASGEELA,QEMVQVQAAS	CRC
RLBP1	c.841G>A	p.D281N	PFLKSKLLERVFVHGDDLSGFYQEI[p.D281N]NENILPSDFGGTLPKYDGKAVAEQLF	FYQEINENI,YQEINENIL,NENILPSDF,GFYQEINENI,FYQEINENIL,QEINENILPS	CRC
RLIM	c.1502C>T	p.S501L	SPSSSSGGESSETSSDLFEGSNEGS[p.S501L]LSSGSSGARREGRHRAPVTFDESGSL	SLSSGSSGA,FEGSNEGSL	KIRC
RLN2	c.412A>T	p.S138C	QQHVPVLKDSSLLFEEFKKLIRNRQ[p.S138C]CEAADSSPSELKYLGLDTHSRKKRQL	LIRNRQCEA,RQCEAADSS,CEAADSSPS,KLIRNRQCEA,LIRNRQCEAA,RQCEAADSSP	LUAD
RNASET2	c.380C>T	p.A127V	HSFPNRSRFWKHEWEKHGTCAAQVD[p.A127V]VLNSQKKYFGRSLELYRELDLNSVLL	QVDVLNSQK,VLNSQKKYF,AQVDVLNSQK,QVDVLNSQKK	CRC
RNF111	c.2313delC	p.R771fs	HEVMQRMEVQRRRMMQHPTRAHERP[p.R771fs]HPIHIGCTQTMVMGIIFMCLRLCPHILDRLQRGLPGNWELKLE*	TMVMGIIFM,VMGIIFMCL,HIGCTQTMV,RLCPHILDR,QTMVMGIIF,RGLPGNWEL,RAHERPHPI,MGIIFMCLR,CTQTMVMGI,MVMGIIFMC,CLRLCPHIL,HERPHPIHI,IHIGCTQTM,IGCTQTMVM,FMCLRLCPH,LQRGLPGNW,LPGNWELKL,MVMGIIFMCL,FMCLRLCPHI,RLCPHILDRL,VMGIIFMCLR,RGLPGNWELK,RAHERPHPIH,QTMVMGIIFM,RPHPIHIGCT,HIGCTQTMVM,TQTMVMGIIF,RLQRGLPGNW	STAD
RNF113B	c.515C>T	p.A172V	YRGIHSYLRYLKPKDTSMGNSSSGM[p.A172V]VRKGPIRAPGHLRATVRWDYQPDICK	NSSSGMVRK,SMGNSSSGMV	CRC
RNF149	c.25A>G	p.S9G	MAWRRREA[p.S9G]GVGARGVLALALALALCVPGARGRA	AWRRREAGV,MAWRRREAG,RRREAGVGAR,MAWRRREAGV,REAGVGARGV	ACC
RNF150	c.623C>T	p.S208L	LERNITVTMYITIGTRNLQKYVSRT[p.S208L]LVVFVSISFIVLMIISLAWLVFYYIQ	RTLVVFVSI,KYVSRTLVV,YVSRTLVVF,VSRTLVVFV,LQKYVSRTL,LVVFVSISF,QKYVSRTLV,YVSRTLVVFV,NLQKYVSRTL,LQKYVSRTLV,LVVFVSISFI,KYVSRTLVVF,RTLVVFVSIS,TLVVFVSISF,QKYVSRTLVV	CRC
RNF150	c.707G>A	p.R236Q	FVSISFIVLMIISLAWLVFYYIQRF[p.R236Q]QYANARDRNQRRLGDAAKKAISKLQI	FYYIQRFQY,YYIQRFQYA,IQRFQYANA,YIQRFQYANA,FYYIQRFQYA,YYIQRFQYAN,IQRFQYANAR,VFYYIQRFQY,FQYANARDRN	CRC
RNF152	c.283C>T	p.P95S	PDDPEVLAVIAIPHTSEHTPVFIKL[p.P95S]SSNGCYMLPLPISKERALLPGDMGCR	KLSSNGCYM,IKLSSNGCY,LSSNGCYML,KLSSNGCYML,FIKLSSNGCY,IKLSSNGCYM,SSNGCYMLPL	SKCM

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RNF17	c.1052C>G	p.S351C	KKYNNKKELSCYDTYPPLEKKKVDM[p.S351C]CVLTSEAPPPPLQPETNDVHLEAKNF	KKKVDMCVL	KIRC
RNF222	c.397G>A	p.A133T	PLAASSPAWRPPPGQARPPGSPGQS[p.A133T]TQLPLDLLPSLPRESQIFVISRHGMP	SPGQSTQLPL,GQSTQLPLDL,TQLPLDLLPS	ACC
RNF39	c.787G>T	p.G263C	HRRLLISADRRSVQLAPPGTPAPPD[p.G263C]CPKRFDQLPAVLGAQGFGAGRHCWEV	GTPAPPDCPK	ACC
RNF43	c.1976delG	p.G659fs	PSTSSLFNLQKSSLSARHPQRKRRG[p.G659fs]VPPSPPLALGPRMQLCTQLARFFPITPPVWHILGPQRHTP*	RMQLCTQLA,TQLARFFPI,RFFPITPPV,FFPITPPVW,ITPPVWHIL,RGVPPSPPL,MQLCTQLAR,HPQRKRRGV,VPPSPPLAL,RKRRGVPPS,LALGPRMQL,QLCTQLARF,FPITPPVWH,RMQLCTQLAR,MQLCTQLARF,CTQLARFFPI,RFFPITPPVW,RGVPPSPPLA,FPITPPVWHI,SPPLALGPRM,GPRMQLCTQL,RRGVPPSPPL,QLCTQLARFF,TQLARFFPIT,ARFFPITPPV	STAD
RNF43	c.348_349insC	p.P116fs	NASDDDNLEPGFISIVKLESPRRAP[p.P116fs]PPLPVTG*	SPRRAPPPL,RRAPPPLPV	STAD
RNF43	c.647C>T	p.S216L	PPAWPDYDVWILMTVVGTIFVIILA[p.S216L]LVLRIRCRPRHSRPDPLQQRTAWAIS	IILALVLRI,IFVIILALV,VIILALVLR,TIFVIILAL,FVIILALVL,TIFVIILALV,VIILALVLRI,IFVIILALVL,LVLRIRCRPR,FVIILALVLR,IILALVLRIR,LALVLRIRCR,GTIFVIILAL	CRC
RNMT	c.1174delA	p.K392fs	PEFLVYFPLLNEMAKKYNMKLVYKK[p.K392fs]HFWNSTKKRLRTMKIKCS*	VYKKHFWNS,KKHFWNSTK,KHFWNSTKK,STKKRLRTM,KKRLRTMKI,RLRTMKIKC,HFWNSTKKR,MKLVYKKHF,YKKHFWNST,STKKRLRTMK,KKHFWNSTKK,KKRLRTMKIK,RLRTMKIKCS,FWNSTKKRLR,NMKLVYKKHF,MKLVYKKHFW	STAD
RNPC3	c.347delA	p.E116fs	LVVEFAKEQDRVHSPCPTSGSEKKK[p.E116fs]GLMTLSKMIKKKKNLVI*	GLMTLSKMI,LMTLSKMIK,MTLSKMIKK,TLSKMIKKK,LSKMIKKKK,MIKKKKNLV,KGLMTLSKM,IKKKKNLVI,KMIKKKKNLV,GLMTLSKMIK,LMTLSKMIKK,MTLSKMIKKK,TLSKMIKKKK,KKKGLMTLSK,MIKKKKNLVI,SKMIKKKKNL,SEKKKGLMTL,KKGLMTLSKM	CESC
ROBO2	c.3052G>A	p.D1018N	SQITQATPYATTQILHSNSIHELAV[p.D1018N]NLPDPQWKSSIQQKTDLMGFGYSLPD	SIHELAVNL,HELAVNLPD,AVNLPDPQWK,NSIHELAVNL,LAVNLPDPQW,HELAVNLPDP	UCEC
ROBO2	c.3238_3239insC	p.P1080fs	KNKNSSKPQKNNGSTWANVPLPPPP[p.P1080fs]SPAPSWHGAGTLCSGTTRKWL*	TLCSGTTRK,GTLCSGTTR,SPAPSWHGA,APSWHGAGT,GTLCSGTTRK,VPLPPPPSPA,SPAPSWHGAG,APSWHGAGTL	STAD
ROBO2	c.3877delA	p.K1293fs	PTSPFSTDSNTSAALSQSQRPRPTK[p.K1293fs]NTREGGWTNNQHCLIEGKE*	WTNNQHCLI,REGGWTNNQH	STAD
ROCK1	c.1552A>T	p.T518S	HRINEYQRKAEQENEKRRNVENEVS[p.T518S]SLKDQLEDLKKVSQNSQLANEKLSQL	EVSSLKDQL,NVENEVSSLK,RNVENEVSSL,NEVSSLKDQL	PRAD
ROR2	c.2014G>A	p.D672N	KLLGNSLLPIRWMAPEAIMYGKFSI[p.D672N]NSDIWSYGVVLWEVFSYGLQPYCGYS	NSDIWSYGV,KFSINSDIW,SINSDIWSY,IMYGKFSIN,GKFSINSDI,FSINSDIWSY,NSDIWSYGVV,IMYGKFSINS,INSDIWSYGV,GKFSINSDIW	CRC
RORB	c.280G>T	p.G94W	NRNRCQHCRLQKCLALGMSRDAVKF[p.G94W]WRMSKKQRDSLYAEVQKHQQRLQEQR	AVKFWRMSK,MSRDAVKFW,AVKFWRMSKK,MSRDAVKFWR,DAVKFWRMSK,GMSRDAVKFW	LUAD
ROS1	c.734G>T	p.R245I	FPGGPILGYNLRLISKNQKLDAGTQ[p.R245I]ITSFQFYSTLPNTIYRFSIAAVNEVG	GTQITSFQF,TQITSFQFY,QKLDAGTQI,GTQITSFQFY,ITSFQFYSTL,NQKLDAGTQI,LDAGTQITSF,AGTQITSFQF	UCEC
RP1	c.5312C>T	p.S1771L	WLLKENHLLRMSSENPGMCGNADTT[p.S1771L]LVDTLLDNNSSEVPYSHFGNLAPGPT	DTTLVDTLL,GMCGNADTTL	LUSC
RPA1	c.92G>A	p.R31H	SEGAIAAIMQKGDTNIKPILQVINI[p.R31H]HPITTGNSPPRYRLLMSDGLNTLSSF	LQVINIHPI,ILQVINIHPI,LQVINIHPIT	HNSC
RPL10L	c.560A>C	p.K187T	RQKIHISKKWGFTKFNADEFEDMVA[p.K187T]TKCLIPDGCGVKYVPSHGPLDKWRVL	DEFEDMVAT,DEFEDMVATK,FEDMVATKCL	LUAD
RPL13AP20	c.319G>C	p.G107R	QTMRGMPPHKTKPGQAALDCLKVFD[p.G107R]RIPPPYDKKKRMVVPAALKVVRLKPA	VFDRIPPPY,RIPPPYDKK,KVFDRIPPP,KVFDRIPPPY,RIPPPYDKKK	UCS

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RPL19	c.451C>T	p.R151C	KVKGNVFKNKRILMEHIHKLKADKA[p.R151C]CKKLLADQAEARRSKTKEARKRREER	KLKADKACK,KLKADKACKK	TGCT
RPL22	c.44delA	p.K15fs	MAPVKKLVVKGGKK[p.K15fs]RSKF*	VVKGGKKRSK,VKGGKKRSKF	UCEC
RPL5	c.172_173delAG	p.R58fs	KRLVIQDKNKYNTPKYRMIVRVTNR[p.R58fs]YHLSDCLCPYRGGYDSLRSVCTRTAKIWCEGWPDKLCCSILYWPAAGPQASQ*	HLSDCLCPY,RSVCTRTAK,MIVRVTNRY,IVRVTNRYH,RVTNRYHLS,RTAKIWCEG,CLCPYRGGY,DSLRSVCTR,VRVTNRYHL,KLCCSILYW,CSILYWPAA,DKLCCSILY,WPAAGPQAS,WPDKLCCSI,SLRSVCTRTA,RMIVRVTNRY,KIWCEGWPDK,HLSDCLCPYR,IWCEGWPDKL,IVRVTNRYHL,RSVCTRTAKI,YHLSDCLCPY,CPYRGGYDSL,WPDKLCCSIL,RTAKIWCEGW	TGCT
RPL6	c.578T>G	p.F193C	LASGLLLVTGPLVLNRVPLRRTHQK[p.F193C]CVIATSTKIDISNVKIPKHLTDAYFK	CVIATSTKI,RTHQKCVIA,KCVIATSTK,HQKCVIATS,RTHQKCVIAT,HQKCVIATST	CRC
RPRD2	c.289C>A	p.R97S	PHRLNLFYLANDVIQNCKRKNAIIF[p.R97S]SESFADVLPEAAALVKDPSVSKSVER	AIIFSESFA,NAIIFSESF,FSESFADVL,IIFSESFADV,IFSESFADVL,NAIIFSESFA,KNAIIFSESF	LUAD
RPS2	c.598A>G	p.R200G	GKPHTVPCKVTGRCGSVLVRLIPAP[p.R200G]GGTGIVSAPVPKKLLMMAGIDDCYTS	RLIPAPGGT,LVRLIPAPG,IPAPGGTGI,LIPAPGGTGI,IPAPGGTGIV	CLL
RPS6KA5	c.496G>A	p.E166K	THLSQRERFTEHEVQIYVGEIVLAL[p.E166K]KHLHKLGIIYRDIKLENILLDSNGHV	VLALKHLHK,LALKHLHKL,LKHLHKLGI,VLALKHLHKL,ALKHLHKLGI,IVLALKHLHK,YVGEIVLALK,KHLHKLGIIY,GEIVLALKHL,LKHLHKLGII	CRC
RPS6KA6	c.1181C>A	p.S394Y	ATSIAEEYKITPITSANVLPIVQIN[p.S394Y]ENAAQFGEVYELKEDIGVGSYSVCKR	ENAAQFGEV,QINENAAQF,VQINENAAQ,VQINENAAQF,ENAAQFGEVY,NENAAQFGEV,LPIVQINENA	UCEC
RPS6KA6	c.327delA	p.K109fs	KKASLKVRDRVRTKMERDILVEVNH[p.K109fs]HLLSNCTMPFRLKGNCT*	ILVEVNHHL,LLSNCTMPF,LSNCTMPFR,HHLLSNCTM,ILVEVNHHLL,LLSNCTMPFR,SNCTMPFRLK,HLLSNCTMPF,NHHLLSNCTM	STAD
RPSA	c.331C>G	p.Q111E	AVLKFAAATGATPIAGRFTPGTFTN[p.Q111E]EIQAAFWEPRLLVVTDPRADHQPLTE	FTNEIQAAF,TPGTFTNEI,FTPGTFTNEI,TFTNEIQAAF,EIQAAFWEPR,NEIQAAFWEP,FTNEIQAAFW	GBM
RPTN	c.1090G>A	p.G364S	QSSHYGQMDRKGQCYHYDQTNRQGQ[p.G364S]SSHYSQPNRQGQSSHYGQPDTQDQSS	SSHYSQPNR,TNRQGQSSHY,GQSSHYSQPN	CLL
RPTN	c.1614G>A	p.M538I	QTDRQGQSFHYGQPDRQGQSSHYSQ[p.M538I]IDRQGQSSHYGQTDRQGQSSHYGQTD	GQSSHYSQI,SSHYSQIDR,SQIDRQGQSS,IDRQGQSSHY	TGCT
RPTN	c.886G>A	p.G296S	CGQSERLGQELGCGQTDRQGQSSHY[p.G296S]SQTDRQDQSYHYGQTDRQGQSSHYSQ	SQTDRQDQSY	PRAD
RRAD	c.833C>A	p.A278E	LRRDSKEANARRQAGTRRRESLGKK[p.A278E]EKRFLGRIVARNSRKMAFRAKSKSCH	KEKRFLGRI,KEKRFLGRIV	KIRC,TGCT
RREB1	c.2348G>T	p.G783V	CGEDLKHYRALRIHMRTHCGRGLGG[p.G783V]VHKGRKPFECKECSAAFAAKRNCIHH	GVHKGRKPF,CGRGLGGVHK	ACC
RRN3	c.25C>T	p.R9C	MAAPLLHT[p.R9C]CLPGDAAASSSAVKKLGASRTGISNM	MAAPLLHTC,LLHTCLPGDA,MAAPLLHTCL,HTCLPGDAAA	KIRP
RRN3	c.31C>T	p.P11S	MAAPLLHTRL[p.P11S]SGDAAASSSAVKKLGASRTGISNMRA	HTRLSGDAA,LLHTRLSGDA,HTRLSGDAAA	KIRP
RRP15	c.642G>T	p.L214F	KEAGSSMRKRAKLISTVSKKDFISV[p.L214F]FRGMDGSTNETASSRKKPKAKQTEVK	SKKDFISVF,VSKKDFISVF,KDFISVFRGM	LUSC
RRS1	c.135delC	p.N45fs	QRITVHKELELQFDLGNLLASDRNP[p.N45fs]RPGCGAPDPRRRPSYRPWRGTTRNCSSTSCGSCPRSAWKRR*	GSCPRSAWK,STSCGSCPR,RRRPSYRPW,SYRPWRGTT,LLASDRNPR,APDPRRRPS,CGSCPRSAW,SSTSCGSCPR,CGSCPRSAWK,GSCPRSAWKR,RRRPSYRPWR,SYRPWRGTTR,NLLASDRNPR,APDPRRRPSY,RPSYRPWRGT,RPWRGTTRNC	STAD
RSBN1	c.1714G>A	p.E572K	SPFKRRRSMNEIKNLQYLPRTSEPR[p.E572K]KVLFEDRTRAHADHVGQGFDWQSTAA	RTSEPRKVL,RTSEPRKVLF,LPRTSEPRKV	UCEC
RSF1	c.1158delA	p.K386fs	HEITEKSTEETEKLKNDQQAKIPLK[p.K386fs]NEKLN*	QAKIPLKNEK,AKIPLKNEKL	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
RSPO2	c.82C>T	p.R28C	FRLFSFALIILNCMDYSHCQGNRWR[p.R28C]CSKRASYVSNPICKGCLSCSKDNGCS	QGNRWRCSK,RWRCSKRAS,RCSKRASYV,WRCSKRASY,CQGNRWRCSK,RWRCSKRASY,QGNRWRCSKR	CRC
RTN1	c.308C>G	p.S103W	ASTGVAGVSSAMDHTFSTTSKDGEG[p.S103W]WCYTSLISDICYPPQEDSTYFTGILQ	EGWCYTSLI,GEGWCYTSL,TSKDGEGWCY,GEGWCYTSLI	LUAD
RTN2	c.938delC	p.P313fs	KTVPILELSPPLWTAIGWVQRGPTP[p.P313fs]LLLSSGFY*	VQRGPTPLL,PLLLSSGFY,WVQRGPTPL,TPLLLSSGF,VQRGPTPLLL,GWVQRGPTPL,TPLLLSSGFY	STAD
RUNX1	c.286_287insG	p.D96fs	LCSVLPTHWRCNKTLPIAFKVVALG[p.D96fs]GCSRWHSGHCDGWQ*	VVALGGCSR,VALGGCSRW,KVVALGGCSR,RWHSGHCDGW	BRCA
RUNX1	c.403A>G	p.R135G	DENYSAELRNATAAMKNQVARFNDL[p.R135G]GFVGRSGRGKSFTLTITVFTNPPQVA	LGFVGRSGR,VARFNDLGF,VARFNDLGFV,RFNDLGFVGR,DLGFVGRSGR,QVARFNDLGF	LAML
RUNX1	c.424_425insA	p.R142fs	LRNATAAMKNQVARFNDLRFVGRSG[p.R142fs]KREKLHSDHHCLHKPTASRHLPQSHQNHSGWAPRTSKTSAETR*	KLHSDHHCL,CLHKPTASR,HSDHHCLHK,SGWAPRTSK,VGRSGKREK,ASRHLPQSH,RTSKTSAET,RFVGRSGKR,QNHSGWAPR,APRTSKTSA,QSHQNHSGW,HQNHSGWAP,HSGWAPRTSK,RTSKTSAETR,KLHSDHHCLH,HQNHSGWAPR,HCLHKPTASR,LHKPTASRHL	BRCA
RUNX2	c.1010G>T	p.R337M	SPSIHSTTPLSSTRGTGLPAITDVP[p.R337M]MRISDDDTATSDFCLWPSTLSKKSQA	AITDVPMRI,LPAITDVPM,GLPAITDVPM	LUAD
RUNX2	c.1397C>A	p.P466H	STPYLYYGTSSGSYQFPMVPGGDRS[p.P466H]HSRMLPPCTTTSNGSTLLNPNLPNQN	RSHSRMLPP,HSRMLPPCT,RSHSRMLPPC,HSRMLPPCTT	KIRC
RUNX2	c.211C>G	p.Q71E	VAAQQQQQQQQQQQQQQQQQQQQQQQ[p.Q71E]EEAAAAAAAAAAAAAAAAAVPRLRPP	QQQQEEAAA,QQQEEAAAA,QQEEAAAAA,QQQQEEAAAA,QQQEEAAAAA,QQEEAAAAAA,QEEAAAAAAA	KIRP,TGCT
RUSC2	c.1456delC	p.P486fs	SSTQAAAAVGPTVLEGQVYTNTSPP[p.P486fs]TSALDVSAPAAMIAACSAALLSAWARWNVC*	AMIAACSAA,MIAACSAAL,AALLSAWAR,ALLSAWARW,NTSPPTSAL,SALDVSAPA,DVSAPAAMI,SAPAAMIAA,IAACSAALL,SAALLSAWA,LSAWARWNV,APAAMIAAC,LDVSAPAAM,CSAALLSAW,AMIAACSAAL,MIAACSAALL,LLSAWARWNV,SAALLSAWAR,YTNTSPPTSA,TSALDVSAPA,DVSAPAAMIA,CSAALLSAWA,ALDVSAPAAM,AAMIAACSAA,ACSAALLSAW,AALLSAWARW	STAD
RUVBL1	c.1291G>A	p.E431K	SVQLLTPANLLAKINGKDSIEKEHV[p.E431K]KEISELFYDAKSSAKILADQQDKYMK	HVKEISELF,VKEISELFY,IEKEHVKEI,HVKEISELFY,KEHVKEISEL,KEISELFYDA	CRC
RUVBL1	c.349C>T	p.R117C	PFCPMVGSEVYSTEIKKTEVLMENF[p.R117C]CRAIGLRIKETKEVYEGEVTELTPCE	VLMENFCRA,EVLMENFCR,NFCRAIGLR,LMENFCRAI,VLMENFCRAI,NFCRAIGLRI,FCRAIGLRIK,ENFCRAIGLR,EVLMENFCRA,MENFCRAIGL	CRC
RWDD2B	c.761G>A	p.R254H	VEGPQSACEEFWSRLRKLNWKRILI[p.R254H]HHREDIPFDGTNDETERQRKFSIFEE	ILIHHREDI,IHHREDIPF,KLNWKRILIH,RILIHHREDI,NWKRILIHHR,LIHHREDIPF	CRC
RXFP1	c.668C>A	p.S223Y	HRLEWLIIEDNHLSRISPPTFYGLN[p.S223Y]YLILLVLMNNVLTRLPDKPLCQHMPR	GLNYLILLV,TFYGLNYLI,FYGLNYLIL,YGLNYLILL,NYLILLVLM,LNYLILLVL,YGLNYLILLV,GLNYLILLVL,TFYGLNYLIL,FYGLNYLILL,LNYLILLVLM,SPPTFYGLNY	UCEC
RXRA	c.1280C>A	p.S427Y	AYCKHKYPEQPGRFAKLLLRLPALR[p.S427Y]YIGLKCLEHLFFFKLIGDTPIDTFLM	LLRLPALRY,LPALRYIGL,LRYIGLKCL,RLPALRYIGL,LLRLPALRYI,ALRYIGLKCL,YIGLKCLEHL,LLLRLPALRY	BLCA
RXRA	c.1280C>T	p.S427F	AYCKHKYPEQPGRFAKLLLRLPALR[p.S427F]FIGLKCLEHLFFFKLIGDTPIDTFLM	LPALRFIGL,LLRLPALRF,LRFIGLKCL,RLPALRFIGL,FIGLKCLEHL,LLRLPALRFI,LLLRLPALRF	BLCA
RYR1	c.2002G>T	p.D668Y	IRPNIFVGRAEGTTQYSKWYFEVMV[p.D668Y]YEVTPFLTAQATHLRVGWALTEGYTP	MVYEVTPFL,KWYFEVMVY,VMVYEVTPF,YEVTPFLTA,FEVMVYEVT,WYFEVMVYEV,VMVYEVTPFL,MVYEVTPFLT,EVMVYEVTPF,SKWYFEVMVY,YEVTPFLTAQ,FEVMVYEVTP	TGCT
RYR1	c.7726G>A	p.A2576T	NRYLCLAVLPLITKCAPLFAGTEHR[p.A2576T]TIMVDSMLHTVYRLSRGRSLTKAQRD	RTIMVDSML,HRTIMVDSM,RTIMVDSMLH,LFAGTEHRTI,FAGTEHRTIM	UCEC
RYR2	c.13002G>T	p.M4334I	ICSLLLGGSLVEGAKKIKVAELLAN[p.M4334I]IPDPTQDEVRGDGEEGERKPLEAALP	KVAELLANI,LLANIPDPT,IPDPTQDEV,NIPDPTQDEV,IKVAELLANI,AELLANIPDP	LUAD

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RYR2	c.2131G>A	p.E711K	VTAEATHLRVGWASTEGYSPYPGGG[p.E711K]KEWGGNGVGDDLFSYGFDGLHLWSGC	KEWGGNGVG,SPYPGGGKEW	LUSC
RYR2	c.6069A>C	p.L2023F	DFHEDLMTHCGIELDEDGSLDGNSD[p.L2023F]FTIRGRLLSLVEKVTYLKKKQAEKPV	GSLDGNSDF,SLDGNSDFTI,FTIRGRLLSL	TGCT
RYR2	c.7239G>C	p.K2413N	IMTFYSALIDLLGRCAPEMHLIHAG[p.K2413N]NGEAIRIRSILRSLIPLGDLVGVISI	LIHAGNGEA,IHAGNGEAI,HLIHAGNGEA,LIHAGNGEAI	LUAD
RYR3	c.5008C>A	p.P1670T	DESKRHGLPGVGLRTCLKPGFRFST[p.P1670T]TCFVVTGEDHQKQSPEIPLESLRTKA	RFSTTCFVV,GFRFSTTCF,FRFSTTCFV,GFRFSTTCFV,PGFRFSTTCF,FRFSTTCFVV	LUAD
RYR3	c.8114G>A	p.R2705Q	LAVGWTVERTKEGEALVQQRENEKL[p.R2705Q]QSVSQANQGNSYSPAPLDLSNVVLSR	RENEKLQSV,RENEKLQSVS,NEKLQSVSQA	CRC
SACS	c.8717G>A	p.R2906Q	FHVNGHFALDSARRNLWRDDNGVGV[p.R2906Q]QSDWNNSLMTALIAPAYVELLIQLKK	QSDWNNSLM,VQSDWNNSL,VQSDWNNSLM	UCEC
SAFB	c.2393delG	p.W798fs	REGQHYPERHGGPERHGRDSRDGWG[p.W798fs]AMALTRG*	DSRDGWGAM,RDGWGAMAL,DGWGAMALTR,RDSRDGWGAM,SRDGWGAMAL	STAD
SAFB	c.2396G>T	p.G799V	EREGQHYPERHGGPERHGRDSRDGW[p.G799V]VGYGSDKRMSEGRGLPPPPRGRRDWG	DSRDGWVGY,VGYGSDKRM,RDSRDGWVGY	TGCT
SAGE1	c.685C>T	p.R229C	HNVCEQKMENVQPAPDNVLLTLRPR[p.R229C]CINMTDTGISPMSTRDPYATITYNVP	TLRPRCINM,RPRCINMTDT,RCINMTDTGI	CRC
SAGE1	c.894C>A	p.H298Q	STGLINVAGAGTPAISTNGLYSTVP[p.H298Q]QNVCEEKMENDQPQPNNVLSTVQPVI	LYSTVPQNV,GLYSTVPQNV	LUAD
SALL3	c.1777C>G	p.L593V	PGLNHVESGVSATAESPQSLLGGPP[p.L593V]VTKAEPVSLPCTNARAGDAPVGAQAS	SLLGGPPVT,LLGGPPVTK,LLGGPPVTKA,SLLGGPPVTK	ACC
SALL4	c.2983delG	p.V995fs	NQYTSMLNGGLAVKTNEISVIQSGG[p.V995fs]FLPSRFPWGPPPL*	FLPSRFPWG,GFLPSRFPW,RFPWGPPPL,ISVIQSGGF,IQSGGFLPS,SGGFLPSRF,SRFPWGPPP,FLPSRFPWGP,QSGGFLPSRF,GGFLPSRFPW,SRFPWGPPPL	STAD
SALL4	c.560G>T	p.R187L	PPTPQDISYLAKGKVANTNVTLQAL[p.R187L]LGTKVAVNQRSADALPAPVPGANSIP	ALLGTKVAV,LQALLGTKV,TLQALLGTK,TLQALLGTKV,VTLQALLGTK,NTNVTLQALL,LQALLGTKVA	LUAD
SAMD3	c.618G>T	p.Q206H	DMTKYLEGSLYPSTQQYNDVVNALL[p.Q206H]HAHPFLDEDGCGFFLWKRALKDRFKY	ALLHAHPFL,NALLHAHPF,VNALLHAHPF	LUSC
SAMD4B	c.1429C>T	p.R477W	APAPTDGSEPAPAPVADGDIPSQFT[p.R477W]WVMGKVCTQLLVSRPDEENITSYLQL	SQFTWVMGK,DIPSQFTWV,IPSQFTWVM,GDIPSQFTW,SQFTWVMGKV,WVMGKVCTQL,PSQFTWVMGK,DIPSQFTWVM	UCS
SBF1	c.3228delC	p.P1076fs	SRNLVKNAKKTIGRQHVTRKKYNPP[p.P1076fs]AGSTGASRPLRTRRTRSQCRRSWSPAR*	STGASRPLR,ASRPLRTRR,RTRRTRSQC,RTRSQCRRS,RSQCRRSWS,VTRKKYNPPA,ASRPLRTRRT,RTRRTRSQCR,RTRSQCRRSW,RSQCRRSWSP,QCRRSWSPAR,RPLRTRRTRS,KKYNPPAGST,SQCRRSWSPA	STAD
SBNO1	c.3415_3416insA	p.N1139fs	EVHQQNALFQYFADTLTAVVQNAKK[p.N1139fs]KWKI*	AVVQNAKKK,VQNAKKKWK,VVQNAKKKWK	STAD
SBSPON	c.397G>T	p.G133W	GGAPCPPLEERAGCLEYSTPQGQDC[p.G133W]WHTYVPAFITTSAFNKERTRQATSPH	GQDCWHTYV,CWHTYVPAF,QGQDCWHTY,CWHTYVPAFI,PQGQDCWHTY,YSTPQGQDCW	LUAD
SCAF1	c.624_625insC	p.P208fs	PPPAPSSASSSPSPSPSSSSPSPPP[p.P208fs]TPTAPCTPSPTCPPIRYL*	SPSPPPTPT,TPSPTCPPI,SPTCPPIRY,CTPSPTCPPI,SPSPPPTPTA,SPTCPPIRYL	KIRC
SCAF11	c.2776_2777delGA	p.E926fs	SSPGEKSRSQSRERESDRDGQRRER[p.E926fs]KENQKVV*	RERKENQKV,RERKENQKVV	GBM,KIRP
SCAF8	c.2218G>T	p.G740C	LVQPSLSMTPETVKDVGFGSLVIPG[p.G740C]CSVASNLATSALPAGNVFNAPTKQAE	SLVIPGCSV,LVIPGCSVA,SLVIPGCSVA,IPGCSVASNL	LUAD

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SCAPER	c.1097G>A	p.R366Q	AEKTQFTVSTLDDVKNSGSIRDNYV[p.R366Q]QTSEISAVHIDTECVSVMLQAGTPPL	VQTSEISAV,YVQTSEISAV,QTSEISAVHI,RDNYVQTSEI,VQTSEISAVH	UCEC
SCARF1	c.1841G>A	p.R614Q	SVSFAEGTKFAPQSRRSSGELSSPL[p.R614Q]QKPKRLSRGAQSGPEGREAEESTGPE	LSSPLQKPK,LQKPKRLSR,SPLQKPKRL	STAD
SCFD2	c.1633C>T	p.R545W	TDWDSSINLTFHKSKIAVDELFTSL[p.R545W]WDIAGARSLLKQFKSVYVPGNHTHQA	ELFTSLWDI,SLWDIAGAR,TSLWDIAGA,WDIAGARSL,FTSLWDIAGA,ELFTSLWDIA,TSLWDIAGAR,WDIAGARSLL,DELFTSLWDI	CRC
SCLT1	c.327delA	p.K109fs	MKLQLENVIKENERLHSELKDAVEK[p.K109fs]NWRPFPWAQR*	KNWRPFPWA,AVEKNWRPF,EKNWRPFPW,NWRPFPWAQR,VEKNWRPFPW,DAVEKNWRPF	STAD
SCML4	c.581G>A	p.R194Q	GKQHLRSLPVVNSIGYVLRFLAKLC[p.R194Q]QSLLCDDLFSHQPFPRGCSASEKVQE	FLAKLCQSL,FLAKLCQSLL,RFLAKLCQSL,CQSLLCDDLF	CRC
SCML4	c.783G>T	p.L261F	YLVNPVGMNRYSVDTSASTFNHRGS[p.L261F]FHPSSSLYCKRQNSGDSHLGGGPAAT	STFNHRGSF,SFHPSSSLY,GSFHPSSSL,STFNHRGSFH,GSFHPSSSLY,RGSFHPSSSL,ASTFNHRGSF	LUAD
SCN10A	c.3425G>A	p.R1142H	EGCIRHCPCCKLDTTKSPWDVGWQV[p.R1142H]HKTCYRIVEHSWFESFIIFMILLSSG	WQVHKTCYR,WQVHKTCYRI,VGWQVHKTCY,SPWDVGWQVH	MM
SCN10A	c.4709C>T	p.T1570M	IVVVLSIASLIFSAILKSLQSYFSP[p.T1570M]MLFRVIRLARIGRILRLIRAAKGIRT	SLQSYFSPM,LQSYFSPML,YFSPMLFRV,MLFRVIRLA,SYFSPMLFR,QSYFSPMLF,SPMLFRVIR,SLQSYFSPML,QSYFSPMLFR,MLFRVIRLAR,LQSYFSPMLF,SYFSPMLFRV,YFSPMLFRVI,KSLQSYFSPM,FSPMLFRVIR,SPMLFRVIRL	CRC
SCN2A	c.107G>A	p.R36K	PDSFRFFTRESLAAIEQRIAEEKAK[p.R36K]KPKQERKDEDDENGPKPNSDLEAGKS	RIAEEKAKK,KAKKPKQER,KAKKPKQERK	BRCA
SCN2A	c.464C>A	p.T155K	LFNMLIMCTILTNCVFMTMSNPPDW[p.T155K]KKNVEYTFTGIYTFESLIKILARGFC	TMSNPPDWK,MSNPPDWKK,WKKNVEYTF,MTMSNPPDWK,TMSNPPDWKK,DWKKNVEYTF	LUAD
SCN7A	c.4073G>A	p.R1358H	MTVGSYLVPPSLVQLILLSRIIHML[p.R1358H]HLGKGPKVFHNLMLPLMLSLPALLNI	IIHMLHLGK,MLHLGKGPK,LSRIIHMLH,SRIIHMLHL,HLGKGPKVF,MLHLGKGPKV,RIIHMLHLGK,HMLHLGKGPK,LSRIIHMLHL,LHLGKGPKVF	GBM
SCNN1G	c.1691G>A	p.R564H	MSCSVVCVIEIIEVFFIDFFSIIAR[p.R564H]HQWQKAKEWWAWKQAPPCPEAPRSPQ	IIARHQWQK,IARHQWQKA,DFFSIIARH,FSIIARHQW,HQWQKAKEW,IIARHQWQKA,SIIARHQWQK,FFSIIARHQW,IARHQWQKAK,HQWQKAKEWW	GBM
SCRIB	c.995G>T	p.G332V	SLGKLTKLTNLNVDRNHLEALPPEI[p.G332V]VGCVALSVLSLRDNRLAVLPPELAHT	IVGCVALSV,ALPPEIVGC,LEALPPEIV,PEIVGCVAL,LPPEIVGCV,ALPPEIVGCV,EIVGCVALSV,LPPEIVGCVA	TGCT
SCRT1	c.397T>G	p.S133A	VSEGYAADAFFITDGRSRRKASNAG[p.S133A]AAAAPSTASAAAPDGDAGGGGGAGGR	RRKASNAGA,KASNAGAAA,RKASNAGAA,KASNAGAAAA,RKASNAGAAA,AAAAPSTASA	ACC
SCUBE2	c.1024G>A	p.V342M	DGKTCKDIDECQTRNGGCDHFCKNI[p.V342M]MGSFDCGCKKGFKLLTDEKSCQDVDE	FCKNIMGSF,CDHFCKNIM,IMGSFDCGCK,HFCKNIMGSF	CRC
SDAD1	c.824delA	p.K275fs	YATGKKSSKNKKKLEKAMKVLKKQK[p.K275fs]RRKNQRCLTFQPFT*	KVLKKQKRR,VLKKQKRRK,KQKRRKNQR,RKNQRCLTF,QRCLTFQPF,KVLKKQKRRK,AMKVLKKQKR,NQRCLTFQPF,RRKNQRCLTF	STAD
SDHAP1	c.196C>T	p.H66Y	DYKVRIDEYDHSKPIQGQQKKPFEE[p.H66Y]YWRKHTLSYVDVSTGKVTVEYRPIID	YWRKHTLSY,QQKKPFEEY,EEYWRKHTL,EYWRKHTLSY,YWRKHTLSYV,GQQKKPFEEY,QQKKPFEEYW,FEEYWRKHTL	CESC
SDHAP2	c.110_111insTT	p.S37fs	VGRPPVPLHMVSTASGQTRCWTWLS[p.S37fs]LVRHVP*	CWTWLSLVR,TRCWTWLSL,WTWLSLVRHV,QTRCWTWLSL	CESC
SDHAP2	c.91C>T	p.R31C	LCPACTPVGRPPVPLHMVSTASGQT[p.R31C]CCWTWLSGQACALSIAESCRPGDKVP	SGQTCCWTW,GQTCCWTWL,TASGQTCCW	GBM,PRAD
SDHAP3	c.196G>A	p.A66T	AACASVHGANRLGANSLLDLVVFGQ[p.A66T]TCALSIEESCRPGDKVPPIKPNAGEE	VVFGQTCAL,FGQTCALSI,VFGQTCALSI,LVVFGQTCAL	GBM
SDK1	c.1524_1525insC	p.K508fs	RPVDTTVTDGMTAILRCEVSGAPKP[p.K508fs]RHHLEKRKPHSGQWLCPDS*	EVSGAPKPR,KRKPHSGQW,RKPHSGQWL,APKPRHHLEK,KPRHHLEKRK,KRKPHSGQWL	KIRC

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SDK1	c.3542C>T	p.T1181M	PSPYSPSSRVIQTLQAPPDVAPTSV[p.T1181M]MVRTASETSLRLRWVPLPDSQYNGNP	DVAPTSVMV,MVRTASETSL,DVAPTSVMVR,APTSVMVRTA	CRC
SDK1	c.6437A>G	p.Y2146C	ADASESEATDSDYEDALPKHSFVNH[p.Y2146C]CMSDPTYYNSWKRRAQGRAPAPHRYE	HCMSDPTYY,KHSFVNHCM,NHCMSDPTY,FVNHCMSDPT,VNHCMSDPTY	TGCT
SEC24D	c.150_151insC	p.A50fs	YGHYGDPSHTASPTGMMKPAGPLGA[p.A50fs]HRH*	MKPAGPLGAH	LUAD
SEC31B	c.2713C>T	p.P905S	GVRPASSQPQLLGGQRVQVPNPVGF[p.P905S]SGTWPLPGSPLPMACPGIMRPGSTSL	VGFSGTWPL,NPVGFSGTW	TGCT
SEC61A2	c.377G>T	p.G126V	EVGDTPKDRALFNGAQKLFGMIITI[p.G126V]VQAIVYVMTGMYGDPAEMGAGICLLI	ITIVQAIVY,MIITIVQAI,TIVQAIVYV,GMIITIVQA,IITIVQAIV,IVQAIVYVM,KLFGMIITIV,GMIITIVQAI,MIITIVQAIV,ITIVQAIVYV,IITIVQAIVY,TIVQAIVYVM	LUAD
SECISBP2	c.1824C>G	p.D608E	GMDELISTPSVEDKSEEPPGTELQR[p.D608E]ETEASHLAPNHTTFPKIHSRRFRDYC	LQRETEASH,RETEASHLA,TELQRETEA,LQRETEASHL,RETEASHLAP	KIRC
SELP	c.1285C>T	p.R429W	RAFQYDTNCSFRCAEGFMLRGADIV[p.R429W]WCDNLGQWTAPAPVCQALQCQDLPVP	VWCDNLGQW,MLRGADIVW,FMLRGADIVW,IVWCDNLGQW	UCEC
SELP	c.889G>A	p.A297T	NMTCLHSAKAFQHQSSCSFSCEEGF[p.A297T]TLVGPEVVQCTASGVWTAPAPVCKAV	FTLVGPEVV,FSCEEGFTL,FSCEEGFTLV,EGFTLVGPEV	TGCT
SEMA3A	c.241G>A	p.D81N	SYHTFLLDEERSRLYVGAKDHIFSF[p.D81N]NLVNIKDFQKIVWPVSYTRRDECKWA	FSFNLVNIK,IFSFNLVNI,KDHIFSFNL,HIFSFNLVNI,NLVNIKDFQK,SFNLVNIKDF,KDHIFSFNLV	CRC
SEMA4D	c.755G>A	p.R252Q	EDDRVYFFFTEVSVEYEFVFRVLIP[p.R252Q]QIARVCKGDQGGLRTLQKKWTSFLKA	VLIPQIARV,RVLIPQIAR,FVFRVLIPQI,RVLIPQIARV,VFRVLIPQIA	CRC
SEMG2	c.874C>T	p.R292C	QHQTKNLSQDQEHGRKAHKISYPSS[p.R292C]CTEERQLHHGEKSVQKDVSKGSISIQ	CTEERQLHH,HKISYPSSC	GBM
SENP7	c.2018C>A	p.S673Y	ELELSYPLSWVQAFPLFQNLSSKES[p.S673Y]YFIHYYCVSTCSFPAGVAVAEEMKLK	SYFIHYYCV,SSKESYFIH,KESYFIHYY,ESYFIHYYC,QNLSSKESY,NLSSKESYF,SKESYFIHY,NLSSKESYFI,SSKESYFIHY,FQNLSSKESY,SKESYFIHYY,ESYFIHYYCV,QNLSSKESYF,KESYFIHYYC	UCEC
SEPHS1	c.1112G>A	p.R371Q	GEGHQAWIIGIVEKGNRTARIIDKP[p.R371Q]QIIEVAPQVATQNVNPTPGATS*	QIIEVAPQV,RIIDKPQII,IIDKPQIIEV	CRC
SEPHS1	c.37G>A	p.E13K	MSTRESFNPESY[p.E13K]KLDKSFRLTRFTELKGTGCKVPQDVL	ESFNPESYK,SFNPESYKL,SYKLDKSFR,ESYKLDKSF,YKLDKSFRL,KLDKSFRLTR,SYKLDKSFRL,ESYKLDKSFR,ESFNPESYKL	UCEC
SERPINA12	c.631C>G	p.R211G	HGKINNLIENIDPGTVMLLANYIFF[p.R211G]GARWKHEFDPNVTKEEDFFLEKNSSV	LLANYIFFG,YIFFGARWK,NYIFFGARW,FGARWKHEF,ANYIFFGAR,LANYIFFGA,MLLANYIFFG,LLANYIFFGA,LANYIFFGAR,FFGARWKHEF,ANYIFFGARW	BLCA
SERPINA12	c.757G>T	p.D253Y	FFLEKNSSVKVPMMFRSGIYQVGYD[p.D253Y]YKLSCTILEIPYQKNITAIFILPDEG	YQVGYDYKL,GIYQVGYDY,YDYKLSCTI,GIYQVGYDYK,IYQVGYDYKL,SGIYQVGYDY,YDYKLSCTIL,YKLSCTILEI	LUAD
SERPINA3	c.474G>C	p.K158N	LQLSMGNAMFVKEQLSLLDRFTEDA[p.K158N]NRLYGSEAFATDFQDSAAAKKLINDY	FTEDANRLY,NRLYGSEAF,RFTEDANRLY,ANRLYGSEAF	CESC
SERPINA4	c.292C>T	p.R98C	HQQILETGEGSPSLKIAPANADFAF[p.R98C]CFYYLIASETPGKNIFFSPLSISAAY	NADFAFCFY,FAFCFYYLI,DFAFCFYYL,ADFAFCFYY,ANADFAFCF,NADFAFCFYY,FAFCFYYLIA,DFAFCFYYLI,ANADFAFCFY,ADFAFCFYYL	CESC
SERPINA9	c.1242G>T	p.M414I	TTKFIVRSKDGPSYFTVSFNRTFLM[p.M414I]IITNKATDGILFLGKVENPTKS*	FLMIITNKA,TFLMIITNK,SFNRTFLMI,FNRTFLMII,FLMIITNKAT,RTFLMIITNK,VSFNRTFLMI,SFNRTFLMII	LUAD
SERPINB12	c.503delA	p.Q168fs	PICQEYLDGVIQFYHTTIESVDFQK[p.Q168fs]TLKNPDKRLTSGLNVNPKVKSRNSSARTLLMLRLCWYW*	NSSARTLLM,SVDFQKTLK,KTLKNPDKR,TSGLNVNPK,SARTLLMLR,LMLRLCWYW,KVKSRNSSA,KSRNSSART,RNSSARTLL,LLMLRLCWY,NVNPKVKSR,KRLTSGLNV,SRNSSARTL,SSARTLLML,IESVDFQKT,LTSGLNVNPK,SSARTLLMLR,RTLLMLRLCW,LLMLRLCWYW,FQKTLKNPDK,SGLNVNPKVK,KVKSRNSSAR,KSRNSSARTL,RNSSARTLLM,SARTLLMLRL,TLLMLRLCWY,NPDKRLTSGL,IESVDFQKTL,SRNSSARTLL	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SERPINB3	c.626C>G	p.S209C	GQWENKFKKENTKEEKFWPNKNTYK[p.S209C]CVQMMRQYNSFNFALLEDVQAKVLEI	KCVQMMRQY,TYKCVQMMR,NTYKCVQMM,NTYKCVQMMR,WPNKNTYKCV,NKNTYKCVQM,YKCVQMMRQY	KIRC
SERPINC1	c.134G>T	p.R45L	SLLLIGFWDCVTCHGSPVDICTAKP[p.R45L]LDIPMNPMCIYRSPEKKATEDEGSEQ	TAKPLDIPM,VDICTAKPL,CTAKPLDIPM,KPLDIPMNPM	LUAD
SERPINI1	c.243delA	p.L81fs	GMMELGAQGSTQKEIRHSMGYDSLK[p.L81fs]MVKNFLS*	SLKMVKNFL,SMGYDSLKM,SMGYDSLKMV,MGYDSLKMVK,SLKMVKNFLS,HSMGYDSLKM	STAD
SESTD1	c.918T>G	p.I306M	VMQVVNWLEGPGSEQLRAQWGIGDS[p.I306M]MRASQALQQKHEEIESQHSEWFAVYV	SMRASQALQ,DSMRASQAL,AQWGIGDSM,SMRASQALQQ,RAQWGIGDSM	KIRC
SETDB2	c.2145delA	p.R715fs	YGYEAGTVPEKEIFCQCGVNKCRKK[p.R715fs]YYKYVTNACL*	KYYKYVTNA,KCRKKYYKY,GVNKCRKKY,YKYVTNACL,KYYKYVTNAC,YYKYVTNACL,VNKCRKKYYK,KCRKKYYKYV,GVNKCRKKYY,KKYYKYVTNA	STAD
SEZ6L	c.620C>T	p.S207L	VPLWLDRKESAVPTTPAPLQISPFT[p.S207L]LQPYVAHTLPQRPEPGEPGPDMAQEA	TLQPYVAHT,LQPYVAHTL,ISPFTLQPY,LQISPFTLQ,SPFTLQPYV,TLQPYVAHTL,QISPFTLQPY,ISPFTLQPYV,APLQISPFTL,LQISPFTLQP,SPFTLQPYVA	CRC
SEZ6L2	c.221G>C	p.R74P	EALAELLHGALLRRGPEMGYLPGSD[p.R74P]PDPTLATPPAGQTLAVPSLPRATEPG	YLPGSDPDPT,LPGSDPDPTL	ACC
SF1	c.763C>T	p.R255W	IETPEDQNDLRKMQLRELARLNGTL[p.R255W]WEDDNRILRPWQSSETRSITNTTVCT	TLWEDDNRI,LARLNGTLW,TLWEDDNRIL	CESC
SF3B1	c.1868A>G	p.Y623C	SNLAKAAGLATMISTMRPDIDNMDE[p.Y623C]CVRNTTARAFAVVASALGIPSLLPFL	CVRNTTARA,CVRNTTARAF	CLL
SF3B1	c.1876A>T	p.N626Y	AKAAGLATMISTMRPDIDNMDEYVR[p.N626Y]YTTARAFAVVASALGIPSLLPFLKAV	NMDEYVRYT,YTTARAFAV,YVRYTTARA,RYTTARAFA,EYVRYTTAR,VRYTTARAF,DEYVRYTTA,NMDEYVRYTT,YTTARAFAVV,RYTTARAFAV,YVRYTTARAF,IDNMDEYVRY,DEYVRYTTAR	CLL
SF3B1	c.1996A>G	p.K666E	IPSLLPFLKAVCKSKKSWQARHTGI[p.K666E]EIVQQIAILMGCAILPHLRSLVEIIE	QARHTGIEI,EIVQQIAIL,IEIVQQIAI,WQARHTGIEI,EIVQQIAILM,IEIVQQIAIL	CLL
SF3B1	c.2098A>G	p.K700E	MGCAILPHLRSLVEIIEHGLVDEQQ[p.K700E]EVRTISALAIAALAEAATPYGIESFD	GLVDEQQEV,EVRTISALA,QEVRTISAL,DEQQEVRTI,EVRTISALAI,QQEVRTISAL,DEQQEVRTIS,QEVRTISALA	BRCA,CLL
SF3B1	c.2704G>A	p.E902K	GNLGAADIDHKLEEQLIDGILYAFQ[p.E902K]KQTTEDSVMLNGFGTVVNALGKRVKP	ILYAFQKQT,KQTTEDSVM,ILYAFQKQTT,FQKQTTEDSV,QKQTTEDSVM,KQTTEDSVML	BLCA
SF3B1	c.2870G>A	p.R957Q	ICGTVLWRLNNKSAKVRQQAADLIS[p.R957Q]QTAVVMKTCQEEKLMGHLGVVLYEYL	DLISQTAVV,ISQTAVVMK,LISQTAVVM,ADLISQTAV,LISQTAVVMK,QAADLISQTA,DLISQTAVVM,RQQAADLISQ	UCEC
SFI1	c.2462G>A	p.R821Q	THHLQCVRKRLLHRQSTQLLAQRLS[p.R821Q]QTCFRQWRQQLAARRQEQRATVRALW	LLAQRLSQT,SQTCFRQWR,AQRLSQTCF,LSQTCFRQW,LLAQRLSQTC,AQRLSQTCFR,LSQTCFRQWR,LAQRLSQTCF,RLSQTCFRQW	HNSC
SFPQ	c.1832G>A	p.R611Q	EEQMRRQREESYSRMGYMDPRERDM[p.R611Q]QMGGGGAMNMGDPYGSGGQKFPPLGG	MQMGGGGAM,DMQMGGGGAM,QMGGGGAMNM,MQMGGGGAMN	CRC
SFRP4	c.695G>A	p.R232Q	QRSGCNEVTTVVDVKEIFKSSSPIP[p.R232Q]QTQVPLITNSSCQCPHILPHQDVLIM	IPQTQVPLI,SSSPIPQTQV,SPIPQTQVPL	UCEC
SFSWAP	c.1850C>A	p.S617Y	PLEKNRVKLDDDSDDDEESKEGQES[p.S617Y]YSSAANTNPAVAPPCVVVEEKKPQLT	ESKEGQESY,GQESYSSAA,YSSAANTNPA,KEGQESYSSA,EESKEGQESY,QESYSSAANT	CRC
SGCG	c.659C>T	p.A220V	ESPTRSLSMDAPRGVHIQAHAGKIE[p.A220V]VLSQMDILFHSSDGMLVLDAETVCLP	EVLSQMDIL,VLSQMDILF,GKIEVLSQM,IEVLSQMDI,IQAHAGKIEV,QAHAGKIEVL,IEVLSQMDIL,EVLSQMDILF	CRC
SGCZ	c.123T>G	p.I41M	REQYILATQQNNLPRTENAQLYPVG[p.I41M]MYGWRKRCLYFFVLLLLVTMIVNLAM	LYPVGMYGW,MYGWRKRCL,AQLYPVGMY,GMYGWRKRCL,MYGWRKRCLY,NAQLYPVGMY,QLYPVGMYGW	CRC
SGIP1	c.1505G>T	p.R502L	GVGDVSRPFSPPIHSSSPPPIAPLA[p.R502L]LAESTSSISSTNSLSAATTPTVENEQ	ALAESTSSI,ALAESTSSIS,SPPPIAPLAL,LALAESTSSI	LUAD

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SGK1	c.1100_1102delAGA	p.K367del	AKDDFMEIKSHVFFSLINWDDLINK[p.K367del]ITPPFNPNVSGPNDLRHFDPEFTEEPVP	LINKITPPF,DLINKITPPF	UCEC
SGK3	c.183delA	p.L61fs	SEWFVFRRYAEFDKLYNTLKKQFPA[p.L61fs]WP*	TLKKQFPAW	STAD
SGOL2	c.1220delA	p.E407fs	KKSNKKTNEHGMKTFRKVKDSSSEK[p.E407fs]REKDQRDSLKIVQMSILGKRLKTGQKDLMSWMAKGVQKIPVLFSIMNSWLR*	LMSWMAKGV,WMAKGVQKI,SLKIVQMSI,IVQMSILGK,MSILGKRLK,SWMAKGVQK,FSIMNSWLR,GVQKIPVLF,KDLMSWMAK,GQKDLMSWM,REKDQRDSL,RDSLKIVQM,LKIVQMSIL,KGVQKIPVL,QKIPVLFSI,KIPVLFSIM,VLFSIMNSW,DLMSWMAKGV,VLFSIMNSWL,SLKIVQMSIL,KIVQMSILGK,QMSILGKRLK,MSWMAKGVQK,SWMAKGVQKI,KGVQKIPVLF,KVKDSSSEKR,REKDQRDSLK,LGKRLKTGQK,RLKTGQKDLM,MAKGVQKIPV,IVQMSILGKR,LFSIMNSWLR,VQMSILGKRL,KRLKTGQKDL,GQKDLMSWMA,AKGVQKIPVL,VQKIPVLFSI,QKIPVLFSIM	STAD
SGSM1	c.2452G>A	p.E818K	VLDAQRNTPTVLRPRDGSVDDRQSS[p.E818K]KATTSQDEAPREELAVQDSLESDLLA	SVDDRQSSK,RQSSKATTS,GSVDDRQSSK,RQSSKATTSQ	CESC
SGSM1	c.3351C>A	p.F1117L	IALALVEVYRDIILENNMDFTDIIK[p.F1117L]LFNEMAERHNTKQVLKLARDLVYKVQ	FTDIIKLFN,KLFNEMAER,DFTDIIKLF,DIIKLFNEM,MDFTDIIKL,NMDFTDIIKL,DIIKLFNEMA,MDFTDIIKLF	CRC
SH3KBP1	c.1688_1689insC	p.P563fs	ISQVSDNKASLPPKPGTMAAGGGGP[p.P563fs]SPSVLSGALPPVILFGNSWTQSQLPVSVRHGRKTKDGACGQQPGGRGGAKDTGPRAEEHHRDHEGPAETRD*	VLSGALPPV,TQSQLPVSV,GALPPVILF,PVSVRHGRK,SVRHGRKTK,LPVSVRHGR,SPSVLSGAL,SWTQSQLPV,SQLPVSVRH,SVLSGALPPV,VLSGALPPVI,ILFGNSWTQS,WTQSQLPVSV,VSVRHGRKTK,QLPVSVRHGR,NSWTQSQLPV,SGALPPVILF,FGNSWTQSQL,SQLPVSVRHG,PPVILFGNSW	KIRC
SH3KBP1	c.1720delC	p.L574fs	LPPKPGTMAAGGGGPAPLSSAAPSP[p.L574fs]CHPLWEQLDTEPTPRLCSARKENQRWSLRPAARRPWRS*	RWSLRPAAR,RPAARRPWR,CSARKENQR,WSLRPAARR,RKENQRWSL,NQRWSLRPA,QRWSLRPAA,WEQLDTEPT,APSPCHPLW,RWSLRPAARR,SLRPAARRPW,EQLDTEPTPR,SAAPSPCHPL,RPAARRPWRS,NQRWSLRPAA	STAD
SH3PXD2A	c.2276C>T	p.S759L	SSDLITLPATTPPCPTKKEWEGPAT[p.S759L]LYMTCSAYQKVQDSEISFPAGVEVQV	TLYMTCSAY,ATLYMTCSA,KEWEGPATL,WEGPATLYM,ATLYMTCSAY,LYMTCSAYQK,KEWEGPATLY,KKEWEGPATL,WEGPATLYMT	LUAD
SH3RF2	c.952C>T	p.R318C	RKVPGQFSITTALNTLNRMVHSPSG[p.R318C]CHMVEISTPVLISSSNPSVITQPMEK	HSPSGCHMV,VHSPSGCHM,MVHSPSGCHM,SPSGCHMVEI,RMVHSPSGCH,CHMVEISTPV	GBM
SH3TC2	c.265C>T	p.R89C	RCVNGPLQEAARRRLWALENEDQEV[p.R89C]CMLFKDLSARLVSIQSQRAQFLITFK	NEDQEVCML,CMLFKDLSAR,LENEDQEVCM,NEDQEVCMLF,QEVCMLFKDL	CRC
SHB	c.1378G>A	p.A460T	RNSQTSKHDYSLSLRSNQGFMHMKL[p.A460T]TKTKEKYVLGQNSPPFDSVPEVIHYY	FMHMKLTKT,GFMHMKLTK,KLTKTKEKY,KLTKTKEKYV,FMHMKLTKTK,QGFMHMKLTK,HMKLTKTKEK,LTKTKEKYVL,MKLTKTKEKY	GBM
SHROOM4	c.3468_3470delAGA	p.1156_1157EE>E	EEEEEEEEEEEEEEEEEEEAEEEEE[p.1156_1157EE>E]LPPQYFSSETSGSCALNPEEVLEQPQPL	EEAEEEEEL	PAAD
SI	c.3649G>T	p.V1217F	LDFYMFLGPTPEVATKQYHEVIGHP[p.V1217F]FMPAYWALGFQLCRYGYANTSEVREL	FMPAYWALG,PFMPAYWAL,IGHPFMPAY,HPFMPAYWA,YHEVIGHPF,HEVIGHPFM,FMPAYWALGF,QYHEVIGHPF,VIGHPFMPAY,EVIGHPFMPA,HPFMPAYWAL,YHEVIGHPFM,IGHPFMPAYW	LUAD
SI	c.5042T>A	p.I1681K	WFDYHTGKDIGVRGQFQTFNASYDT[p.I1681K]KNLHVRGGHILPCQEPAQNTFYSRQK	TFNASYDTK,QTFNASYDTK,ASYDTKNLHV	TGCT
SIGLEC1	c.954delC	p.P318fs	QAAWSDAGVYTCQAENGVGSLVSPP[p.P318fs]SASTSSWLRSR*	SASTSSWLR,STSSWLRSR,PPSASTSSW,ASTSSWLRSR,SPPSASTSSW	STAD
SIGLEC10	c.749C>T	p.T250M	SAQRTVRLRVAYAPRDLVISISRDN[p.T250M]MPALEPQPQGNVPYLEAQKGQFLRLL	ISRDNMPAL,MPALEPQPQ,SISRDNMPAL,LVISISRDNM,ISISRDNMPA,MPALEPQPQG	GBM
SIGLEC11	c.1088C>T	p.S363F	NRLGSQQQALDLSVQYPPENLRVMV[p.S363F]FQANRTVLENLGNGTSLPVLEGQSLR	MVFQANRTV,RVMVFQANR,VMVFQANRTV,RVMVFQANRT,MVFQANRTVL,FQANRTVLEN	CRC

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SIK1	c.2032delC	p.Q678fs	EVLEQQRLLQLQHHPAAAPGCSQAP[p.Q678fs]SRPLPRL*	QAPSRPLPR,APSRPLPRL,CSQAPSRPL,SQAPSRPLP,SQAPSRPLPR	STAD
SIM1	c.637G>A	p.V213M	YLKIRQYSLDMSPFDGCYQNVGLVA[p.V213M]MGHSLPPSAVTEIKLHSNMFMFRASL	YQNVGLVAM,GLVAMGHSL,MGHSLPPSA,VAMGHSLPP,AMGHSLPPSA,CYQNVGLVAM,YQNVGLVAMG,MGHSLPPSAV	CESC
SIPA1L1	c.3188G>A	p.R1063Q	SETYRMPVMEYKMNEGVSYEFKFPF[p.R1063Q]QNNNKWQRNASKGPHSPQVPSQVQSP	KFPFQNNNK,FQNNNKWQR,FPFQNNNKW,YEFKFPFQN,KFPFQNNNKW,YEFKFPFQNN	CRC
SIPA1L1	c.3680C>A	p.S1227Y	PSWQRSEDSIADQMAYSYRGPQDFN[p.S1227Y]YFVLEQHEYTEPTCHLPAVSKVLPAF	RGPQDFNYF,YFVLEQHEY,YRGPQDFNY,YRGPQDFNYF,SYRGPQDFNY,NYFVLEQHEY,GPQDFNYFVL	CRC
SIPA1L3	c.2330G>C	p.G777A	RVHNPCTDNVCYSMAVTRSKDAPPF[p.G777A]APPIPSGTTFRKSDVFRDFLLAKVIN	RSKDAPPFA,DAPPFAPPI,RSKDAPPFAP,APPIPSGTTF,KDAPPFAPPI	KIRC
SIRPA	c.387_389delCGA	p.D131del	IRIGNITPADAGTYYCVKFRKGSPD[p.D131del]VEFKSGAGTELSVRAKPSAPVVSGPAAR	KGSPDVEFK,KFRKGSPDV,RKGSPDVEF,VKFRKGSPDV,FRKGSPDVEF	KIRC
SIRPA	c.697G>A	p.V233I	SIHSTAKVVLTREDVHSQVICEVAH[p.V233I]ITLQGDPLRGTANLSETIRVPPTLEV	QVICEVAHI,VICEVAHITL,SQVICEVAHI	PRAD
SIX1	c.571G>A	p.E191K	TQVSNWFKNRRQRDRAAEAKERENT[p.E191K]KNNNSSSNKQNQLSPLEGGKPLMSSS	KNNNSSSNK	UCEC
SIX3	c.79A>C	p.I27L	VFRSPLDLYSSHFLLPNFADSHHRS[p.I27L]LLLASSGGGNGAGGGGGAGGGSGGGN	FADSHHRSL,FADSHHRSLL	CLL
SKI	c.185C>G	p.A62G	AFSARWAQEAYKKESAKEAGAAAAVP[p.A62G]GPVPAATEPPPVLHLPAIQPPPPVLP	GAAAVPGPV,KEAGAAAVPG	KIRP
SKOR1	c.2648A>G	p.Y883C	EEMVQQLQIVRDTLCNELDQERKAR[p.Y883C]CAIQQKLKEAHDALHHFSCKMLTPRH	KARCAIQQK,RCAIQQKLK,QERKARCAI,KARCAIQQKL	LUAD
SLAMF1	c.829delA	p.S277fs	LIMVVILQLRRRGKTNHYQTTVEKK[p.S277fs]ALRSMPKSRNQVLFRRNLTPSQLRTLAPPYMLLPQSLSQSLSRKQIPSQSMLV*	TLAPPYMLL,SMPKSRNQV,KQIPSQSML,QIPSQSMLV,KSRNQVLFR,SLSQSLSRK,QSLSQSLSR,RTLAPPYML,PYMLLPQSL,KKALRSMPK,ALRSMPKSR,RSMPKSRNQ,RNLTPSQLR,QLRTLAPPY,TTVEKKALR,MPKSRNQVL,TPSQLRTLA,LPQSLSQSL,VEKKALRSM,NQVLFRRNL,RRNLTPSQL,SQLRTLAPP,LRTLAPPYM,SQSLSRKQI,RKQIPSQSM,LLPQSLSQSL,KQIPSQSMLV,SMPKSRNQVL,KSRNQVLFRR,QSLSQSLSRK,RTLAPPYMLL,KALRSMPKSR,RSMPKSRNQV,QLRTLAPPYM,SQLRTLAPPY,QTTVEKKALR,MPKSRNQVLF,PPYMLLPQSL,YQTTVEKKAL,FRRNLTPSQL,YMLLPQSLSQ,SRKQIPSQSM,RKQIPSQSML	BLCA
SLC10A4	c.843C>G	p.F281L	YKYSRVADYIVKVSLWSLLVTLVVL[p.F281L]LIMTGTMLGPELLASIPAAVYVIAIF	LLVTLVVLL,LLIMTGTML,VLLIMTGTM,SLLVTLVVLL,LLVTLVVLLI	CESC
SLC10A6	c.326delG	p.G109fs	YLLAISFSLKPVQAIAVLIMGCCPG[p.G109fs]APSLTFSPSGLMEIWISASV*	LIMGCCPGA,GLMEIWISA,SLTFSPSGL,FSPSGLMEI,LTFSPSGLM,MEIWISASV,CPGAPSLTF,APSLTFSPS,SPSGLMEIW,VLIMGCCPGA,GLMEIWISAS,LMEIWISASV,SLTFSPSGLM,TFSPSGLMEI,MGCCPGAPSL,SPSGLMEIWI	STAD
SLC10A7	c.782C>T	p.S261L	LILFIIFSIQLSFMLLTFIFSTRNN[p.S261L]LGFTPADTVAIIFCSTHKSLTLGIPM	FIFSTRNNL,STRNNLGFT,RNNLGFTPA,FSTRNNLGF,NLGFTPADTV,TFIFSTRNNL,IFSTRNNLGF	UCEC
SLC12A1	c.875C>T	p.S292L	ANAVAVAMYVVGFAETVVDLLKESD[p.S292L]LMMVDPTNDIRIIGSITVVILLGISV	LLKESDLMM,LLKESDLMMV,LMMVDPTNDI	CRC
SLC12A2	c.2483G>A	p.R828Q	ALLHLVHDFTKNVGLMICGHVHMGP[p.R828Q]QRQAMKEMSIDQAKYQRWLIKNKMKA	MGPQRQAMK,HMGPQRQAM,PQRQAMKEM,HMGPQRQAMK,HVHMGPQRQA,GPQRQAMKEM,VHMGPQRQAM	UCEC
SLC12A7	c.2056delC	p.H686fs	WGDGIRGLSLNAARYALLRVEHGPP[p.H686fs]TPRTGGPRCW*	LRVEHGPPT,RVEHGPPTPR	STAD

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SLC13A2	c.1478_1479insG	p.L493fs	IVLLLGGGYALAKGSERSGLSEWLG[p.L493fs]KQADPTAECASSSHCHHPLPPGGHLHRVH*	SGLSEWLGK,SSHCHHPLP,HPLPPGGHL,KQADPTAEC,SSSHCHHPL,SEWLGKQAD,GLSEWLGKQA,RSGLSEWLGK,KQADPTAECA,ASSSHCHHPL,SEWLGKQADP,LPPGGHLHRV	KIRC
SLC13A5	c.818A>C	p.Q273P	VNFASWFAFAFPNMLVMLLFAWLWL[p.Q273P]PFVYMRFNFKKSWGCGLESKKNEKAA	LLFAWLWLP,FAWLWLPFV,WLWLPFVYM,LFAWLWLPF,AWLWLPFVY,WLPFVYMRF,PFVYMRFNF,LWLPFVYMR,FAWLWLPFVY,LLFAWLWLPF,LFAWLWLPFV,AWLWLPFVYM,LWLPFVYMRF,PFVYMRFNFK,WLWLPFVYMR,LPFVYMRFNF	GBM
SLC16A14	c.1484G>A	p.R495Q	YDFSFYICGLLYMIGILFLLIQPCI[p.R495Q]QIIEQSRRKYMDGAHV*	LLIQPCIQI,CIQIIEQSR,FLLIQPCIQI,LLIQPCIQII,QIIEQSRRKY,CIQIIEQSRR	UCEC
SLC16A6	c.293_294insG	p.G98fs	LTFSAPLATVLSNRFGHRLVVMLGG[p.G98fs]ATCQHRDGGRLLLTRGFSYVRRHRHHLWSGILL*	LLTRGFSYV,RLVVMLGGA,LTRGFSYVR,YVRRHRHHL,RHRHHLWSG,LLLTRGFSY,GFSYVRRHR,CQHRDGGRL,GRLLLTRGF,RGFSYVRRH,RHHLWSGIL,HHLWSGILL,LLLTRGFSYV,RLLLTRGFSY,SYVRRHRHHL,LTRGFSYVR,RGFSYVRRHR,RHRHHLWSGI,MLGGATCQHR,ATCQHRDGGR,LLTRGFSYVR,VMLGGATCQH,CQHRDGGRLL,FSYVRRHRHH,YVRRHRHHLW,HRHHLWSGIL,RHHLWSGILL	STAD
SLC16A9	c.1407_1424delCTGCGTCCTGCTGGGAGG	p.CVLLGG470del	LGPPIVGWFYDWTQTYDIAFYFSGF[p.CVLLGG470del]FILLLAALPSWDTCNKQLPKPAPTTFLYKVASNV*	AFYFSGFFI,FYFSGFFIL,YFSGFFILL,IAFYFSGFF,IAFYFSGFFI,AFYFSGFFIL,FYFSGFFILL,YFSGFFILLL,DIAFYFSGFF	KIRC
SLC17A9	c.970G>A	p.V324I	HLINQGYRAITVRKLMQGMGLGLSS[p.V324I]IFALCLGHTSSFCESVVFASASIGLQ	GMGLGLSSI,GLSSIFALC,SIFALCLGH,MGLGLSSIF,LGLSSIFAL,LSSIFALCL,GLGLSSIFAL,GLSSIFALCL,GMGLGLSSIF,QGMGLGLSSI	GBM
SLC1A2	c.1044_1045insT	p.F348fs	LIIHGGIFLPLIYFVVTRKNPFSFF[p.F348fs]CWHFPSLDHCPGHRFQCWNFACHLSLPGRKSGD*	KNPFSFFCW,PFSFFCWHF,SFFCWHFPS,FFCWHFPSL,LDHCPGHRF,GHRFQCWNF,FQCWNFACH,WNFACHLSL,NPFSFFCWH,FPSLDHCPG,CPGHRFQCW,SFFCWHFPSL,FQCWNFACHL,CWNFACHLSL,FACHLSLPGR,FSFFCWHFPS,RKNPFSFFCW,NPFSFFCWHF,SLDHCPGHRF,FPSLDHCPGH	LUAD
SLC20A1	c.984_985delAG	p.P328fs	PLQAVVEERTVSFKLGDLEEAPERE[p.P328fs]ASQRGLERGNQHR*	LEEAPEREA,RGLERGNQHR	UCEC
SLC22A15	c.602C>T	p.S201L	NGGMSLVAFVLLNECVGTAYWALAG[p.S201L]LIGGLFFAVGIAQYALLGYFIRSWRT	ALAGLIGGL,GLIGGLFFA,LIGGLFFAV,TAYWALAGL,AYWALAGLI,LAGLIGGLF,AGLIGGLFF,GLIGGLFFAV,GTAYWALAGL,ALAGLIGGLF,TAYWALAGLI,LAGLIGGLFF	CRC
SLC22A9	c.1220G>A	p.R407Q	LQTLFGAVILLANCVAPWALKYMNR[p.R407Q]QASQMLLMFLLAICLLAIIFVPQEMQ	YMNRQASQM,ALKYMNRQA,KYMNRQASQ,RQASQMLLM,MNRQASQML,QASQMLLMF,LKYMNRQAS,YMNRQASQML,KYMNRQASQM,RQASQMLLMF,MNRQASQMLL,LKYMNRQASQ,NRQASQMLLM	GBM
SLC24A2	c.401C>T	p.A134V	SENSTDHAQGDYPKDIFSLEERRKG[p.A134V]VIILHVIGMIYMFIALAIVCDEFFVP	RKGVIILHV,VIILHVIGMI,SLEERRKGVI,RKGVIILHVI,EERRKGVIIL	CRC
SLC24A5	c.103C>A	p.R35S	ARRALLLGILWATAHLPLSGTSLPQ[p.R35S]SLPRATGNSTQCVISPSSEFPEGFFT	SLPQSLPRA,TSLPQSLPR,LPQSLPRAT,GTSLPQSLPR	LUAD
SLC25A17	c.84delT	p.F28fs	LSYESLVHAVAGAVGSVTAMTVFFP[p.F28fs]WIQLDFDFRLMRKENPKLHTWCSWRSLKKKDSWHHIEGGFQ*	AMTVFFPWI,IQLDFDFRL,RLMRKENPK,KLHTWCSWR,CSWRSLKKK,TWCSWRSLK,TAMTVFFPW,FFPWIQLDF,PWIQLDFDF,SWHHIEGGF,LMRKENPKL,HTWCSWRSL,WIQLDFDFR,DFDFRLMRK,TVFFPWIQL,KENPKLHTW,RSLKKKDSW,KKKDSWHHI,RLMRKENPKL,HTWCSWRSLK,TWCSWRSLKK,VTAMTVFFPW,TAMTVFFPWI,VFFPWIQLDF,LMRKENPKLH,MTVFFPWIQL,IQLDFDFRLM,RKENPKLHTW,LHTWCSWRSL,LKKKDSWHHI,FPWIQLDFDF,NPKLHTWCSW	STAD
SLC25A32	c.247C>G	p.Q83E	LRPKYNGILHCLTTIWKLDGLRGLY[p.Q83E]EGVTPNIWGAGLSWGLYFFFYNAIKS	GLYEGVTPN,GLRGLYEGV,LYEGVTPNI,YEGVTPNIW,GLYEGVTPNI,LYEGVTPNIW	BRCA
SLC25A40	c.287G>A	p.R96Q	EGGNKLWYKKPGNFQGTLDAFFKII[p.R96Q]QNEGIKSLWSGLPPTLVMAVPATVIY	IQNEGIKSL,KIIQNEGIK,FKIIQNEGI,IQNEGIKSLW	CRC
SLC25A45	c.316G>T	p.G106C	LLVLTATSHQERRAQPPSYMHIFLA[p.G106C]CCTGGFLQAYCLAPFDLIKVRLQNQT	FLACCTGGF,YMHIFLACC,SYMHIFLAC,YMHIFLACCT,FLACCTGGFL,SYMHIFLACC,IFLACCTGGF,CCTGGFLQAY	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLC25A48	c.199G>A	p.A67T	TLSCIRVVYRRESMFGFFKGMSFPL[p.A67T]TSIAVYNSVVFGVFSNTQRFLSQHRC	GMSFPLTSI,TSIAVYNSV,MSFPLTSIA,FPLTSIAVY,MSFPLTSIAV,GMSFPLTSIA,LTSIAVYNSV,KGMSFPLTSI,SFPLTSIAVY,TSIAVYNSVV	DLBCL
SLC25A48	c.301C>A	p.R101S	VFGVFSNTQRFLSQHRCGEPEASPP[p.R101S]STLSDLLLASMVAGVVSVGLGGPVDL	SPPSTLSDL,EPEASPPSTL	LUAD
SLC25A5	c.235A>T	p.I79F	HDCVVRIPKEQGVLSFWRGNLANV[p.I79F]FRYFPTQALNFAFKDKYKQIFLGGVD	NLANVFRYF,RGNLANVFR,VFRYFPTQA,GNLANVFRY,WRGNLANVF,FRYFPTQAL,NVFRYFPTQA,FWRGNLANVF,VFRYFPTQAL,RGNLANVFRY,GNLANVFRYF	CESC
SLC25A5	c.352G>A	p.A118T	DKYKQIFLGGVDKRTQFWLYFAGNL[p.A118T]TSGGAAGATSLCFVYPLDFARTRLAA	WLYFAGNLT,LTSGGAAGA,NLTSGGAAGA,WLYFAGNLTS	KIRC
SLC26A3	c.262G>A	p.V88I	WLPAYRLKEWLLSDIVSGISTGIVA[p.V88I]ILQGLAFALLVDIPPVYGLYASFFPA	GISTGIVAI,GIVAILQGL,AILQGLAFA,ILQGLAFAL,VAILQGLAF,ISTGIVAIL,AILQGLAFAL,ILQGLAFALL,GISTGIVAIL,GIVAILQGLA,IVAILQGLAF,SGISTGIVAI	GBM
SLC26A7	c.1886delT	p.I629fs	LAHCTASLIKAMTYYGNLDSEKPIF[p.I629fs]LNRYLLQ*	KPIFLNRYL,NLDSEKPIFL,SEKPIFLNRY,DSEKPIFLNR,KPIFLNRYLL	STAD
SLC27A3	c.1927delC	p.P643fs	VNVYGVTVPGHEGRAGMAALVLRPP[p.P643fs]TLWTLCSSTPTCLRTCHLMPGPDSSGSRSLWPPQRPSNSRKFGWQMRASTPAPCLTHCTFWTRL*	WQMRASTPA,ALVLRPPTL,CSSTPTCLR,LTHCTFWTR,GSRSLWPPQ,PQRPSNSRK,QMRASTPAP,RASTPAPCL,NSRKFGWQM,LVLRPPTLW,RKFGWQMRA,APCLTHCTF,VLRPPTLWTL,TLCSSTPTCL,GSRSLWPPQR,RSLWPPQRPS,NSRKFGWQMR,QMRASTPAPC,LTHCTFWTRL,CLTHCTFWTR,TPTCLRTCHL,GPDSSGSRSL,AALVLRPPTL,ALVLRPPTLW,PQRPSNSRKF,SNSRKFGWQM,RKFGWQMRAS,WQMRASTPAP,MRASTPAPCL,RPSNSRKFGW,APCLTHCTFW	STAD
SLC2A6	c.689C>A	p.A230D	LIMILLLSFMPNSPRFLLSRGRDEE[p.A230D]DLRALAWLRGTDVDVHWEFEQIQDNV	DLRALAWLR,EEDLRALAW,DEEDLRALAW,EEDLRALAWL	PRAD
SLC2A7	c.193G>A	p.A65T	YNLSVVNTPHKVFKSFYNETYFERH[p.A65T]TTFMDGKLMLLLWSCTVSMFPLGGLL	TYFERHTTF,ETYFERHTT,HTTFMDGKL,YFERHTTFM,TTFMDGKLM,TYFERHTTFM,ETYFERHTTF	CRC
SLC2A7	c.804C>A	p.H268Q	LRGHTDMEAELEDMRAEARAERAEG[p.H268Q]QLSVLHLCALRSLRWQLLSIIVLMAG	RAEGQLSVL,AERAEGQLS,AEGQLSVLH,QLSVLHLCAL,AERAEGQLSV,AEGQLSVLHL,GQLSVLHLCA	TGCT
SLC30A9	c.581G>A	p.R194H	LRSDVEAKSLEVWGSPEALAREKKL[p.R194H]HKEAEIEYRERLFRNQKILREYRDFL	LAREKKLHK,LHKEAEIEY,REKKLHKEA,ALAREKKLHK,KLHKEAEIEY	CRC
SLC32A1	c.1480G>A	p.V494I	CFLLPSLFHLRLLWRKLLWHQVFFD[p.V494I]IAIFVIGGICSVSGFVHSLEGLIEAY	VFFDIAIFV,LWHQVFFDI,FFDIAIFVI,IAIFVIGGI,QVFFDIAIF,HQVFFDIAI,LLWHQVFFDI,QVFFDIAIFV,VFFDIAIFVI,DIAIFVIGGI,HQVFFDIAIF,WHQVFFDIAI	STAD
SLC33A1	c.1625C>T	p.S542L	CVFIGFGWWFFLGPKFKKLQDEGSS[p.S542L]LWKCKRNN*	KLQDEGSSL,LQDEGSSLW,KKLQDEGSSL,KLQDEGSSLW	CRC
SLC35D3	c.1250G>C	p.*417S	VWRLVRGTRYMKKDYLIENEELPSP[p.*417S]SEGGACTYLCAYTYFIC*	PSEGGACTY,CTYLCAYTY,YLCAYTYFI,TYLCAYTYF,GACTYLCAY,SEGGACTYL,YLCAYTYFIC,CTYLCAYTYF,TYLCAYTYFI,GGACTYLCAY,ACTYLCAYTY,SPSEGGACTY	HNSC
SLC35F3	c.838G>A	p.A280T	CNKAFVFLLSWIVLRDRFMGVRIVA[p.A280T]TILAIAGIVMMTYADGFHSHSVIGIA	FMGVRIVAT,RIVATILAI,IVATILAIA,ATILAIAGI,GVRIVATIL,TILAIAGIV,MGVRIVATI,FMGVRIVATI,RIVATILAIA,ATILAIAGIV,RFMGVRIVAT,GVRIVATILA,MGVRIVATIL,VRIVATILAI,TILAIAGIVM	CRC
SLC35G2	c.184delA	p.K62fs	INEGYGNFMEENPKKGLLSEMKKKG[p.K62fs]ELSLEPWIPYLHQQKTQ*	LSLEPWIPY,SLEPWIPYL,SEMKKKGEL,MKKKGELSL,GELSLEPWI,IPYLHQQKT,LSLEPWIPYL,EMKKKGELSL,ELSLEPWIPY,KKGELSLEPW	CESC
SLC37A1	c.1582G>A	p.V528I	ACALLFLIRLIHKELSCPGSATGDQ[p.V528I]IPFKEQ*	ATGDQIPFK,SATGDQIPF,SATGDQIPFK,GSATGDQIPF,CPGSATGDQI	TGCT
SLC38A1	c.298G>A	p.G100R	MSVFNLSNAIMGSGILGLAFALANT[p.G100R]RILLFLVLLTSVTLLSIYSINLLLIC	ALANTRILL,RILLFLVLL,LAFALANTR,NTRILLFLV,LANTRILLF,FALANTRIL,TRILLFLVL,ALANTRILLF,NTRILLFLVL,GLAFALANTR,LAFALANTRI,FALANTRILL	TGCT
SLC38A10	c.3213_3215delCAT	p.1071_1072IIL>I	SDLRRRRRDLGPHAEGQLAPRDGVI[p.1071_1072IIL>I]GLNPLPDVQVNDLRGALDAQLRQAAGGA	APRDGVIGL,RDGVIGLNPL	PAAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLC39A12	c.1883G>C	p.C628S	ILMNFISSLTAFMGLYIGLSVSADP[p.C628S]SVQDWIFTVTAGMFLYLSLVEMLPEM	SVQDWIFTV,DPSVQDWIF,GLSVSADPSV	LUAD
SLC39A6	c.158G>T	p.R53L	AFPQTTEKISPNWESGINVDLAIST[p.R53L]LQYHLQQLFYRYGENNSLSVEGFRKL	TLQYHLQQL,AISTLQYHL,LQYHLQQLF,DLAISTLQY,LQYHLQQLFY,TLQYHLQQLF,INVDLAISTL,VDLAISTLQY,LAISTLQYHL,STLQYHLQQL	LUAD
SLC39A7	c.1144C>T	p.R382C	LHEVPHEVGDFAILVQSGCSKKQAM[p.R382C]CLQLLTAVGALAGTACALLTEGGAVG	KQAMCLQLL,AMCLQLLTA,KKQAMCLQL,AMCLQLLTAV,SKKQAMCLQL,KKQAMCLQLL,KQAMCLQLLT	CRC
SLC39A7	c.1367_1368insG	p.L456fs	SVLPELLREASPLQSLLEVLGLLGG[p.L456fs]SYHDGADCPP*	VLGLLGGSY,LLGGSYHDGA,EVLGLLGGSY,LEVLGLLGGS	CLL
SLC43A1	c.398C>T	p.P133L	LVGSACFTASCTLMALASRDVEALS[p.P133L]LLIFLALSLNGFGGICLTFTSLTLPN	ALSLLIFLA,LLIFLALSL,EALSLLIFL,RDVEALSLL,VEALSLLIF,LSLLIFLAL,ALSLLIFLAL,SLLIFLALSL,ASRDVEALSL,EALSLLIFLA,RDVEALSLLI,VEALSLLIFL	CRC
SLC43A3	c.647G>A	p.R216H	LLYEKGISLRASFIFISVCSTWHVA[p.R216H]HTFLLMPRGHIPYPLPPNYSYGLCPG	STWHVAHTF,TWHVAHTFL,HVAHTFLLM,WHVAHTFLL,STWHVAHTFL,VAHTFLLMPR,CSTWHVAHTF,TWHVAHTFLL,WHVAHTFLLM	CRC
SLC44A5	c.208G>T	p.V70F	KPADTPSEEEDFGDPRTYDPDFKGP[p.V70F]FANRSCTDVLCCMIFLLCIIGYIVLG	FANRSCTDV,DFKGPFANR,TYDPDFKGPF,FANRSCTDVL	KIRC
SLC44A5	c.554G>A	p.R185H	CPEKFLTYVEMQLLYTKDKSYWEDY[p.R185H]HQFCKTTAKPVKSLTQLLLDDDCPTA	HQFCKTTAK,SYWEDYHQF,YHQFCKTTA,KSYWEDYHQF,SYWEDYHQFC,HQFCKTTAKP,WEDYHQFCKT	CRC
SLC4A3	c.3183delG	p.L1061fs	SQKARRLLKGSGFHLDLLLIGSLGG[p.L1061fs]SVGCLGCPGSRLPRSAPSPMSMR*	LLIGSLGGS,LIGSLGGSV,SLGGSVGCL,RSAPSPMSM,SAPSPMSMR,LPRSAPSPM,LLIGSLGGSV,RLPRSAPSPM,RSAPSPMSMR,GSRLPRSAPS	STAD
SLC4A5	c.1597A>G	p.I533V	WFPSDFYDGFHIQSISAILFIYLGC[p.I533V]VTNAITFGGLLGDATDNYQGVMESFL	ILFIYLGCV,YLGCVTNAI,GCVTNAITF,AILFIYLGCV,FIYLGCVTNA,YLGCVTNAIT,ILFIYLGCVT,IYLGCVTNAI,LGCVTNAITF	LUAD
SLC4A8	c.687C>G	p.N229K	LNDSMRVKVREALLKKHHHQNEKKR[p.N229K]KNLIPIVRSFAEVGKKQSDPHLMDKH	KKRKNLIPI,KRKNLIPIV,KKRKNLIPIV,EKKRKNLIPI,HQNEKKRKNL,KNLIPIVRSF	KIRC
SLC52A1	c.1108_1110delGGC	p.G370del	LSLLGMLFGAYLMALAILSPCPPLV[p.G370del]TTAGVVLVVLSWVLCLCVFSYVKVAASS	VTTAGVVLV,LVTTAGVVL,LVTTAGVVLV,VTTAGVVLVV,CPPLVTTAGV	KIRC
SLC52A2	c.1197_1198insG	p.G399fs	LSWVLCLGVFSYVKVAASSLLHGGG[p.G399fs]PAGIAGSRRGHPGGLSARRCCYVPPDQHLSRVPQQKGLCRPL*	SLLHGGGPA,LSARRCCYV,HLSRVPQQK,CYVPPDQHL,GSRRGHPGG,RGHPGGLSA,GLSARRCCY,QQKGLCRPL,LLHGGGPAGI,GLSARRCCYV,GSRRGHPGGL,RGHPGGLSAR,SARRCCYVPP,VPPDQHLSRV	KIRC
SLC5A1	c.157G>T	p.G53W	DISIIVIYFVVVMAVGLWAMFSTNR[p.G53W]WTVGGFFLAGRSMVWWPIGASLFASN	WTVGGFFLA,WAMFSTNRW,MFSTNRWTV,RWTVGGFFL,AMFSTNRWT,TNRWTVGGF,NRWTVGGFF,AMFSTNRWTV,LWAMFSTNRW,RWTVGGFFLA,STNRWTVGGF,TNRWTVGGFF	LUAD
SLC5A7	c.1006G>T	p.G336C	KTTEEADMILPIVLQYLCPVYISFF[p.G336C]CLGAVSAAVMSSADSSILSASSMFAR	YISFFCLGA,CLGAVSAAV,ISFFCLGAV,VYISFFCLG,YISFFCLGAV,FCLGAVSAAV,VYISFFCLGA,CLGAVSAAVM,CPVYISFFCL	HNSC
SLC5A7	c.1325G>T	p.G442V	IFPQLLCVLFVKGTNTYGAVAGYVS[p.G442V]VLFLRITGGEPYLYLQPLIFYPGYYP	AVAGYVSVL,YVSVLFLRI,VAGYVSVLF,GYVSVLFLR,AGYVSVLFL,AGYVSVLFLR,AVAGYVSVLF,GYVSVLFLRI,YGAVAGYVSV,GAVAGYVSVL	LUAD
SLC6A10P	c.264A>C	p.K88N	WSFFTPLVCMGIFIFNVVYYKPLVY[p.K88N]NNTNVYPWWGEAMGWAFVLSSMLCMP	YYKPLVYNN,YYKPLVYNNT,KPLVYNNTNV	GBM,KIRC
SLC6A11	c.896G>T	p.W299L	TLPGASEGIKFYLYPDLSRLSDPQV[p.W299L]LVDAGTQIFFSYAICLGCLTALGSYN	RLSDPQVLV,VLVDAGTQI,SRLSDPQVL,LVDAGTQIF,LVDAGTQIFF,VLVDAGTQIF,LSRLSDPQVL	LUAD
SLC6A14	c.255_256insG	p.A85fs	FPYLTYSNGGGAFLIPYAIMLALAG[p.A85fs]FTFVLSGVFTGTIC*	LALAGFTFV,ALAGFTFVL,VLSGVFTGT,MLALAGFTF,FTFVLSGVF,AIMLALAGF,MLALAGFTFV,FVLSGVFTGT,VLSGVFTGTI,AIMLALAGFT,ALAGFTFVLS,AGFTFVLSGV,YAIMLALAGF,IMLALAGFTF,GFTFVLSGVF,FTFVLSGVFT,LALAGFTFVL	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLC6A9	c.281G>A	p.R94K	LLPQLMAQHSLAMAQNGAVPSEATK[p.R94K]KDQNLKRGNWGNQIEFVLTSVGYAVG	AVPSEATKK,ATKKDQNLK,ATKKDQNLKR	CLL
SLC6A9	c.727C>T	p.R243W	AYCNNPWNTHDCAGVLDASNLTNGS[p.R243W]WPAALPSNLSHLLNHSLQRTSPSEEY	NLTNGSWPA,WPAALPSNL,ASNLTNGSW,NLTNGSWPAA,SWPAALPSNL,LTNGSWPAAL,DASNLTNGSW	BLCA
SLC7A10	c.471delC	p.P157fs	TSLAVISMTFSNYVLQPVFPNCIPP[p.P157fs]PQPPGCCPWPA*	FPNCIPPPQ	STAD
SLC7A2	c.964C>T	p.R322W	TLAGAATCFYAFVGFDCIATTGEEV[p.R322W]WNPQKAIPIGIVTSLLVCFMAYFGVS	EVWNPQKAI,EEVWNPQKA,IATTGEEVW,EEVWNPQKAI,GEEVWNPQKA	UCEC
SLC8A1	c.1292G>A	p.R431H	VSKIFFEQGTYQCLENCGTVALTII[p.R431H]HRGGDLTNTVFVDFRTEDGTANAGSD	GTVALTIIH,TVALTIIHR,GTVALTIIHR	CRC
SLC8A1	c.1297G>T	p.G433C	KIFFEQGTYQCLENCGTVALTIIRR[p.G433C]CGDLTNTVFVDFRTEDGTANAGSDYE	CGDLTNTVF,RCGDLTNTVF	LUAD
SLC9A2	c.2237delC	p.T746fs	SPQSYKMEWKNEVDVDSGRDMPSTP[p.T746fs]QHPTAEKRAPRRQAYYSSPFSLKTSLAQRGKTV*	SLAQRGKTV,KTSLAQRGK,RQAYYSSPF,AYYSSPFSL,RAPRRQAYY,YYSSPFSLK,SLKTSLAQR,KRAPRRQAY,PTAEKRAPR,MPSTPQHPT,SPFSLKTSL,AYYSSPFSLK,STPQHPTAEK,FSLKTSLAQR,RQAYYSSPFS,QAYYSSPFSL,KRAPRRQAYY,PTAEKRAPRR,MPSTPQHPTA,SPFSLKTSLA,RRQAYYSSPF,AEKRAPRRQA	STAD
SLC9A4	c.1892G>A	p.R631H	RTLSYNKYNLKPQTSEKQAKEILIR[p.R631H]HQNTLRESMRKGHSLPWGKPAGTKNI	ILIRHQNTL,LIRHQNTLR,HQNTLRESM,KEILIRHQN,ILIRHQNTLR,HQNTLRESMR,EILIRHQNTL,KQAKEILIRH,RHQNTLRESM,KEILIRHQNT	GBM
SLC9A5	c.1341G>C	p.L447F	TKVPAKDYFVATTIVVVFFTVIVQG[p.L447F]FTIKPLVKWLKVKRSEHHKPTLNQEL	VIVQGFTIK,FFTVIVQGF,FTIKPLVKW,GFTIKPLVK,FTVIVQGFT,TVIVQGFTI,VQGFTIKPL,FTIKPLVKWL,TVIVQGFTIK,QGFTIKPLVK,VFFTVIVQGF,GFTIKPLVKW,FTVIVQGFTI	BLCA
SLC9B1	c.1338_1339delGT	p.V446fs	FAGFSFKEKIFIALAWMPKATVQAV[p.V446fs]RSSGSRNSKSLRTPLGTICEGCDDSSIFSHLDHSSKWSSTYGHSGA*	HSSKWSSTY,SLRTPLGTI,RSSGSRNSK,FSHLDHSSK,GSRNSKSLR,SSKWSSTYG,NSKSLRTPL,SHLDHSSKW,SKWSSTYGH,AVRSSGSRNS,KSLRTPLGTI,IFSHLDHSSK,SSKWSSTYGH,MPKATVQAVR,RNSKSLRTPL,CEGCDDSSIF,FSHLDHSSKW	KIRC
SLCO2A1	c.1437G>C	p.M479I	IFHPVCGDNGIEYLSPCHAGCSNIN[p.M479I]ISSATSKQLIYLNCSCVTGGSASAKT	ISSATSKQL,NINISSATSK,ISSATSKQLI	CESC
SLIT1	c.4379G>T	p.R1460L	SGTKGAHCVCDPGFSGELCEQESEC[p.R1460L]LGDPVRDFHQVQRGYAICQTTRPLSW	ESECLGDPV,CLGDPVRDF,QESECLGDPV	LUAD
SLITRK1	c.134delA	p.K45fs	TGDVCKEKICSCNEIEGDLHVDCEK[p.K45fs]RASQVCSVSLPRLPSFTIYFCMAIPSLDFSLMSSLTFIMRLVCTWKTMACMKSFRGLFWGCSW*	FTIYFCMAI,SLMSSLTFI,LMSSLTFIM,SLTFIMRLV,IMRLVCTWK,TMACMKSFR,QVCSVSLPR,MSSLTFIMR,VSLPRLPSF,RLPSFTIYF,YFCMAIPSL,CMAIPSLDF,FSLMSSLTF,FIMRLVCTW,KTMACMKSF,CMKSFRGLF,RGLFWGCSW,TWKTMACMK,KSFRGLFWG,LPRLPSFTI,IPSLDFSLM,RLVCTWKTM,KRASQVCSV,ASQVCSVSL,SQVCSVSLP,LDFSLMSSL,CTWKTMACM,MKSFRGLFW,CEKRASQVC,LPSFTIYFC,SLPRLPSFTI,RLPSFTIYFC,SLDFSLMSSL,FSLMSSLTFI,SLMSSLTFIM,RLVCTWKTMA,LMSSLTFIMR,FIMRLVCTWK,CTWKTMACMK,KTMACMKSFR,SQVCSVSLPR,SFTIYFCMAI,IYFCMAIPSL,FCMAIPSLDF,DFSLMSSLTF,TFIMRLVCTW,CMKSFRGLFW,SSLTFIMRLV,MAIPSLDFSL,MSSLTFIMRL,RASQVCSVSL,LPRLPSFTIY,LPSFTIYFCM,MACMKSFRGL,SVSLPRLPSF,MRLVCTWKTM,WKTMACMKSF,ACMKSFRGLF,FRGLFWGCSW,CEKRASQVCS	STAD
SLITRK1	c.155G>A	p.R52H	KICSCNEIEGDLHVDCEKKGFTSLQ[p.R52H]HFTAPTSQFYHLFLHGNSLTRLFPNE	SLQHFTAPT,KGFTSLQHF,HFTAPTSQF,FTSLQHFTA,LQHFTAPTS,HFTAPTSQFY,KKGFTSLQHF,LQHFTAPTSQ,QHFTAPTSQF	CRC
SLITRK3	c.641G>T	p.R214L	PTNLFKAVSLTHLDLRGNRLKVLFY[p.R214L]LGMLDHIGRSLMELQLEENPWNCTCE	FYLGMLDHI,RLKVLFYLG,KVLFYLGML,LKVLFYLGM,LFYLGMLDHI,RLKVLFYLGM,YLGMLDHIGR,LKVLFYLGML	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLITRK3	c.893C>T	p.S298L	REIRKTELCPLLSDSEVEASLGIPH[p.S298L]LSSSKENAWPTKPSSMLSSVHFTASS	GIPHLSSSK,LSSSKENAW,LGIPHLSSSK,VEASLGIPHL,HLSSSKENAW	CRC
SLITRK5	c.1403G>T	p.R468M	NRISMIQDRAFGDLTNLRRLYLNGN[p.R468M]MIERLSPELFYGLQSLQYLFLQYNLI	RLYLNGNMI,YLNGNMIER,RRLYLNGNM,YLNGNMIERL,NMIERLSPEL,LYLNGNMIER,LRRLYLNGNM,RRLYLNGNMI,MIERLSPELF	LUAD
SLITRK5	c.203G>T	p.R68L	YYGEICDNACPCEEKDGILTVSCEN[p.R68L]LGIISLSEISPPRFPIYHLLLSGNLL	ILTVSCENL,TVSCENLGI,CENLGIISL,NLGIISLSEI,LTVSCENLGI,CENLGIISLS	LUAD
SLITRK6	c.2223C>A	p.N741K	HLQRSLLEQENHSPLTGSNMKYKTT[p.N741K]KQSTEFLSFQDASSLYRNILEKEREL	KQSTEFLSF,SNMKYKTTK,KYKTTKQST,TTKQSTEFL,KTTKQSTEF,GSNMKYKTTK,KTTKQSTEFL,MKYKTTKQST,YKTTKQSTEF,TKQSTEFLSF	LUAD
SMAD2	c.962G>A	p.R321Q	SLTVDGFTDPSNSERFCLGLLSNVN[p.R321Q]QNATVEMTRRHIGRGVRLYYIGGEVF	LLSNVNQNA,VNQNATVEM,GLLSNVNQNA,NVNQNATVEM	CRC
SMAD4	c.1082G>A	p.R361H	GETFKVPSSCPIVTVDGYVDPSGGD[p.R361H]HFCLGQLSNVHRTEAIERARLHIGKG	YVDPSGGDHF,DPSGGDHFCL	CRC
SMAP1	c.506delA	p.E169fs	QPLVSSPSLQAAVDKNKLEKEKEKK[p.E169fs]RKRKREKRSQKSRQNHLQLKSCRRKISNWSLKKVPALKKLRSPLWIF*	ALKKLRSPL,KISNWSLKK,SLKKVPALK,KLRSPLWIF,KKRKRKREK,RKREKRSQK,RSQKSRQNH,SQKSRQNHL,KSRQNHLQL,RRKISNWSL,RKISNWSLK,KVPALKKLR,HLQLKSCRR,WSLKKVPAL,RQNHLQLKS,KKVPALKKL,LKKLRSPLW,KKLRSPLWI,KISNWSLKKV,KSRQNHLQLK,SLKKVPALKK,WSLKKVPALK,KRKREKRSQK,RSQKSRQNHL,HLQLKSCRRK,RRKISNWSLK,CRRKISNWSL,NWSLKKVPAL,QKSRQNHLQL,RQNHLQLKSC,LQLKSCRRKI,ALKKLRSPLW,KKLRSPLWIF	UCS
SMARCA4	c.1142G>A	p.R381Q	QKPRGLDPVEILQEREYRLQARIAH[p.R381Q]QIQELENLPGSLAGDLRTKATIELKA	LQARIAHQI,RIAHQIQEL,HQIQELENL,RLQARIAHQI,ARIAHQIQEL	CRC
SMARCA4	c.2738C>T	p.P913L	NHHCKLTQVLNTHYVAPRRLLLTGT[p.P913L]LLQNKLPELWALLNFLLPTIFKSCST	RLLLTGTLL,LLQNKLPEL,LTGTLLQNK,RRLLLTGTL,TLLQNKLPEL,LLTGTLLQNK,RRLLLTGTLL	HNSC
SMARCA5	c.468_471delAGAA	p.T156fs	KQNLLSVGDYRHRRTEQEEDEELLT[p.T156fs]APKQPMFALDLKTLHRM*	APKQPMFAL,LLTAPKQPM,LTAPKQPMF,KQPMFALDL,LDLKTLHRM,KQPMFALDLK,LTAPKQPMFA,FALDLKTLHR,TAPKQPMFAL,LLTAPKQPMF,PMFALDLKTL,QEEDEELLTA	TGCT
SMC3	c.2908G>C	p.E970Q	ELGSLPQEAFEKYQTLSLKQLFRKL[p.E970Q]QQCNTELKKYSHVNKKALDQFVNFSE	KLQQCNTEL,KLQQCNTELK,QQCNTELKKY,RKLQQCNTEL	TGCT
SMCR8	c.523G>A	p.E175K	VRPFCMAYISADQHKIMQQFQELSA[p.E175K]KFSRASECLKTGNRKAFAGELEKKLK	ELSAKFSRA,QQFQELSAK,QFQELSAKF,AKFSRASEC,MQQFQELSAK,KFSRASECLK,QQFQELSAKF,AKFSRASECL,QELSAKFSRA	UCEC
SMG1	c.8087C>A	p.P2696H	LICNTTVERCQELYRKYEMQYAPQP[p.P2696H]HPTVCQFITATEMTLQRYAADINSRL	YAPQPHPTV,APQPHPTVC,QPHPTVCQF,MQYAPQPHP,QYAPQPHPTV,YEMQYAPQPH,MQYAPQPHPT,HPTVCQFITA,QPHPTVCQFI	TGCT
SMG7	c.2536_2537insA	p.E846fs	TQDPIKLFEPSLQPPVMQQQPLEKK[p.E846fs]NEAFSHGAI*	NEAFSHGAI,QPLEKKNEAF,KKNEAFSHGA	PRAD
SNAPC1	c.633delT	p.D211fs	QNMKHVISVDKSKPDKALSLIKDDF[p.D211fs]LTILRT*	LIKDDFLTI,IKDDFLTIL,SLIKDDFLTI,ALSLIKDDFL,LIKDDFLTIL	STAD
SNAPC2	c.875delC	p.T292fs	IPAGGSLGPAAEGDGAGSKAPEETP[p.T292fs]QPPRRPSTAN*	TPQPPRRPS,TPQPPRRPST	STAD
SND1	c.112C>G	p.Q38E	GPAVPTVQRGIIKMVLSGCAIIVRG[p.Q38E]EPRGGPPPERQINLSNIRAGNLARRA	AIIVRGEPR,CAIIVRGEPR	CESC
SND1	c.2163delC	p.H721fs	VQDVETGTQLEKLMENMRNDIASHP[p.H721fs]L*	RNDIASHPL,MRNDIASHPL	STAD
SOAT1	c.190delT	p.F64fs	GRIDIKQLIAKKIKLTAEAEELKPF[p.F64fs]L*	AEAEELKPFL	STAD
SOLH	c.2141G>A	p.R714H	GFLMGASCGGGNMKVDDSAYESLGL[p.R714H]HPRHAYSILDVRDVQGTRLLRLRNPW	GLHPRHAYS,LGLHPRHAY,HPRHAYSIL,SAYESLGLH,YESLGLHPR,GLHPRHAYSI,SLGLHPRHAY,YESLGLHPRH	LIHC
SON	c.2723C>T	p.S908L	AQMLASGTMDAQMLASSTQDSAMLG[p.S908L]LKSPDPYRLAQDPYRLAQDPYRLGHD	GLKSPDPYR,LGLKSPDPY,TQDSAMLGL,LKSPDPYRL,GLKSPDPYRL,TQDSAMLGLK,MLGLKSPDPY,STQDSAMLGL	LUSC

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SON	c.4075_4098delGTCCTGGAGTCTTCGGCTGTGACC	p.VLESSAVT1359del	LAESILEPPAMAAPESSAMAVLESS[p.VLESSAVT1359del]TVTVLESSTVTVLEPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVL	AMAVLESST,MAVLESSTV,AMAVLESSTV,AVLESSTVTV	KIRC
SORBS1	c.1710C>A	p.F570L	VLTNEKMSRDISPEEIDLKNEPWYK[p.F570L]LFSELEFGKPPPKKIWDYTPGDCSIL	KNEPWYKLF,PWYKLFSEL,LKNEPWYKL,YKLFSELEF,KLFSELEFGK,WYKLFSELEF,EPWYKLFSEL,LKNEPWYKLF	CRC
SORBS1	c.3466G>A	p.V1156M	AERGAGERGPGGPKISKKSCLKPSD[p.V1156M]MVRCLSTEQRLSDLNTPEESRPGKPL	CLKPSDMVR,KPSDMVRCL,MVRCLSTEQR,KKSCLKPSDM	CRC
SORBS2	c.2596C>T	p.P866S	VFEALDSALKDICDQIKAEKKRGSL[p.P8665]SDNSILHRLISELLPDVPERNSSLRA	RGSLSDNSI,LSDNSILHRL,SLSDNSILHR,RGSLSDNSIL	PAAD
SORBS2	c.3472delG	p.E1158fs	DRIHSLSSNKPQRPVFTHENIQGGG[p.E1158fs]NRFRLCITILPGMKMSWSSEKVMSLMSWKSVMTAGLWGPQEEPNSLVLSPETTSRGCELRSLLL*	SSEKVMSLM,KMSWSSEKV,SLMSWKSVM,LMSWKSVMT,KVMSLMSWK,CITILPGMK,RFRLCITIL,ILPGMKMSW,MSLMSWKSV,MSWKSVMTA,TTSRGCELR,MTAGLWGPQ,ETTSRGCEL,GPQEEPNSL,MSWSSEKVM,NRFRLCITI,ITILPGMKM,WSSEKVMSL,EKVMSLMSW,WKSVMTAGL,KSVMTAGLW,QEEPNSLVL,SEKVMSLMS,VMSLMSWKSV,SLMSWKSVMT,LMSWKSVMTA,RLCITILPGM,GMKMSWSSEK,LVLSPETTSR,RFRLCITILP,MSLMSWKSVM,SWKSVMTAGL,NIQGGGNRFR,ETTSRGCELR,WSSEKVMSLM,KMSWSSEKVM,IQGGGNRFRL,NRFRLCITIL,MKMSWSSEKV,SEKVMSLMSW,MSWKSVMTAG,WKSVMTAGLW	STAD
SORCS2	c.958C>T	p.R320W	FWSVSGVDADPDLVHVEAQDLGGDF[p.R320W]WYVTCAIHNCSEKMLTAPFAGPIDHG	DLGGDFWYV,DFWYVTCAI,GDFWYVTCA,AQDLGGDFWY,GDFWYVTCAI,EAQDLGGDFW	CRC
SORL1	c.614G>T	p.R205L	ADAYAQYLWITFDFCNTLQGFSIPF[p.R205L]LAADLLLHSKASNLLLGFDRSHPNKQ	LQGFSIPFL,PFLAADLLL,IPFLAADLL,TLQGFSIPFL,FLAADLLLHS,LAADLLLHSK,FSIPFLAADL,IPFLAADLLL	LUAD
SOS1	c.697A>T	p.N233Y	FMAEIRQYIRELNLIIKVFREPFVS[p.N233Y]YSKLFSANDVENIFSRIVDIHELSVK	PFVSYSKLF,VFREPFVSY,VSYSKLFSA,EPFVSYSKL,REPFVSYSK,FVSYSKLFSA,KVFREPFVSY,VFREPFVSYS,REPFVSYSKL,EPFVSYSKLF	LUAD,UCEC
SOWAHA	c.371G>C	p.R124P	AAQPSKPTSTVLPRSASAPGAPPLV[p.R124P]PVPRPVEPPGDLGLPTEPQDTPGGPA	APGAPPLVPV	ACC
SOX17	c.1208G>T	p.S403I	PYQGHDSGVNLPDSHGAISSVVSDA[p.S403I]ISAVYYCNYPDV*	VSDAISAVY,ISAVYYCNY,VVSDAISAV,ISSVVSDAI,SDAISAVYY,VVSDAISAVY,VSDAISAVYY,SVVSDAISAV,AISSVVSDAI,AISAVYYCNY	UCEC
SOX6	c.2155C>T	p.R719W	HLEKYPNYKYKPRPKRTCIVDGKKL[p.R719W]WIGEYKQLMRSRRQEMRQFFTVGQQP	LWIGEYKQL,GKKLWIGEY,KLWIGEYKQL,LWIGEYKQLM,WIGEYKQLMR	CRC
SOX7	c.925delC	p.L309fs	RRIPHLPGHPYSPEYAPSPLHCSHP[p.L309fs]WAPWPLASPPASP*	SHPWAPWPL,SPLHCSHPW,HPWAPWPLA,HCSHPWAPW,WPLASPPAS,CSHPWAPWPL,APWPLASPPA,LHCSHPWAPW,HPWAPWPLAS	STAD
SOX9	c.223G>A	p.E75K	ENTFPKGEPDLKKESEEDKFPVCIR[p.E75K]KAVSQVLKGYDWTLVPMPVRVNGSSK	CIRKAVSQV,RKAVSQVLK,FPVCIRKAV,IRKAVSQVL,CIRKAVSQVL,IRKAVSQVLK,KAVSQVLKGY,FPVCIRKAVS	LUAD
SP4	c.17_19delAGG	p.E11del	MSDQKKEEEE[p.E11del]AAAAAAMATEGGKTSEPENNNKKPKTSG	KEEEEAAAA,KEEEEAAAAA	LUSC
SP4	c.19G>A	p.E7K	MSDQKK[p.E7K]KEEEEAAAAAAMATEGGKTSEPENNN	KEEEEAAAA,KEEEEAAAAA	TGCT
SPAG16	c.1315G>T	p.V439L	GDTTVKLWDLCKGDCILTFEGHSRA[p.V439L]LWSCTWHSCGNFVASSSLDKTSKIWD	ALWSCTWHS,HSRALWSCT,FEGHSRALW,SRALWSCTW,RALWSCTWH,ALWSCTWHSC,LTFEGHSRAL,TFEGHSRALW,HSRALWSCTW	LUAD
SPAG16	c.1462C>T	p.P488S	WDVNSERCRCTLYGHTDSVNSIEFF[p.P488S]SFSNTLLTSSADKTLSIWDARTGICE	EFFSFSNTL,NSIEFFSFS,VNSIEFFSF,IEFFSFSNT,FSFSNTLLT,SVNSIEFFSF,EFFSFSNTLL,IEFFSFSNTL,FSFSNTLLTS	SKCM
SPAG17	c.3790delC	p.Q1264fs	GQESTGQYVIDEEPTWDIMVRQSYP[p.Q1264fs]RG*	IMVRQSYPR,MVRQSYPRG,DIMVRQSYPR	STAD

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SPAM1	c.1037G>A	p.R346Q	LVYTFGETVALGASGIVIWGTLSIM[p.R346Q]QSMKSCLLLDNYMETILNPYIINVTL	IMQSMKSCL,MQSMKSCLL,TLSIMQSMK,GTLSIMQSM,QSMKSCLLL,IMQSMKSCLL,SIMQSMKSCL,MQSMKSCLLL,GTLSIMQSMK,WGTLSIMQSM	GBM
SPATA17	c.215G>A	p.R72K	QVRAYIRHLNRIVTIIQKWWRSFLG[p.R72K]KKQYQLTVQVAYYTMMMNLYNAMAVR	FLGKKQYQL,KWWRSFLGK,WWRSFLGKK,RSFLGKKQY,GKKQYQLTV,FLGKKQYQLT,SFLGKKQYQL,KWWRSFLGKK,WRSFLGKKQY,KKQYQLTVQV	CESC
SPATA22	c.449C>T	p.S150L	NDFKPQCKRTNLVANDGKNSCPVSS[p.S150L]VAQQQKQLRIPEPPNLSRNKETELLR	VSSVAQQQK,SVAQQQKQLR,GKNSCPVSSV	CRC
SPATA5L1	c.2055delT	p.C685fs	KVCTKTMPIGPDVSLENLAAETCFF[p.C685fs]LELILETSAQKLLCWLCKKMD*	LAAETCFFL,LILETSAQK,KLLCWLCKK,ETCFFLELI,AETCFFLEL,LETSAQKLL,LELILETSA,NLAAETCFFL,FLELILETSA,LILETSAQKL,KLLCWLCKKM,AQKLLCWLCK,ETCFFLELIL,AETCFFLELI	STAD
SPATA9	c.566G>T	p.C189F	AVLKKVKNIFQEEESIRQNREESEN[p.C189F]FRKAFSEPVLSEPMFAEGEIKAKPYR	FRKAFSEPV,EESENFRKA,NFRKAFSEPV,RQNREESENF,EESENFRKAF,FRKAFSEPVL,REESENFRKA	KIRC
SPEG	c.2831C>T	p.A944V	EAEGGLCRLRILAAERGDAGFYTCK[p.A944V]VVNEYGARQCEARLEVRAHPESRSLA	YTCKVVNEY,DAGFYTCKV,FYTCKVVNEY	CRC
SPEG	c.2975_2976insG	p.A992fs	AVLAPLQDVDVGAGEMALFECLVAG[p.A992fs]AH*	FECLVAGAH,ALFECLVAGA	KIRC
SPEN	c.2407_2408delGA	p.E803fs	RLERYTKNEKTDKERTFDPERVERE[p.E803fs]TLNTEGKSGKGQN*	TLNTEGKSGK	GBM
SPESP1	c.363C>G	p.F121L	EETTTFPTGGFTPEIGKKKHTESTP[p.F121L]LWSIKPNNVSIVLHAEEPYIENEEPE	KKHTESTPL,KHTESTPLW,TESTPLWSI,KKKHTESTPL,KKHTESTPLW	BLCA
SPG20	c.696delT	p.F232fs	QPPPLETLGLDADELILIPNGVQIF[p.F232fs]L*	IPNGVQIFL,LIPNGVQIFL	STAD
SPIN2B	c.448A>G	p.M150V	ANTIIGKAVEHMFEGEHGSKDEWRG[p.M150V]VVLAQAPIMKAWFYITYEKDPVLYMY	KDEWRGVVL,VVLAQAPIM,DEWRGVVLA,VVLAQAPIMK,SKDEWRGVVL,RGVVLAQAPI,DEWRGVVLAQ	TGCT
SPIN4	c.512A>G	p.Y171C	PVMDTWFYITYEKDPVLYMYTLLDD[p.Y171C]CKDGDLRIIPDSNYYFPTAEQEPGEV	YMYTLLDDC,YMYTLLDDCK	LUAD
SPINT1	c.947C>T	p.A316V	LREEECILACRGVQGGPLRGSSGAQ[p.A316V]VTFPQGPSMERRHPVCSGTCQPTQFR	VTFPQGPSM,GSSGAQVTF,RGSSGAQVTF,AQVTFPQGPS	GBM
SPOP	c.148G>A	p.E50K	TQIKVVKFSYMWTINNFSFCREEMG[p.E50K]KVIKSSTFSSGANDKLKWCLRVNPKG	KVIKSSTFS,GKVIKSSTF,FSFCREEMGK,MGKVIKSSTF	UCEC
SPOP	c.304T>G	p.F102V	DEESKDYLSLYLLLVSCPKSEVRAK[p.F102V]VKFSILNAKGEETKAMESQRAYRFVQ	KSEVRAKVK,RAKVKFSIL,KVKFSILNA,SEVRAKVKF,KVKFSILNAK,RAKVKFSILN,EVRAKVKFSI,KSEVRAKVKF,VRAKVKFSIL,AKVKFSILNA,CPKSEVRAKV	PRAD
SPOP	c.305T>G	p.F102C	DEESKDYLSLYLLLVSCPKSEVRAK[p.F102C]CKFSILNAKGEETKAMESQRAYRFVQ	KSEVRAKCK,RAKCKFSIL,KCKFSILNA,SEVRAKCKF,RAKCKFSILN,KCKFSILNAK,EVRAKCKFSI,KSEVRAKCKF,VRAKCKFSIL	PRAD
SPOP	c.391T>G	p.W131G	ILNAKGEETKAMESQRAYRFVQGKD[p.W131G]GGFKKFIRRDFLLDEANGLLPDDKLT	QGKDGGFKK,GGFKKFIRR,GKDGGFKKF,RFVQGKDGGF	PRAD
SPOP	c.397T>A	p.F133I	NAKGEETKAMESQRAYRFVQGKDWG[p.F133I]IKKFIRRDFLLDEANGLLPDDKLTLF	FVQGKDWGI,DWGIKKFIR,WGIKKFIRR,GKDWGIKKF,RFVQGKDWGI,DWGIKKFIRR	PRAD
SPOP	c.397T>G	p.F133V	NAKGEETKAMESQRAYRFVQGKDWG[p.F133V]VKKFIRRDFLLDEANGLLPDDKLTLF	FVQGKDWGV,DWGVKKFIR,GKDWGVKKF,DWGVKKFIRR	PRAD
SPOP	c.398T>G	p.F133C	NAKGEETKAMESQRAYRFVQGKDWG[p.F133C]CKKFIRRDFLLDEANGLLPDDKLTLF	DWGCKKFIR,GKDWGCKKF,DWGCKKFIRR	PRAD
SPOP	c.399C>G	p.F133L	NAKGEETKAMESQRAYRFVQGKDWG[p.F133L]LKKFIRRDFLLDEANGLLPDDKLTLF	FVQGKDWGL,DWGLKKFIR,GKDWGLKKF,LKKFIRRDF,FVQGKDWGLK,RFVQGKDWGL,DWGLKKFIRR	PRAD

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SPTA1	c.5195A>C	p.K1732T	EKLKEAYALFQFFQDLDDEESWIEE[p.K1732T]TLIRVSSQDYGRDLQGVQNLLKKHKR	WIEETLIRV,EESWIEETL,SWIEETLIRV,TLIRVSSQDY,ESWIEETLIR,DEESWIEETL,EESWIEETLI	STAD
SPTA1	c.6032C>T	p.A2011V	PEITDLKDKLISAQHNQSKAIEERY[p.A2011V]VALLKRWEQLLEASAVHRQKLLEKQL	RYVALLKRW,AIEERYVAL,KAIEERYVA,IEERYVALL,AIEERYVALL,KAIEERYVAL	GBM
SPTA1	c.6727G>T	p.D2243Y	DLGDNLEDALILDIKYSTIGLAQQW[p.D2243Y]YQLYQLGLRMQHNLEQQIQAKDIKGV	LAQQWYQLY,GLAQQWYQL,QQWYQLYQL,WYQLYQLGL,AQQWYQLYQ,STIGLAQQWY,AQQWYQLYQL,QWYQLYQLGL,GLAQQWYQLY,WYQLYQLGLR,YQLYQLGLRM	LUAD
SPTA1	c.7099G>T	p.G2367C	FLIDKESENIKSSDEIENAFQALAE[p.G2367C]CKSYITKEDMKQALTPEQVSFCATHM	ALAECKSYI,QALAECKSY,ALAECKSYIT,NAFQALAECK,FQALAECKSY,CKSYITKEDM	LUAD
SPTB	c.256C>T	p.R86C	KWVNSHLARVSCRITDLYKDLRDGR[p.R86C]LLIKLLEVLSGEMLPKPTKGKMRIHC	RLLIKLLEV,LLIKLLEVL,RDGRLLIKL,RLLIKLLEVL,DLRDGRLLIK	CRC
SPTB	c.5591C>T	p.T1864I	AFERELHLLGVQVQQFQDVATRLQT[p.T1864I]VYAGEKAEAIQNKEQEVSAAWQALLD	ATRLQTVYA,VATRLQTVY,DVATRLQTV,RLQTVYAGEK,VYAGEKAEAI,ATRLQTVYAG,TVYAGEKAEA,DVATRLQTVY,LQTVYAGEKA	KIRC
SPTBN4	c.5978C>T	p.A1993V	ADKPRDVSSVEVLMNYHQGLKTELE[p.A1993V]VRVPELTTCQELGRSLLLNKSAMADE	ELEVRVPEL,TELEVRVPE,GLKTELEVRV,HQGLKTELEV,TELEVRVPEL,LEVRVPELTT	CRC
SPTLC3	c.290G>A	p.R97K	IGTLFGYLRDFLRNWGIEKCNAAVE[p.R97K]KKEQKDFVPLYQDFENFYTRNLYMRI	KKEQKDFVPL	SKCM
SPTY2D1	c.1454delC	p.P485fs	GSSRGPGRPVSSPHELRRPVSGLGP[p.P485fs]RGGLSVALGDP*	GPRGGLSVA,GLGPRGGLSV,GPRGGLSVAL	STAD
SRCAP	c.5625_5626insC	p.Q1875fs	RSGPPSPPSTATSFGGPRPRRQPPP[p.Q1875fs]TTSFPFLSGLPGGKAEAAAV*	GLPGGKAEA,RQPPPTTSF,TSFPFLSGL,RPRRQPPPT,FPFLSGLPG,FLSGLPGGKA,GLPGGKAEAA,TTSFPFLSGL,RPRRQPPPTT,QPPPTTSFPF,RRQPPPTTSF,FPFLSGLPGG	KIRP
SRCAP	c.5626_5627insC	p.P1876fs	RSGPPSPPSTATSFGGPRPRRQPPP[p.P1876fs]TTSFPFLSGLPGGKAEAAAV*	GLPGGKAEA,RQPPPTTSF,TSFPFLSGL,RPRRQPPPT,FPFLSGLPG,FLSGLPGGKA,GLPGGKAEAA,TTSFPFLSGL,RPRRQPPPTT,QPPPTTSFPF,RRQPPPTTSF,FPFLSGLPGG	STAD
SRCIN1	c.2595delC	p.P865fs	LSQSPKKVTAETDFNKSVDFEMPPP[p.P865fs]APR*	FEMPPPAPR,VDFEMPPPA,DFEMPPPAPR	STAD
SREBF2	c.2289delC	p.H763fs	LSRAQSLCGPEHSAVPDSLRWLCHP[p.H763fs]WARSFSWSGAGL*	RWLCHPWAR,RSFSWSGAG,HPWARSFSW,SLRWLCHPW,LCHPWARSF,SLRWLCHPWA,CHPWARSFSW,RWLCHPWARS,WARSFSWSGA,RSFSWSGAGL,HPWARSFSWS,WLCHPWARSF,DSLRWLCHPW	STAD
SRGAP1	c.182C>T	p.T61M	EQQTEMRVQLLQDLQDFFRKKAEIE[p.T61M]MEYSRNLEKLAERFMAKTRSTKDHQQ	MEYSRNLEK,KKAEIEMEY,IEMEYSRNL,RKKAEIEMEY,MEYSRNLEKL	MM
SRPRB	c.40G>A	p.G14S	MASADSRRVADGG[p.G14S]SAGGTFQPYLDTLRQELQQTDPTLLS	SAGGTFQPY,GSAGGTFQPY,ADGGSAGGTF	BLCA
SRRM2	c.6769G>T	p.A2257S	IPAASAAAMNLASARTPAIPTAVNL[p.A2257S]SDSRTPAAAAAMNLASPRTAVAPSAV	NLSDSRTPA,NLSDSRTPAA	TGCT
SRSF11	c.51_52insG	p.G17fs	MSNTTVVPSTAGPGPSGG[p.G17fs]ARWRRWWWRRRRRHRGNPGD*	RWRRWWWRR,RWWWRRRRR,GARWRRWWWR,RWRRWWWRRR,RWWWRRRRRH,WWWRRRRRHR	PRAD
SSPO	c.12593delC	p.S4198fs	PRGQQSRFRSSTSGSWAPECREEQS[p.S4198fs]RASPALSPRAHPCACRALAPAPWGTAGCRGSASGAPAPRRV*	ALAPAPWGT,ALSPRAHPC,RASPALSPR,SASGAPAPR,QSRASPALS,RAHPCACRA,RGSASGAPA,SPALSPRAH,SPRAHPCAC,APAPWGTAG,EQSRASPAL,CRALAPAPW,EEQSRASPA,ALAPAPWGTA,ALSPRAHPCA,GSASGAPAPR,RASPALSPRA,RAHPCACRAL,REEQSRASPA,EEQSRASPAL,ACRALAPAPW	PRAD
ST18	c.2334C>A	p.H778Q	KTLKSLMAANSQELKCPTPGCDGSG[p.H778Q]QVTGNYASHRSLSGCPRARKGGVKMT	GSGQVTGNY,GQVTGNYAS,QVTGNYASHR,GQVTGNYASH	LUAD
ST6GALNAC1	c.1061G>A	p.S354N	ELNYSLVQKVVTRFPPVPQQQLLLA[p.S354N]NLPAGSLRCITCAVVGNGGILNNSHM	LLANLPAGS,QQQLLLANL,LANLPAGSL,LLANLPAGSL,NLPAGSLRCI,LANLPAGSLR,QQLLLANLPA	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
STAB1	c.3358_3359insC	p.P1120fs	ASVDVADLLATNGVLHILSQVLLPP[p.P1120fs]PRGCARWAGVAAAAGLGACLQPLPGIAAAPWVGAPD*	GLGACLQPL,RGCARWAGV,CARWAGVAA,RWAGVAAAA,IAAAPWVGA,QPLPGIAAA,ARWAGVAAA,LQPLPGIAA,LPGIAAAPW,GIAAAPWVGA,RGCARWAGVA,CARWAGVAAA,LLPPPRGCAR,ARWAGVAAAA,AAAAGLGACL,AGLGACLQPL,LQPLPGIAAA,LPPPRGCARW,LPGIAAAPWV	STAD
STAC3	c.349G>T	p.G117W	FKDHFFKKPKFCDVCARMIVLNNKF[p.G117W]WLRCKNCKTNIHEHCQSYVEMQRCFG	VLNNKFWLR,WLRCKNCKT,IVLNNKFWLR,RMIVLNNKFW,KFWLRCKNCK,MIVLNNKFWL	LUAD
STAMBPL1	c.427T>C	p.Y143H	TDELKNDLLKKYNVEYQEYLQSKNK[p.Y143H]HKAEILKKLEHQRLIEAERKRIAQMR	KHKAEILKK,YLQSKNKHKA,KNKHKAEILK,SKNKHKAEIL	TGCT
STARD8	c.1985G>C	p.G662A	RRNKTPDYRGQHVFGVPPLIHVQRT[p.G662A]AQPLPQSIQQAMRYLRSQCLDQVGIF	HVQRTAQPL,RTAQPLPQSI,IHVQRTAQPL	TGCT
STAT2	c.1466_1467insC	p.P489fs	AWASVLWFNLLSPNLQNQQFFSNPP[p.P489fs]NGPLELAGPCSQLAVLLLCWPRPQLRPAEHAEKQAVRAEL*	LLCWPRPQL,AVLLLCWPR,FSNPPNGPL,ELAGPCSQL,NPPNGPLEL,WPRPQLRPA,RPQLRPAEH,QQFFSNPPN,AEHAEKQAV,LLLCWPRPQL,QLRPAEHAEK,SQLAVLLLCW,LAVLLLCWPR,LLCWPRPQLR,ELAGPCSQLA,WPRPQLRPAE,RPQLRPAEHA,RPAEHAEKQA,QQFFSNPPNG,FFSNPPNGPL,LELAGPCSQL,AEKQAVRAEL	STAD
STAT3	c.1982A>T	p.D661V	SVEPYTKQQLNNMSFAEIIMGYKIM[p.D661V]VATNILVSPLVYLYPDIPKEEAFGKY	IIMGYKIMV,IMGYKIMVA,IMVATNILV,KIMVATNIL,YKIMVATNI,IIMGYKIMVA,KIMVATNILV,IMGYKIMVAT,GYKIMVATNI,EIIMGYKIMV,YKIMVATNIL,IMVATNILVS,VATNILVSPL	HNSC
STAT5B	c.1101_1102insC	p.P367fs	KTQTKFAATVRLLVGGKLNVHMNPP[p.P367fs]PGEGHHHQ*	HMNPPPGEGH	STAD
STAT6	c.1061_1062insC	p.P354fs	QVLKTQTKFQAGVRFLLGLRFLGAP[p.P354fs]SQASAGQGRHGDREAGAGAECASGSWGWSRKHWRNHQQHCALGEQHSWELLLCPVQEPASQEDQAV*	LLCPVQEPA,ASGSWGWSR,SGSWGWSRK,SWGWSRKHW,RFLGAPSQA,WSRKHWRNH,WGWSRKHWR,REAGAGAEC,RNHQQHCAL,CALGEQHSW,GEQHSWELL,EQHSWELLL,WELLLCPVQ,FLGAPSQASA,ALGEQHSWEL,HSWELLLCPV,LLLCPVQEPA,CASGSWGWSR,ASGSWGWSRK,HWRNHQQHCA,SWGWSRKHWR,LRFLGAPSQA,SQASAGQGRH,REAGAGAECA,AGAECASGSW,AECASGSWGW,GSWGWSRKHW,RKHWRNHQQH,WRNHQQHCAL,QQHCALGEQH,GEQHSWELLL	KIRC
STAT6	c.1402G>C	p.D468H	LGPGKLPIQLQALSLPLVVIVHGNQ[p.D468H]HNNAKATILWDNAFSEMDRVPFVVAE	HGNQHNNAK,NQHNNAKAT,NQHNNAKATI	DLBCL
STK11	c.837delC	p.G279fs	EGDNIYKLFENIGKGSYAIPGDCGP[p.G279fs]RSLTC*	YAIPGDCGPR,IPGDCGPRSL	LUSC
STK11IP	c.464C>A	p.A155E	PLHCLHGLRGIYSQLETLICSRSLQ[p.A155E]ELEELLSACGGDFCSALPWLALLSAN	SLQELEELL,QELEELLSA,LICSRSLQEL,RSLQELEELL,LQELEELLSA,QELEELLSAC	KIRC
STK19	c.265G>A	p.D89N	RGARPGGGDAGGTPGETVRHCSAPE[p.D89N]NPIFRFSSLHSYPFPGTIKSRDMSWK	SAPENPIFR,NPIFRFSSL,CSAPENPIF,CSAPENPIFR,SAPENPIFRF,RHCSAPENPI,HCSAPENPIF,NPIFRFSSLH	SKCM
STK19	c.52_53insG	p.R18fs	MQKWFSAFDDAIIQRQWR[p.R18fs]GKPLPGRGRCELHEGG*	IIQRQWRGK,LPGRGRCEL,QRQWRGKPL,RQWRGKPLP,AIIQRQWRGK,QWRGKPLPGR,RGKPLPGRGR,IQRQWRGKPL,RQWRGKPLPG	PRAD
STOML3	c.256G>T	p.D86Y	VVFRLGRIQADKAKGPGLILVLPCI[p.D86Y]YVFVKVDLRTVTCNIPPQEILTRDSV	ILVLPCIYV,VLPCIYVFV,YVFVKVDLR,LVLPCIYVF,IYVFVKVDL,LILVLPCIY,LILVLPCIYV,LVLPCIYVFV,VLPCIYVFVK,ILVLPCIYVF,GLILVLPCIY,IYVFVKVDLR,LPCIYVFVKV	LUAD
STON1-GTF2A1L	c.1352A>G	p.N451S	KVTKEGKFVESAVITQIYCLCFVNG[p.N451S]SLECFLTLNDLELPKRDESYYEKDSE	CLCFVNGSL,FVNGSLECF,GSLECFLTL,FVNGSLECFL,CFVNGSLECF	TGCT
STRA6	c.203A>G	p.Q68R	QPAGNQTSPGATEDYSYGSWYIDEP[p.Q68R]RGGEELQPEGEVPSCHTSIPPGLYHA	GSWYIDEPR	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
STRADA	c.997delC	p.R333fs	EELTMSPSRSVANSGLSDSLTTSTP[p.R333fs]GPPTVTRPPTPTTEPSPPTSTTLWSSAFSATRMPGPVPAPS*	TLWSSAFSA,WSSAFSATR,VTRPPTPTT,ATRMPGPVP,TTLWSSAFS,STTLWSSAF,SSAFSATRM,TRMPGPVPA,MPGPVPAPS,SPPTSTTLW,TLWSSAFSAT,FSATRMPGPV,TTLWSSAFSA,ATRMPGPVPA,STPGPPTVTR,LWSSAFSATR,TTSTPGPPTV,EPSPPTSTTL,TSTTLWSSAF,WSSAFSATRM	STAD
STRN3	c.654G>T	p.K218N	LDVRSQRVRSLLGLSNSEPNGSVET[p.K218N]NNLEQILNGGESPKQKGQEIKRSSGD	ETNNLEQIL,VETNNLEQI,VETNNLEQIL	UCEC
STT3B	c.1747G>T	p.D583Y	TSNAYSSPSVVLASYNHDGTRNILD[p.D583Y]YFREAYFWLRQNTDEHARVMSWWDYG	ILDYFREAY,NILDYFREA,DYFREAYFW,YFREAYFWL,GTRNILDYF,LDYFREAYF,GTRNILDYFR,DYFREAYFWL,YFREAYFWLR,NILDYFREAY,ILDYFREAYF	CRC
STX2	c.320G>T	p.R107L	KKTANKIRAKLKAIEQSFDQDESGN[p.R107L]LTSVDLRIRRTQHSVLSRKFVEAMAE	DESGNLTSV,LTSVDLRIRR	LUAD
STX2	c.756delA	p.K252fs	MINNIERNVMNATDYVEHAKEETKK[p.K252fs]LSNIRARQEGKSG*	NIRARQEGK,ETKKLSNIR	STAD
STXBP6	c.274G>A	p.D92N	QFEGSTSFVRRSQWMLEQLRQVNGI[p.D92N]NPNGDSAEFDLLFENAFDQWVASTAS	RQVNGINPN,NPNGDSAEF,RQVNGINPNG	UCEC
SULT1C4	c.254G>A	p.R85Q	WTQEIVELIQNEGDVEKSKRAPTHQ[p.R85Q]QFPFLEMKIPSLGSGLEQAHAMPSPR	QQFPFLEMK,QFPFLEMKI,APTHQQFPF,HQQFPFLEM,KRAPTHQQF,HQQFPFLEMK,RAPTHQQFPF,KSKRAPTHQQ,APTHQQFPFL,SKRAPTHQQF,THQQFPFLEM,QQFPFLEMKI	CRC
SULT1E1	c.230G>A	p.R77Q	WVSEIVYMIYKEGDVEKCKEDVIFN[p.R77Q]QIPFLECRKENLMNGVKQLDEMNSPR	VIFNQIPFL,DVIFNQIPF,KEDVIFNQI,DVIFNQIPFL	UCEC
SUMF2	c.329G>A	p.G110E	IFPVTNKDFRDFVREKKYRTEAEMF[p.G110E]EWSFVFEDFVSDELRNKATQPMKSVL	EMFEWSFVF,EWSFVFEDF,AEMFEWSFV,FEWSFVFED,EAEMFEWSF,TEAEMFEWS,AEMFEWSFVF,EAEMFEWSFV,TEAEMFEWSF,FEWSFVFEDF	LUAD
SUN3	c.1016C>A	p.P339Q	TFELQHAVSEYLLCVKLNIFSNWGH[p.P339Q]QKYTCLYRFRVHGTPGKHI*	FSNWGHQKY,IFSNWGHQK,HQKYTCLYR,GHQKYTCLY,WGHQKYTCL,QKYTCLYRF,NIFSNWGHQK,HQKYTCLYRF,IFSNWGHQKY,WGHQKYTCLY	LUAD
SUN3	c.370C>A	p.L124I	LRMPKEQLELLKKESQNLENNFRQI[p.L124I]IFLIEQIDVLKALLRDMKDGMDNNHN	QIIFLIEQI,NFRQIIFLI,LENNFRQII,RQIIFLIEQ,RQIIFLIEQI,IFLIEQIDVL,LENNFRQIIF	UCEC
SUN3	c.382G>A	p.E128K	KEQLELLKKESQNLENNFRQILFLI[p.E128K]KQIDVLKALLRDMKDGMDNNHNWNTH	FLIKQIDVL,KQIDVLKAL,LIKQIDVLK,ILFLIKQIDV,KQIDVLKALL,RQILFLIKQI,FLIKQIDVLK,NFRQILFLIK,IKQIDVLKAL	CRC
SUPT6H	c.2869G>A	p.A957T	SSDEDILCLKFHPLQEHVVKEELLN[p.A957T]TLYCEFINRVNEVGVDVNRAIAHPYS	TLYCEFINR,LLNTLYCEF,VKEELLNTL,KEELLNTLY,LLNTLYCEFI,TLYCEFINRV,NTLYCEFINR,ELLNTLYCEF,VKEELLNTLY	CRC
SUSD1	c.1027C>T	p.R343C	SRRINPKISYVISIKGQRLDPMESV[p.R343C]CEETVNLTTDSRTPEVCLALYPGTNY	MESVCEETV,CEETVNLTT	UCEC
SUSD5	c.1538C>T	p.T513M	YELTSSTLEILTVNTVKQTPNHIPS[p.T513M]MIMATTQPPVETTVPEIQDSFPYLLS	TPNHIPSMI,SMIMATTQP,MIMATTQPP,IPSMIMATT,MIMATTQPPV,KQTPNHIPSM,QTPNHIPSMI,TPNHIPSMIM,SMIMATTQPP	GBM
SV2A	c.412delG	p.E138fs	MADGAPLAGVRGGLSDGEGPPGGRG[p.E138fs]RHNDGKNEKNWPNSMKPSYGSVATAASSGHCILCLVWR*	SMKPSYGSV,KPSYGSVAT,WPNSMKPSY,NEKNWPNSM,MKPSYGSVA,AASSGHCIL,SMKPSYGSVA,GGRGRHNDGK,NWPNSMKPSY,NSMKPSYGSV,KPSYGSVATA,KNEKNWPNSM,MKPSYGSVAT,TAASSGHCIL,SGHCILCLVW	STAD
SV2C	c.179C>A	p.P60Q	DRAQDEYTQRSYSRFQDEEDDDDYY[p.P60Q]QAGETYNGEANDDEGSSEATEGHDED	YYQAGETYNG,DDYYQAGETY	LUAD
SVIL	c.278T>C	p.M93T	EKQTRSKYCTETSGVHGDSPYGSGT[p.M93T]TDTHSLESKAERIARYKAERRRQLAE	TTDTHSLESK	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SVIL	c.5586delG	p.G1862fs	EERGAQVQVLQGKEPPCFLQCFQGG[p.G1862fs]WWCTRGGGKRKKKMCKVSGGCTACVERCPWKGICWKWPVTVAA*	KGICWKWPV,PWKGICWKW,CTRGGGKRK,RGGGKRKKK,CWKWPVTVA,FQGGWWCTR,LQCFQGGWW,CKVSGGCTA,WKWPVTVAA,VERCPWKGI,KVSGGCTACV,GICWKWPVTV,TACVERCPWK,CFLQCFQGGW,GWWCTRGGGK,CTRGGGKRKK,GGKRKKKMCK,CWKWPVTVAA,CFQGGWWCTR,CPWKGICWKW	STAD
SYCP2	c.1422A>T	p.K474N	KPSKYIKNSDKGNRNNSQLEKTTPS[p.K474N]NRKMSEASMIVSGADRYTMRSPVLFS	KTTPSNRKM,NRKMSEASM,TPSNRKMSEA,SQLEKTTPSN,SNRKMSEASM	HNSC
SYMPK	c.1007C>G	p.A336G	HPASLEFQAQITTLLVDLGTPQAEI[p.A336G]GRNMPSSKDTRKRPRDDSDSTLKKMK	IGRNMPSSK,PQAEIGRNM,AEIGRNMPS,TPQAEIGRNM,AEIGRNMPSS	TGCT
SYN2	c.99_101delAGC	p.A34del	LSDSSFIANLPNGYMTDLQRPEPQQ[p.A34del]PTPPPPGPGAASAAAPPTASPGPERTPP	LQRPEPQQPT	BLCA,KIRP,PRAD
SYNDIG1	c.403G>T	p.D135Y	CCETTFIEDRSPTKDSLEYPDGKFI[p.D135Y]YLSADDIKIHTLSYDVEEEEEFQELE	YLSADDIKI,FIYLSADDI,YPDGKFIYL,FIYLSADDIK,EYPDGKFIYL,KFIYLSADDI,IYLSADDIKI,LEYPDGKFIY	LUAD
SYNE2	c.9309G>T	p.K3103N	ESRRLNAQILSQRIEKAKCLCDEII[p.K3103N]NKLNENKTFDDSFKEKEILQIKLNAE	CLCDEIINK,IINKLNENK,NKLNENKTF,CLCDEIINKL	CRC
SYNGR4	c.506G>A	p.R169Q	QAAIAFTFFSILVWIFQAYLAFQDL[p.R169Q]QNDAPVPYKRFLDEGGMVLTTLPLPS	LQNDAPVPY,FQDLQNDAPV,LQNDAPVPYK,DLQNDAPVPY	CRC
SYNJ1	c.2041A>T	p.I681F	KTISRDNKYVLLASEQLVGVCLFVF[p.I681F]FRPQHAPFIRDVAVDTVKTGMGGATG	FVFFRPQHA,GVCLFVFFR,VGVCLFVFF,FFRPQHAPF,VFFRPQHAPF,FFRPQHAPFI,VGVCLFVFFR	CLL
SYNJ2	c.2495A>C	p.K832T	WRKKHPFDKTAGELNLLDSDLDVDT[p.K832T]TVRHTWSPGALQYYGRAELQASDHRP	TVRHTWSPG,TVRHTWSPGA	KIRC
SYNJ2	c.3331_3332insC	p.P1111fs	HRSPSRSLSVPNRPRPPQPPQRPPP[p.P1111fs]SNRFNGEKVGFRCVHLLRHPWTVFNFADGKTSTRSTSATSQGSDWNK*	HLLRHPWTV,TVFNFADGK,TSQGSDWNK,RFNGEKVGF,RHPWTVFNF,KVGFRCVHL,GFRCVHLLR,KTSTRSTSA,STRSTSATS,LLRHPWTVF,CVHLLRHPW,HPWTVFNFA,GEKVGFRCV,VGFRCVHLLR,WTVFNFADGK,ATSQGSDWNK,HLLRHPWTVF,LRHPWTVFNF,KVGFRCVHLL,GFRCVHLLRH,KTSTRSTSAT,STRSTSATSQ,RFNGEKVGFR,NFADGKTSTR,PQRPPPSNRF,NRFNGEKVGF,RCVHLLRHPW	STAD
SYNM	c.1547G>A	p.R516Q	RTVILGKKTEVKATREQERNRPETI[p.R516Q]QTKPEEKMFDSKEKASEERNLRWEEL	TIQTKPEEK,IQTKPEEKM,RNRPETIQTK,IQTKPEEKMF	UCEC
SYNPO	c.1856_1857insC	p.G619fs	SSHLKGQAVPASKTGILEESMARRG[p.G619fs]QPQIHVYFRGEAQGDPESRLAGSGTDSG*	GQPQIHVYF,MARRGQPQI,RGQPQIHVY,QPQIHVYFR,AQGDPESRL,SMARRGQPQI,RGQPQIHVYF,MARRGQPQIH,RRGQPQIHVY	KIRC
SYT4	c.1delA	p.M1fs	[p.M1fs]WLRSPPAGKNLMKSPQWWGSSVHLAWSSQSLSLHGSAVRENHPSLTRLLHTSLCMCLRELIFTLKT*	HLAWSSQSL,SLSLHGSAV,CLRELIFTL,LLHTSLCMC,SLCMCLREL,WLRSPPAGK,HTSLCMCLR,QWWGSSVHL,AVRENHPSL,LTRLLHTSL,LSLHGSAVR,SPPAGKNLM,SPQWWGSSV,RLLHTSLCM,KNLMKSPQW,PQWWGSSVH,WGSSVHLAW,AWSSQSLSL,CMCLRELIF,RELIFTLKT,SLTRLLHTSL,LLHTSLCMCL,SLCMCLRELI,CLRELIFTLK,WWGSSVHLAW,KSPQWWGSSV,AVRENHPSLT,SLSLHGSAVR,HPSLTRLLHT,LAWSSQSLSL,GKNLMKSPQW,PQWWGSSVHL,VHLAWSSQSL,SQSLSLHGSA,SAVRENHPSL,RENHPSLTRL,TRLLHTSLCM,LCMCLRELIF,SPQWWGSSVH	STAD
SYT7	c.1046C>T	p.T349M	TMKRNLNPIFNESFAFDIPTEKLRE[p.T349M]MTIIITVMDKDKLSRNDVIGKIYLSW	KLREMTIII,IPTEKLREM,REMTIIITV,EMTIIITVM,MTIIITVMDK,KLREMTIIIT,REMTIIITVM	CRC
SYT8	c.1117C>T	p.R373W	GARASGQPLQHWADMLAHARRPIAQ[p.R373W]WHPLRPAREVDRMLALQPRLRLRLPL	QWHPLRPAR,PIAQWHPLR,RPIAQWHPL,HARRPIAQW,AQWHPLRPA,HARRPIAQWH,RPIAQWHPLR,AHARRPIAQW,RRPIAQWHPL	ACC
SYTL2	c.1320C>G	p.I440M	FPINGLHSHSEVLTARPQSMENSPT[p.I440M]MNEPKDKSSELTRLESVLPRSPADEL	QSMENSPTM,PQSMENSPTM	BLCA

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TAB3	c.632G>C	p.R211T	HIPRYSTNPITVTVSQNLPSGQTVP[p.R211T]TALQILPQIPSNLYGSPGSIYIRQTS	QTVPTALQI,LPSGQTVPT,TALQILPQI,GQTVPTALQI,LPSGQTVPTA	BLCA
TADA2B	c.199G>A	p.E67K	IGHHRRYHGYQLVDGGRFTLWGPEA[p.E67K]KGGWTSREEQLLLDAIEQFGFGNWED	FTLWGPEAK,EAKGGWTSR,RFTLWGPEAK	CESC
TAF1	c.2527C>T	p.R843W	SKDRPRRIRMEDIKKAFPSHSESSI[p.R843W]WKRLKLCADFKRTGMDSNWWVLKSDF	IWKRLKLCA,HSESSIWKR,SESSIWKRL,FPSHSESSIW,WKRLKLCADF	UCEC
TAF1A	c.514_515CG>AT	p.R172M	HGMLKDAKRNLSEAETWRHGENTSS[p.R172M]MEILINLIQAYKGLLQYYTWSEKKMEL	SSMEILINL,SMEILINLI,NTSSMEILI,RHGENTSSM,GENTSSMEI,MEILINLIQ,SSMEILINLI,WRHGENTSSM,GENTSSMEIL,MEILINLIQA	SKCM
TAF1B	c.874C>T	p.R292C	GIESWPDYEDIYKKTVEVGTFLDLP[p.R292C]CFPDITEDCYLHPNILCMKYLMEVNL	GTFLDLPCF,LDLPCFPDI,FLDLPCFPDI,VGTFLDLPCF	BLCA
TAF1L	c.2553delA	p.K851fs	QVFIYRLFWKSKDRPRRIRMEDIKK[p.K851fs]PFLPIQKAASGRG*	DIKKPFLPI,RMEDIKKPF,MEDIKKPFL,KPFLPIQKAA,IRMEDIKKPF,RMEDIKKPFL	STAD
TAF5	c.388T>G	p.S130A	RQSKLREAEEALRREAGLLEEAVAG[p.S130A]AGAPGEVDSAGAEVTSALLSRVTASA	LLEEAVAGA,EEAVAGAGA,GLLEEAVAGA,LEEAVAGAGA	ACC
TANK	c.1139C>T	p.S380L	LDSPGKAIRGPQQPIWKPFPNQDSD[p.S380L]LVVLSGTDSELHIPRVCEFCQAVFPP	NQDSDLVVL,FPNQDSDLV,KPFPNQDSDL,FPNQDSDLVV	CRC
TAOK2	c.2696_2697insG	p.Q899fs	QRVEEELLALQTGRSERIRSLLERQ[p.Q899fs]GP*	RIRSLLERQG	KIRC
TARBP1	c.2344C>G	p.L782V	VLTELINLHLKVGWKRGNPIWRVIS[p.L782V]VLKNASIQHLQEMDSGQEPTVGSQIQ	RVISVLKNA,IWRVISVLK,NPIWRVISV,VLKNASIQHL,PIWRVISVLK,NPIWRVISVL	LUSC
TARS2	c.595G>A	p.E199K	RGSELPVLERICQELTAAARPFRRL[p.E199K]KASRDQLRQLFKDNPFKLHLIEEKVT	AARPFRRLK,RLKASRDQL,RPFRRLKAS,AAARPFRRLK,AARPFRRLKA,RPFRRLKASR,RLKASRDQLR,RRLKASRDQL	LUAD
TARSL2	c.1097G>A	p.G366D	KGPHVRHTGKIKTIKIFKNSSTYWE[p.G366D]DNPEMETLQRIYGISFPDNKMMRDWE	TYWEDNPEM,STYWEDNPEM,WEDNPEMETL	GBM
TAS1R2	c.808C>T	p.R270C	PNQNMTSEERQRLVTIVDKLQQSTA[p.R270C]CVVVVFSPDLTLYHFFNEVLRQNFTG	KLQQSTACV,LQQSTACVV,STACVVVVF,QSTACVVVV,QQSTACVVV,KLQQSTACVV,QQSTACVVVV,STACVVVVFS,LQQSTACVVV,QSTACVVVVF	CRC
TAS1R3	c.1573G>A	p.E525K	SRQCQEGQVRRVKGFHSCCYDCVDC[p.E525K]KAGSYRQNPDDIACTFCGQDEWSPER	CVDCKAGSY,CVDCKAGSYR	BLCA
TAS2R1	c.549C>A	p.F183L	KFFSQNATIQKEDTLAIQIFSFVAE[p.F183L]LSVPLLIFLFAVLLLIFSLGRHTRQM	QIFSFVAEL,FVAELSVPL,FSFVAELSV,ELSVPLLIF,AELSVPLLI,IQIFSFVAEL,FVAELSVPLL,IFSFVAELSV,SFVAELSVPL,LSVPLLIFLF,ELSVPLLIFL,FSFVAELSVP,AELSVPLLIF	CRC
TAS2R16	c.531G>T	p.Q177H	IQLLTMEHLPRNSTVTDKLENFHQY[p.Q177H]HFQAHTVALVIPFILFLASTIFLMAS	QYHFQAHTV,HFQAHTVAL,LENFHQYHF,FHQYHFQAH,HQYHFQAHT,YHFQAHTVA,HQYHFQAHTV,KLENFHQYHF,YHFQAHTVAL	LUAD
TAS2R16	c.691G>A	p.V231I	QIQHHSTGHCNPSMKARFTALRSLA[p.V231I]ILFIVFTSYFLTILITIIGTLFDKRC	RSLAILFIV,FTALRSLAI,ILFIVFTSY,SLAILFIVF,ALRSLAILF,TALRSLAIL,ALRSLAILFI,FTALRSLAIL,SLAILFIVFT,RFTALRSLAI,TALRSLAILF,RSLAILFIVF,ILFIVFTSYF,AILFIVFTSY	MM
TAS2R30	c.707_708insT	p.L236fs	HGKGSQDPSTKVHIKALQTVTSFLL[p.L236fs]VMCHLLSVHDHISL*	FLLVMCHLL,LVMCHLLSV,HLLSVHDHI,SFLLVMCHL,QTVTSFLLV,TVTSFLLVM,VMCHLLSVH,LSVHDHISL,LLVMCHLLSV,LLSVHDHISL,SFLLVMCHLL,QTVTSFLLVM,LVMCHLLSVH,LQTVTSFLLV,TSFLLVMCHL	KICH
TAS2R38	c.932T>C	p.I311T	MAACPSGHAAILISGNAKLRRAVMTT[p.I311T]TLLWAQSSLKVRADHKADSRTLC*	AVMTTLLWA,TLLWAQSSL,RAVMTTLLW,KLRRAVMTT,LRRAVMTTL,RRAVMTTLL,KLRRAVMTTL,TLLWAQSSLK,RRAVMTTLLW,RAVMTTLLWA,TTLLWAQSSL,LRRAVMTTLL	KIRC
TAS2R41	c.763G>A	p.A255T	TRALKSLISFLILYALSFLSLIIDA[p.A255T]TKFISMQNDFYWPWQIAVYLCISVHP	FLSLIIDAT,LIIDATKFI,LSLIIDATK,SLIIDATKF,IDATKFISM,SLIIDATKFI,LSLIIDATKF,IIDATKFISM,TKFISMQNDF	GBM
TAS2R8	c.294G>C	p.W98C	PDVYTKNKQQIVIFTFWTFANYLNM[p.W98C]CITTCLNVFYFLKIASSSHPLFLWLK	YLNMCITTC,FANYLNMCI,LNMCITTCL,CITTCLNVF,YLNMCITTCL,NMCITTCLNV,TFANYLNMCI,CITTCLNVFY,MCITTCLNVF	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TAS2R9	c.487G>C	p.E163Q	FLISLIISVPKNDDMWYHLFKVSHE[p.E163Q]QNITWKFKVSKIPGTFKQLTLNLGVM	HEQNITWKF,FKVSHEQNI,VSHEQNITW,VSHEQNITWK,KVSHEQNITW,SHEQNITWKF	BLCA
TAT	c.1100G>A	p.R367H	TLSFLKSNADLCYGALAAIPGLRPV[p.R367H]HPSGAMYLMVGIEMEHFPEFENDVEF	GLRPVHPSG,PVHPSGAMY,RPVHPSGAM,HPSGAMYLM,GLRPVHPSGA,RPVHPSGAMY,HPSGAMYLMV,AAIPGLRPVH,LRPVHPSGAM	GBM
TBC1D1	c.212C>T	p.S71F	EVRRLSRQSTRKEPVTKQVRLCVSP[p.S71F]FGLRCEPEPGRSQQWDPLIYSSIFEC	RLCVSPFGL,QVRLCVSPF,RLCVSPFGLR,KQVRLCVSPF,QVRLCVSPFG,VRLCVSPFGL	BLCA
TBC1D1	c.830A>G	p.H277R	DGGLRSSGFFSSFEESDIENHLISG[p.H277R]RNIVQPTDIEENRTMLFTIGQSEVYL	HLISGRNIV,DIENHLISGR	KIRC
TBC1D12	c.1823T>A	p.F608Y	PDVGYVQGMSFIAAVLILNLEEADA[p.F608Y]YIAFANLLNKPCQLAFFRVDHSMMLK	NLEEADAYI,AYIAFANLL,EADAYIAFA,DAYIAFANL,EEADAYIAF,LNLEEADAY,LEEADAYIA,YIAFANLLNK,ILNLEEADAY,DAYIAFANLL,LEEADAYIAF,EEADAYIAFA,ADAYIAFANL	KIRC
TBC1D2B	c.2759G>A	p.R920Q	ILDARKLISISFGDLNPFPLRQIRN[p.R920Q]QRAYHLEKVRLELTELEAIREDFLRE	QIRNQRAYH,NQRAYHLEK,RQIRNQRAY,IRNQRAYHL,RQIRNQRAYH,QIRNQRAYHL,RNQRAYHLEK,LRQIRNQRAY,NQRAYHLEKV	BLCA,KIRP,PRAD
TBC1D9	c.3697C>A	p.P1233T	DWAITFEQFLASLLTEPALVKYFDK[p.P1233T]TVCMMARITSAKNIRMMGKPLTSASD	ALVKYFDKT,KTVCMMARI,KYFDKTVCM,YFDKTVCMM,ALVKYFDKTV,KYFDKTVCMM,VKYFDKTVCM	PRAD
TBCD	c.1426C>T	p.R476C	DEKRGACSVGTNVRDAACYVCWAFA[p.R476C]CAYEPQELKPFVTAISSALVIAAVFD	YVCWAFACA,CAYEPQELK,VCWAFACAY,YVCWAFACAY,FACAYEPQEL	LUSC
TBL1XR1	c.377delA	p.N126fs	DKLAQQQAAAAAAAAAAASQQGSAK[p.N126fs]MEKTQQMGRRMEHIL*	QMGRRMEHI,KTQQMGRRM,MGRRMEHIL,ASQQGSAKM,AKMEKTQQM,QQMGRRMEH,QQMGRRMEHI,SQQGSAKMEK,AASQQGSAKM,TQQMGRRMEH	STAD
TBX3	c.559C>T	p.H187Y	RYKFHNSRWMVAGKADPEMPKRMYI[p.H187Y]YPDSPATGEQWMSKVVTFHKLKLTNN	YIYPDSPAT,EMPKRMYIY,MYIYPDSPA,RMYIYPDSP,RMYIYPDSPA,PEMPKRMYIY	BRCA
TBX4	c.1109delC	p.S370fs	LDLPCKRSYLEAPSSVGEDHYFRSP[p.S370fs]LPTTSKC*	RSPLPTTSK,GEDHYFRSPL	STAD
TCEB3C	c.922G>A	p.E308K	DLLSAFEAMTSQANPEALSAPALQE[p.E308K]KAAFPGRRVNAKMPVYSGSRPACQLQ	LSAPALQEK,KAAFPGRRV,LQEKAAFPG,ALSAPALQEK,APALQEKAAF	SKCM
TCF7	c.419A>C	p.H140P	GMYKETVYSAFNLLMHYPPPSGAGQ[p.H140P]PPQPQPPLHKANQPPHGVPQLSLYEH	QPPQPQPPL,GQPPQPQPPL	KIRC
TCHP	c.515delA	p.E172fs	KLREMELDLHQKHVVNSWEMQKEEK[p.E172fs]NSKKPPQSKRTNGMKMNMKGPEGRR*	MQKEEKNSK,NSKKPPQSK,QSKRTNGMK,RTNGMKMNM,KMNMKGPEG,MNMKGPEGR,NMKGPEGRR,SKRTNGMKM,RTNGMKMNMK,MQKEEKNSKK,KNSKKPPQSK,KMNMKGPEGR,NSKKPPQSKR,MNMKGPEGRR,KRTNGMKMNM,MKMNMKGPEG	STAD
TCOF1	c.4084_4086delAAG	p.K1366del	GWESRKRKLSGDQPAARTPRSKKKK[p.K1366del]LGAGEGGEASVSPEKTSTTSKGKAKRDK	RSKKKKLGA,TPRSKKKKL,RSKKKKLGAG	PRAD
TCOF1	c.791A>G	p.K264R	APAPGKVGDVTPQVKGGALPPAKRA[p.K264R]RKPEEESESSEEGSESEEEAPAGTRS	ALPPAKRARK	LUAD
TCTE1	c.380G>T	p.S127I	PEHQQKVLNHLSPDLPLAVTANLID[p.S127I]IENYWLRCCMHRWPVCHVAHHGGSWK	NLIDIENYWL,IENYWLRCCM,TANLIDIENY	LUAD
TCTEX1D2	c.221C>T	p.S74L	HAVLKEELANAEYSPEEMPQLTKHL[p.S74L]LENIKDKLKEMGFDRYKMVVQVVIGE	MPQLTKHLL,QLTKHLLENI,LTKHLLENIK	CESC
TDO2	c.591G>C	p.Q197H	RVPYNRRHYRDNFKGEENELLLKSE[p.Q197H]HEKTLLELVEAWLERTPGLEPHGFNF	LLLKSEHEK,LKSEHEKTL,NELLLKSEH,HEKTLLELV,LKSEHEKTLL,SEHEKTLLEL	LUAD
TDRD10	c.828G>T	p.W276C	CLAEYHLGDYGHAWNRCWVLDRVDT[p.W276C]CAVVMFIDFGQLATIPVQSLRSLDSD	DTCAVVMFI,RVDTCAVVM,CAVVMFIDF,VLDRVDTCAV,RVDTCAVVMF	KIRC

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TDRD10	c.965C>T	p.S322L	SLDSDDFWTIPPLTQPFMLEKDILS[p.S322L]LYEVVHRILKGKITGALNSAVTAPAS	MLEKDILSL,SLYEVVHRI,LYEVVHRIL,LEKDILSLY,DILSLYEVV,KDILSLYEV,MLEKDILSLY,FMLEKDILSL,SLYEVVHRIL,ILSLYEVVHR,KDILSLYEVV	CRC
TEAD2	c.894_895insC	p.P298fs	DVRQIYDKFPEKKGGLRELYDRGPP[p.P298fs]PCLLPGQVLGGPELGPKW*	GQVLGGPEL,VLGGPELGPK,RELYDRGPPP	STAD
TECTB	c.85C>A	p.L29I	KAFVLLAIFAEASAKSCAPNKADVI[p.L29I]IVFCYPKTIITKIPECPYGWEVHQLA	VIIVFCYPK,APNKADVII,NKADVIIVF,IVFCYPKTI,KADVIIVFCY,DVIIVFCYPK,APNKADVIIV,IVFCYPKTII	CRC
TEDDM1	c.498G>A	p.M166I	LLVLTAELWAPNMCHLQLMETFLIL[p.M166I]IMGSWLMQAGFILYRPVSGYPWQDDD	LMETFLILI,ILIMGSWLM,IMGSWLMQA,METFLILIM,FLILIMGSW,QLMETFLILI,FLILIMGSWL,LIMGSWLMQA,TFLILIMGSW,ETFLILIMGS,LMETFLILIM,LILIMGSWLM	CESC
TEKT5	c.1202G>A	p.R401H	LLERSIMAKEGPLKVAQTRLECRTR[p.R401H]HPNMELCRDIPQLKLVNEVFTIDDTL	RTRHPNMEL,RTRHPNMELC,LECRTRHPNM,HPNMELCRDI	CRC
TET1	c.4415C>G	p.T1472S	AAVREIMENRYGQKGNAIRIEIVVY[p.T1472S]SGKEGKSSHGCPIAKWVLRRSSDEEK	VVYSGKEGK,RIEIVVYSGK,IVVYSGKEGK	TGCT
TEX15	c.4954G>C	p.E1652Q	ASSLQILQEETKVCLNILPLFVEAF[p.E1652Q]QRKQECSVEQILISRELLVDQNLWNN	FQRKQECSV	CESC
TFE3	c.1444_1445insG	p.G482fs	SLKPEQLDIEEEGRPGAATFHVGGG[p.G482fs]TCPECSPSAAPCTALRCPSGPALSQRPPGGPGRPLPPGAGGHSDGGGGGGGGRTVGGCPVPTAGCLRSPALFSVPCCLQGQQPPQQLQHGRGVLIRPHPSPGTFPPRKGGPVRMRPRLFPHPPMRLPCPGILGEEEM*	ALFSVPCCL,ALRCPSGPA,RMRPRLFPH,RLFPHPPMR,SAAPCTALR,LFPHPPMRL,LIRPHPSPG,PPGGPGRPL,CPVPTAGCL,SPALFSVPC,RPHPSPGTF,FPPRKGGPV,GPVRMRPRL,RPRLFPHPP,LRCPSGPAL,SQRPPGGPG,GCLRSPALF,LRSPALFSV,QQLQHGRGV,LQHGRGVLI,MRLPCPGIL,HPSPGTFPP,CLRSPALFSV,RLFPHPPMRL,ALRCPSGPAL,SQRPPGGPGR,KGGPVRMRPR,RMRPRLFPHP,RPRLFPHPPM,HPSPGTFPPR,SPSAAPCTAL,RPPGGPGRPL,PPRKGGPVRM,GPVRMRPRLF,FPHPPMRLPC,AGCLRSPALF,LQGQQPPQQL,GQQPPQQLQH,QQLQHGRGVL,IRPHPSPGTF,CPGILGEEEM	STAD
TFG	c.1145C>T	p.A382V	YQPRPGFTSLPGSTMTPPPSGPNPY[p.A382V]VRNRPPFGQGYTQPGPGYR*	PYVRNRPPF,YVRNRPPFG,NPYVRNRPPF	CLL
TFPI2	c.616C>T	p.R206C	RTCDAFTYTGCGGNDNNFVSREDCK[p.R206C]CACAKALKKKKKMPKLRFASRIRKIR	CACAKALKK,KCACAKALK,CKCACAKAL,REDCKCACA,CACAKALKKK,KCACAKALKK	GBM
TFPI2	c.664C>T	p.R222C	NFVSREDCKRACAKALKKKKKMPKL[p.R222C]CFASRIRKIRKKQF*	LCFASRIRK,CFASRIRKI,MPKLCFASR,KLCFASRIR,KKKMPKLCF,KKMPKLCFA,KLCFASRIRK,KKKMPKLCFA,KMPKLCFASR,CFASRIRKIR,MPKLCFASRI,KKKKMPKLCF,KKMPKLCFAS	BLCA
TFPT	c.755C>G	p.S252C	EALDSSWVSRGPDKLLPYPTLASPA[p.S252C]CD*	YPTLASPAC	BRCA
TGFBR1	c.722C>T	p.S241L	FGEVWRGKWRGEEVAVKIFSSREER[p.S241L]LWFREAEIYQTVMLRHENILGFIAAD	RLWFREAEI,LWFREAEIY,SSREERLWF,EERLWFREA,FSSREERLW,SSREERLWFR,IFSSREERLW,KIFSSREERL,RLWFREAEIY,FSSREERLWF,REERLWFREA	CRC
TGM6	c.1073delC	p.T358fs	WNESWFARQDLGPSYNGWQVLDATP[p.T358fs]RRRVKVCSGAAQPQSPPSARVMCTWLTMAPSCLRRSTPTTSPGCGTRMRAGSVYTQTRRRLGDASAPRRWAVTPAWTSLTSTSIRKGPGKRGRCTARR*	RVMCTWLTM,VMCTWLTMA,WLTMAPSCL,LTMAPSCLR,TMAPSCLRR,SVYTQTRRR,SLTSTSIRK,RLGDASAPR,TSLTSTSIR,TSIRKGPGK,RVKVCSGAA,SARVMCTWL,GTRMRAGSV,RMRAGSVYT,QTRRRLGDA,ASAPRRWAV,SIRKGPGKR,QVLDATPRR,TTSPGCGTR,WTSLTSTSI,APSCLRRST,AVTPAWTSL,TPRRRVKVC,AQPQSPPSA,TRMRAGSVY,RRWAVTPAW,TPAWTSLTS,RVMCTWLTMA,LTMAPSCLRR,TSLTSTSIRK,STSIRKGPGK,TWLTMAPSCL,RVKVCSGAAQ,SARVMCTWLT,GTRMRAGSVY,RMRAGSVYTQ,RAGSVYTQTR,SVYTQTRRRL,QVLDATPRRR,WLTMAPSCLR,WTSLTSTSIR,TSIRKGPGKR,DASAPRRWAV,WAVTPAWTSL,RLGDASAPRR,QPQSPPSARV,APRRWAVTPA,TPAWTSLTST,RRVKVCSGAA,PQSPPSARVM,ARVMCTWLTM,AWTSLTSTSI,PPSARVMCTW	STAD
THADA	c.5822C>T	p.S1941L	RLLAFLEGKEGEDTLVLSVWDSYAE[p.S1941L]LRQLTLPRTEAAC*	SVWDSYAEL,ELRQLTLPR,YAELRQLTL,SVWDSYAELR,SYAELRQLTL,LSVWDSYAEL	UCEC

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THAP5	c.860C>A	p.S287Y	EELNTNKESVIAIFVPAENSKPSVN[p.S287Y]YFISAQKETTEMEDTDIEDSLYKDVD	VNYFISAQK,NSKPSVNYF,SVNYFISAQK,NSKPSVNYFI,KPSVNYFISA,AENSKPSVNY	CRC
THEM4	c.50T>G	p.L17R	MLRSCAARLRTLGALC[p.L17R]RPPVGRRLPGSEPRPELRSFSSEEVI	ALCRPPVGR,TLGALCRPPV,RLRTLGALCR,RPPVGRRLPG	ACC
THRAP3	c.1652A>G	p.K551R	YKAVQEKSSSPPPRKTSESRDKLGA[p.K551R]RGDFPTGKSSFSITREAQVNVRMDSF	ESRDKLGAR,GARGDFPTGK	KIRC
THSD7B	c.268C>T	p.R90C	VCDWHSDLFQWEVSDWHHCVLVPYA[p.R90C]CGEVKPRTAECVTAQHGLQHRMVRCI	LVPYACGEV,VLVPYACGEV	GBM
THSD7B	c.269G>A	p.R90H	VCDWHSDLFQWEVSDWHHCVLVPYA[p.R90H]HGEVKPRTAECVTAQHGLQHRMVRCI	LVPYAHGEV,YAHGEVKPR,VLVPYAHGEV	CRC
THSD7B	c.376G>A	p.E126K	VTAQHGLQHRMVRCIQKLNRTVVAN[p.E126K]KICEHFALQPPTEQACLIPCPRDCVV	LNRTVVANK,VANKICEHF,NKICEHFAL,KLNRTVVANK,VVANKICEHF	SKCM
TIAM1	c.739_740GG>AT	p.G247M	QLSTCQRANSLGDLYAQKNSGVTAN[p.G247M]MGPGSKFAGYCRNLVSDIPNLANHKMP	TANMGPGSK,KNSGVTANM,ANMGPGSKF,VTANMGPGSK,MGPGSKFAGY,QKNSGVTANM,TANMGPGSKF	TGCT
TIFAB	c.129C>A	p.D43E	GPSAFANVPPRLQHDTSPLLLGRGQ[p.D43E]EAHLQLQLPRLSRRHLSLEPYLEKGS	LLLGRGQEA,RGQEAHLQL,QEAHLQLQL,LLGRGQEAHL,EAHLQLQLPR,GQEAHLQLQL	LUAD
TIGD4	c.935C>T	p.S312F	VESFPAHPEVKNLKSIELAFFPSCL[p.S312F]FSKCIAMKQGVIKSLKIKYRHCLIKK	CLFSKCIAM,LFSKCIAMK,LAFFPSCLF,FPSCLFSKC,AFFPSCLFSK,CLFSKCIAMK,ELAFFPSCLF,SCLFSKCIAM,FPSCLFSKCI	LUAD
TIMD4	c.455_457delCAA	p.T152del	VRLNLQRASTTTHRTATTTTRRTTT[p.T152del]SPTTTRQMTTTPAALPTTVVTTPDLTTG	RTTTSPTTTR,TTRRTTTSPT	PRAD
TIMM44	c.249delA	p.K83fs	GFLSGLLDNVKQELAKNKEMKESIK[p.K83fs]NSVTRPEG*	ESIKNSVTR,KESIKNSVT,EMKESIKNSV,KEMKESIKNS	STAD
TIMP3	c.596_597insC	p.A199fs	YQSKHYACIRQKGGYCSWYRGWAPP[p.A199fs]G*	SWYRGWAPPG	STAD
TINAG	c.1207G>A	p.E403K	MQVREDFFHYKTGIYRHVTSTNKES[p.E403K]KKYRKLQTHAVKLTGWGTLRGAQGQK	VTSTNKESK,STNKESKKY,KKYRKLQTH,VTSTNKESKK,STNKESKKYR,HVTSTNKESK,KKYRKLQTHA	MM
TLL1	c.158C>A	p.P53Q	CAGLDYDYTFDGNEEDKTETIDYKD[p.P53Q]QCKAAVFWGDIALDDEDLNIFQIDRT	KDQCKAAVF,YKDQCKAAVF	LUAD
TLL1	c.458C>T	p.T153M	VKGKVPLQFSGQNEKNRVPRAATSR[p.T153M]MERIWPGGVIPYVIGGNFTGSQRAMF	RAATSRMER,VPRAATSRM,MERIWPGGV,RMERIWPGGV,RVPRAATSRM,RAATSRMERI,MERIWPGGVI	CRC
TLL2	c.2615C>T	p.S872L	LGRFCGSKKPDPTVASGSSMFLRFY[p.S872L]LDASVQRKGFQAVHSTECGGRLKAEV	FLRFYLDAS,SSMFLRFYL,FYLDASVQR,LRFYLDASV,SMFLRFYLDA,FLRFYLDASV,RFYLDASVQR	CRC
TLN2	c.623C>T	p.S208L	REQGVDENETLLLRRKFFYSDQNVD[p.S208L]LRDPVQLNLLYVQARDDILNGSHPVS	FFYSDQNVDL	UCEC
TLR2	c.980A>T	p.D327V	RVIDPGKVETLTIRRLHIPRFYLFY[p.D327V]VLSTLYSLTERVKRITVENSKVFLVP	YLFYVLSTL,YVLSTLYSL,VLSTLYSLT,FYLFYVLST,LFYVLSTLY,IPRFYLFYV,HIPRFYLFYV,YLFYVLSTLY,FYLFYVLSTL,FYVLSTLYSL,RFYLFYVLST,IPRFYLFYVL	CLL
TLR4	c.1492T>G	p.L498V	LEVLKMAGNSFQENFLPDIFTELRN[p.L498V]VTFLDLSQCQLEQLSPTAFNSLSSLQ	DIFTELRNV,FTELRNVTF,TELRNVTFL,LRNVTFLDL,IFTELRNVTF,ELRNVTFLDL	STAD
TM6SF1	c.44C>G	p.S15W	MSASAATGVFVLSL[p.S15W]WAIPVTYVFNHLAAQHDSWTIVGVAA	VLSLWAIPV,VFVLSLWAI,WAIPVTYVF,SLWAIPVTY,GVFVLSLWAI,FVLSLWAIPV,VLSLWAIPVT,SLWAIPVTYV,LWAIPVTYVF,LSLWAIPVTY	BLCA
TM9SF2	c.272G>A	p.R91H	RLDSVESVLPYEYTAFDFCQASEGK[p.R91H]HPSENLGQVLFGERIEPSPYKFTFNK	HPSENLGQV,HPSENLGQVL,SEGKHPSENL	CRC

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TMC5	c.826C>T	p.R276C	DYGSSETPKMTRGVLSRTSSIQPSF[p.R276C]CHRSDDPVGSLWGENDYPEGIEMASM	SIQPSFCHR,SSIQPSFCHR,RTSSIQPSFC	SKCM
TMCC3	c.329G>A	p.R110H	EQTSRDGNVAEYLKLVNNADKQQAG[p.R110H]HIKQVFEKKNQKSAHSIAQLQKKLEQ	QQAGHIKQV,HIKQVFEKK,QAGHIKQVF,AGHIKQVFEK,QQAGHIKQVF,KQQAGHIKQV	CRC
TMCO2	c.43_44delTC	p.S15fs	MSTSSSSSWDNLLESLS[p.S15fs]QHSMELDTSKFFGRD*	SLSQHSMEL,HSMELDTSK,MELDTSKFF,LESLSQHSM,SQHSMELDT,SMELDTSKF,ELDTSKFFGR,ESLSQHSMEL,HSMELDTSKF,LLESLSQHSM,SQHSMELDTS,SMELDTSKFF,MELDTSKFFG	BLCA
TMEM102	c.328G>C	p.A110P	AELLLLRGGIREGSLDLGHAPLGPY[p.A110P]PRGPHYDAGFTLLVPMFSLDGTELQL	HAPLGPYPR,YPRGPHYDA,GPYPRGPHY,LGPYPRGPHY,YPRGPHYDAG	KIRC
TMEM121	c.879_881delGCC	p.P299del	FPPPALSLELQPPPPQRNSVPPPPP[p.P299del]LHGPPGRPHMSSPTRDPLDT*	NSVPPPPPL,RNSVPPPPPL	PRAD
TMEM131	c.3955G>C	p.E1319Q	AHSPLEQHPQPPLPPPVPQPQEPQP[p.E1319Q]QRLSPAPLAHPSHPERASSARHSSED	PQRLSPAPL,QPQEPQPQRL,EPQPQRLSPA,QPQRLSPAPL	CESC
TMEM132A	c.1441C>T	p.R481C	EACDAVFVAGKESRGARGVRVDFWW[p.R481C]CRLRASLRLTVWAPLLPLRIELTDTT	RVDFWWCRLR,FWWCRLRASL,GVRVDFWWCR,WWCRLRASLR,WCRLRASLRL,VRVDFWWCRL	CRC
TMEM132D	c.1732C>T	p.R578W	GDSEEEEDDERRGRGCTLQYQHAMV[p.R578W]WVLTQFVAEAAGPGGHLAHLLGSDWQ	YQHAMVWVL,MVWVLTQFV,AMVWVLTQF,LQYQHAMVW,QYQHAMVWV,LQYQHAMVWV,YQHAMVWVLT,AMVWVLTQFV,MVWVLTQFVA,WVLTQFVAEA,QYQHAMVWVL,HAMVWVLTQF,TLQYQHAMVW	CRC
TMEM132D	c.618delC	p.P206fs	SCRLQGDLGLCVAELELLSSWFSPP[p.P206fs]RWLPGGGSPWTSRRGPPWSSTTPCTQGVREGTASGKTRGEAMGSGQATVTSMSPGPPCRGSGASSFIRHTGNPP*	AMGSGQATV,STTPCTQGV,LSSWFSPPR,SMSPGPPCR,GSGASSFIR,SWFSPPRWL,TSRRGPPWS,GVREGTASG,KTRGEAMGS,RGSGASSFI,SGKTRGEAM,SSWFSPPRW,WLPGGGSPW,WTSRRGPPW,SGQATVTSM,CRGSGASSF,GEAMGSGQA,WLPGGGSPWT,LLSSWFSPPR,GVREGTASGK,TSMSPGPPCR,RWLPGGGSPW,KTRGEAMGSG,RGSGASSFIR,STTPCTQGVR,SSTTPCTQGV,EAMGSGQATV,SPWTSRRGPP,LSSWFSPPRW,SSWFSPPRWL,ASGKTRGEAM,GEAMGSGQAT,GSGQATVTSM	STAD
TMEM147	c.275C>T	p.A92V	FIGEFMKASVDVADLIGLNLVMSRN[p.A92V]VGKGEYKIMVAALGWATAELIMSRCI	LVMSRNVGK,SRNVGKGEY,GLNLVMSRNV,MSRNVGKGEY	GBM
TMEM156	c.241C>T	p.R81C	SFVTFLQPVRETQIIMRIFLNPSNF[p.R81C]CNFTRTCQDITGEFKMCSSCLVCESK	PSNFCNFTR,FLNPSNFCNF,NPSNFCNFTR	GBM
TMEM161B	c.425T>C	p.L142P	VYLVTEVYYNFMKPTQEMNISLVWC[p.L142P]PLVLSFAIKVLFSLTTHYFKVEDGGE	ISLVWCPLV,SLVWCPLVL,VWCPLVLSF,NISLVWCPL,CPLVLSFAI,NISLVWCPLV,ISLVWCPLVL,LVWCPLVLSF,MNISLVWCPL	KIRC
TMEM161B	c.944G>A	p.R315Q	KDYIMNPPLGKESIPLMTEATFDTL[p.R315Q]QLWLIILLCALRLAMMRSHLQAYLNL	TLQLWLIIL,LQLWLIIILL,EATFDTLQL,ATFDTLQLW,TLQLWLIILL,QLWLIIILLCA,ATFDTLQLWL,TFDTLQLWLI,TEATFDTLQL,EATFDTLQLW	UCEC
TMEM19	c.993delT	p.G331fs	LDNNAVNLFSSVLIALLLPTAAWGF[p.G331fs]GPGGELYFISTG*	GFGPGGELY,WGFGPGGEL,GELYFISTG,GFGPGGELYF,WGFGPGGELY	BLCA
TMEM230	c.419A>G	p.D140G	LFLIGAFLIIIGSLLLSGYISKGGA[p.D140G]GRAVPVLIIGILVFLPGFYHLRIAYY	ISKGGAGRA,AGRAVPVLI,YISKGGAGR,SKGGAGRAV,YISKGGAGRA,AGRAVPVLII	KIRC
TMEM247	c.382C>G	p.Q128E	EMELEKVRMEFELTRLKYLHEKNQR[p.Q128E]ERQHEVVMEQLQQ	NQRERQHEV,YLHEKNQRER,NQRERQHEVV	ACC
TMEM41A	c.467delT	p.F156fs	VVSYFPDKVALLQRKVEENRNSLFF[p.F156fs]SYCF*	NSLFFSYCF,NRNSLFFSY,RNSLFFSYCF,ENRNSLFFSY	STAD
TMEM41B	c.690delT	p.F230fs	RITPFLPNWFINITSPVINVPLKVF[p.F230fs]LLVLF*	NVPLKVFLL,LKVFLLVLF,VPLKVFLLV,NVPLKVFLLV,VPLKVFLLVL	STAD
TMEM47	c.259G>A	p.G87S	ASLDIWHCESTLSSDWQIATLALLL[p.G87S]SGAAIILIAFLVGLISICVGSRRRFY	TLALLLSGA,ALLLSGAAI,LLLSGAAII,LLSGAAIIL,ALLLSGAAII,LLLSGAAIIL,LLSGAAIILI,TLALLLSGAA,SGAAIILIAF,LALLLSGAAI	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TMEM55A	c.566G>A	p.R189Q	MELRFNTLAKCPHCKKISSVGSALP[p.R189Q]QRRCCAYITIGMICIFIGVGLTVGTP	SVGSALPQR,LPQRRCCAY,SSVGSALPQR,ALPQRRCCAY,LPQRRCCAYI	CRC
TMEM60	c.231delA	p.K77fs	LIVKMAGRCKSGFDPRHGSHNIKKK[p.K77fs]PGTSLQCYLN*	IKKKPGTSL,NIKKKPGTSL,KKPGTSLQCY	KIRP
TMEM71	c.188G>A	p.R63Q	DSLDGYHSFECGSIDPLTGSHYTCR[p.R63Q]QSPRLLTNGYYIWTEDSFLCDKDGNI	HYTCRQSPR,RQSPRLLTN,SHYTCRQSPR,QSPRLLTNGY,RQSPRLLTNG	BRCA
TMEM74	c.374G>A	p.R125Q	CNCCSQELETSFTYVDKNINLEQRN[p.R125Q]QSSPSAKGHNHPGELGWENPNEWSQE	RNQSSPSAK,EQRNQSSPSA	CRC
TMEM79	c.481_482insC	p.P161fs	ERQPQEDLIVRCEAGEGECRTFMPP[p.P161fs]PGHPPRPH*	RTFMPPPGH,MPPPGHPPR,RTFMPPPGHP,FMPPPGHPPR,GECRTFMPPP	STAD
TMPRSS11A	c.863C>T	p.S288L	IHEKYRSAAREYDIAVVQVSSRVTF[p.S288L]LDDIRQICLPEASASFQPNLTVHITG	QVSSRVTFL,FLDDIRQICL,VQVSSRVTFL,SSRVTFLDDI	CRC
TMPRSS11E	c.775G>T	p.G259C	FTTYKNPARWTASFGVTIKPSKMKR[p.G259C]CLRRIIVHEKYKHPSHDYDISLAELS	KMKRCLRRI,PSKMKRCLR,KPSKMKRCL,MKRCLRRII,CLRRIIVHEK,KMKRCLRRII,SKMKRCLRRI,MKRCLRRIIV	LUAD
TMPRSS11F	c.821G>A	p.R274Q	CFWKNKDPTQWIATFGATITPPAVK[p.R274Q]QNVRKIILHENYHRETNENDIALVQL	KQNVRKIIL,TPPAVKQNV,KQNVRKIILH,ITPPAVKQNV,VKQNVRKIIL	LUSC
TMPRSS3	c.47G>A	p.R16Q	MGENDPPAVEAPFSF[p.R16Q]QSLFGLDDLKISPVAPDADAVAAQIL	FSFQSLFGL,EAPFSFQSL,APFSFQSLF,VEAPFSFQS,QSLFGLDDLK,VEAPFSFQSL,FQSLFGLDDL	UCEC
TMPRSS6	c.904G>A	p.V302I	ITSVYGCSRQEPVVEVLASGAIMAV[p.V302I]IWKKGLHSYYDPFVLSVQPVVFQACE	AIMAVIWKK,GAIMAVIWK,IWKKGLHSY,SGAIMAVIW,IMAVIWKKGL,SGAIMAVIWK,GAIMAVIWKK,VIWKKGLHSY,IWKKGLHSYY,LASGAIMAVI,ASGAIMAVIW	GBM
TMTC2	c.1226C>G	p.T409R	RTQLPSTENIVVLSLSLLIIPFVPA[p.T409R]RNLFFYVGFVIAERVLYIPSMGFCLL	LIIPFVPAR,PFVPARNLF,FVPARNLFF,RNLFFYVGF,PARNLFFYV,VPARNLFFY,IPFVPARNL,FVPARNLFFY,PFVPARNLFF,RNLFFYVGFV,LLIIPFVPAR,VPARNLFFYV,IPFVPARNLF,ARNLFFYVGF	HNSC
TMTC4	c.1831C>T	p.R611C	EAAEQSYRTAIKHRRKYPDCYYNLG[p.R611C]CLYADLNRHVDALNAWRNATVLKPEH	CYYNLGCLY,CLYADLNRHV	STAD
TMX3	c.451C>T	p.R151C	AHRVSGALIRPLPSQQMFEHMQKRH[p.R151C]CVFFVYVGGESPLKEKYIDAASELIV	HMQKRHCVF,MQKRHCVFF,KRHCVFFVY,EHMQKRHCV,MQKRHCVFFV,HMQKRHCVFF,KRHCVFFVYV,QKRHCVFFVY,EHMQKRHCVF,FEHMQKRHCV	LUAD
TNF	c.139C>T	p.L47F	GGPQGSRRCLFLSLFSFLIVAGATT[p.L47F]FFCLLHFGVIGPQREEFPRDLSLISP	ATTFFCLLH,IVAGATTFF,TTFFCLLHF,LIVAGATTF,TFFCLLHFGV,FLIVAGATTF,ATTFFCLLHF,FFCLLHFGVI,LIVAGATTFF	DLBCL
TNFSF9	c.694G>A	p.A232T	SAGQRLGVHLHTEARARHAWQLTQG[p.A232T]TTVLGLFRVTPEIPAGLPSPRSE*	WQLTQGTTV,QLTQGTTVL,GTTVLGLFR,TTVLGLFRV,TQGTTVLGL,TQGTTVLGLF,WQLTQGTTVL	GBM
TNIP2	c.217C>G	p.R73G	LRARLAALEGDAAPSLVDALLEQVA[p.R73G]GFREQLRRQEGGAAEAQMRQEIERLT	ALLEQVAGF,QVAGFREQL,ALLEQVAGFR,QVAGFREQLR,EQVAGFREQL,DALLEQVAGF	ACC
TNIP2	c.415G>A	p.A139T	QPQHEREKEVVLLRRSMAEGERARA[p.A139T]TSDVLCRSLANETHQLRRTLTATAHM	RARATSDVL,AEGERARAT,RARATSDVLC,GERARATSDV	CRC
TNK2	c.1894_1895insC	p.P632fs	PTRALPRPLHPTPVVDWDARPLPPP[p.P632fs]ARL*	RPLPPPARL,DARPLPPPAR	STAD
TNKS2	c.1856_1857insA	p.T619fs	HEAAAKGKYEICKLLLQHGADPTKK[p.T619fs]KQGWKYSFGSC*	PTKKKQGWK,KKQGWKYSF,PTKKKQGWKY,KKKQGWKYSF	CESC,CLL
TNR	c.2074C>A	p.L692I	SAVMNSQQSVPATMNARTELDSPRD[p.L692I]IMVTASSETSISLIWTKASGPIDHYR	IMVTASSET,SPRDIMVTA,TELDSPRDI,DSPRDIMVTA,SPRDIMVTAS,TELDSPRDIM,IMVTASSETS	LUAD
TNS1	c.547C>T	p.P183S	GQPSQRRYVHYFSGLLSGSIKMNNK[p.P183S]SLFLHHVIMHGIPNFESKGGCRPFLR	KMNNKSLFL,KSLFLHHVI,SIKMNNKSL,SLFLHHVIM,IKMNNKSLF,KMNNKSLFLH,SIKMNNKSLF,KSLFLHHVIM,IKMNNKSLFL,NKSLFLHHVI,SLFLHHVIMH	TGCT
TNXB	c.2116_2117delGT	p.V706fs	EEPPASACPGGCGPRELCRAGQCVC[p.V706fs]RGLPRP*	RAGQCVCRGL	ACC

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TOP2A	c.2207G>T	p.R736L	NERSIPSMVDGLKPGQRKVLFTCFK[p.R736L]LNDKREVKVAQLAGSVAEMSSYHHGE	KVLFTCFKL,KLNDKREVK,FTCFKLNDK,KLNDKREVKV,FTCFKLNDKR,RKVLFTCFKL	LUAD
TOP2A	c.3595A>G	p.K1199E	FIEELEAVEAKEKQDEQVGLPGKGG[p.K1199E]EAKGKKTQMAEVLPSPRGQRVIPRIT	KGGEAKGKK,GEAKGKKTQM	THCA
TOP2B	c.1967G>A	p.R656H	IKYYKGLGTSTAKEAKEYFADMERH[p.R656H]HILFRYAGPEDDAAITLAFSKKKIDD	DMERHHILF,MERHHILFR,RHHILFRYA,ADMERHHIL,FADMERHHI,YFADMERHHI,MERHHILFRY,DMERHHILFR,FADMERHHIL,ADMERHHILF	CRC
TOPBP1	c.4141delA	p.I1381fs	ILDVLTGINVQQRRLALAAMRWRKK[p.I1381fs]SSKDKNLALLREHLVGGRLFYMWISLEKQASNAFFSQEEQRCYLVILYLYLKRPHIFFLT*	FSQEEQRCY,LVGGRLFYM,RLFYMWISL,YLVILYLYL,YLYLKRPHI,NLALLREHL,HLVGGRLFY,LVILYLYLK,FYMWISLEK,VILYLYLKR,VGGRLFYMW,CYLVILYLY,LYLKRPHIF,YLKRPHIFF,KSSKDKNLA,SSKDKNLAL,GGRLFYMWI,AFFSQEEQR,AMRWRKKSS,EQRCYLVIL,LKRPHIFFL,LEKQASNAF,REHLVGGRL,EKQASNAFF,KQASNAFFS,SQEEQRCYL,RCYLVILYL,EEQRCYLVI,QEEQRCYLV,NLALLREHLV,HLVGGRLFYM,YMWISLEKQA,YLKRPHIFFL,AMRWRKKSSK,LFYMWISLEK,YLVILYLYLK,LVGGRLFYMW,CYLVILYLYL,LYLYLKRPHI,YLYLKRPHIF,LYLKRPHIFF,RWRKKSSKDK,SSKDKNLALL,EQRCYLVILY,RCYLVILYLY,LLREHLVGGR,NAFFSQEEQR,LVILYLYLKR,SLEKQASNAF,LEKQASNAFF,KSSKDKNLAL,KNLALLREHL,REHLVGGRLF,GRLFYMWISL,KQASNAFFSQ,ILYLYLKRPH,EEQRCYLVIL,QEEQRCYLVI	STAD
TOR1AIP2	c.436G>A	p.G146R	PSDKVGRADAHLGSSSVALPKEASD[p.G146R]RTGASQEPPTTDSQEAQSPGHSSAGQ	KEASDRTGA	TGCT
TOR3A	c.37T>C	p.F13L	MLRGPWRQLWLF[p.F13L]LLLLLPGAPEPRGASRPWEGTDEPGS	RQLWLFLLL,QLWLFLLLL,FLLLLLPGA,PWRQLWLFL,LWLFLLLLL,RQLWLFLLLL,QLWLFLLLLL,PWRQLWLFLL,GPWRQLWLFL	ACC
TOX	c.1061C>T	p.S354L	RASLVSKSYSEPVDVKTSQPPQLIN[p.S354L]LKPSVFHGPSQAHSALYLSSHYHQQP	QLINLKPSV,LINLKPSVF,SQPPQLINL,SQPPQLINLK,QLINLKPSVF	CRC
TP53	c.1010G>T	p.R337L	TSSSPQPKKKPLDGEYFTLQIRGRE[p.R337L]LFEMFRELNEALELKDAQAGKEPGGS	ELFEMFREL,LQIRGRELF,RGRELFEMF,TLQIRGREL,IRGRELFEM,RGRELFEMFR,TLQIRGRELF,IRGRELFEMF,RELFEMFREL	LUAD,LUSC
TP53	c.173delC	p.P58fs	SPLPSQAMDDLMLSPDDIEQWFTED[p.P58fs]QVQMKLPECQRLLPPWPLHQQLLHRRPLHQPPPGPCHLLSLPRKPTRAATVSVWASCILGQPSL*	KLPECQRLL,SLPRKPTRA,RLLPPWPLH,LSLPRKPTR,PTRAATVSV,RAATVSVWA,QMKLPECQR,TVSVWASCI,LPRKPTRAA,QQLLHRRPL,MKLPECQRL,QRLLPPWPL,TRAATVSVW,VSVWASCIL,WPLHQQLLH,TEDQVQMKL,SLPRKPTRAA,CQRLLPPWPL,LLSLPRKPTR,ATVSVWASCI,TVSVWASCIL,LPPWPLHQQL,LPRKPTRAAT,KPTRAATVSV,HQQLLHRRPL,QWFTEDQVQM,MKLPECQRLL,QQLLHRRPLH,HQPPPGPCHL,ASCILGQPSL,IEQWFTEDQV	HNSC
TP53	c.216delC	p.P72fs	DDIEQWFTEDPGPDEAPRMPEAAPP[p.P72fs]WPLHQQLLHRRPLHQPPPGPCHLLSLPRKPTRAATVSVWASCILGQPSL*	SLPRKPTRA,RMPEAAPPW,LSLPRKPTR,PTRAATVSV,RAATVSVWA,TVSVWASCI,LPRKPTRAA,QQLLHRRPL,TRAATVSVW,VSVWASCIL,WPLHQQLLH,PEAAPPWPL,SLPRKPTRAA,LLSLPRKPTR,ATVSVWASCI,TVSVWASCIL,MPEAAPPWPL,APPWPLHQQL,LPRKPTRAAT,KPTRAATVSV,HQQLLHRRPL,QQLLHRRPLH,HQPPPGPCHL,ASCILGQPSL	LUAD
TP53	c.313G>T	p.G105C	PTPAAPAPAPSWPLSSSVPSQKTYQ[p.G105C]CSYGFRLGFLHSGTAKSVTCTYSPAL	YQCSYGFRL,KTYQCSYGF,CSYGFRLGF,SQKTYQCSY,TYQCSYGFR,KTYQCSYGFR,TYQCSYGFRL,PSQKTYQCSY,QKTYQCSYGF,YQCSYGFRLG,CSYGFRLGFL	LUAD
TP53	c.323delG	p.G108fs	AAPAPAPSWPLSSSVPSQKTYQGSY[p.G108fs]VSVWASCILGQPSL*	YVSVWASCI,TYQGSYVSV,YQGSYVSVW,SYVSVWASC,KTYQGSYVS,VSVWASCIL,KTYQGSYVSV,YQGSYVSVWA,SQKTYQGSYV,YVSVWASCIL,TYQGSYVSVW,SYVSVWASCI,ASCILGQPSL	BRCA
TP53	c.328delC	p.R110fs	PAPAPSWPLSSSVPSQKTYQGSYGF[p.R110fs]VWASCILGQPSL*	TYQGSYGFV,YQGSYGFVW,SYGFVWASC,YGFVWASCI,KTYQGSYGFV,YQGSYGFVWA,TYQGSYGFVW,SYGFVWASCI,YGFVWASCIL,ASCILGQPSL	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TP53	c.329G>T	p.R110L	PAPAPSWPLSSSVPSQKTYQGSYGF[p.R110L]LLGFLHSGTAKSVTCTYSPALNKMFC	YQGSYGFLL,FLLGFLHSG,TYQGSYGFL,SYGFLLGFL,GSYGFLLGF,FLLGFLHSGT,KTYQGSYGFL,LLGFLHSGTA,TYQGSYGFLL,YQGSYGFLLG,QGSYGFLLGF	HNSC,LUAD
TP53	c.396G>C	p.K132N	YGFRLGFLHSGTAKSVTCTYSPALN[p.K132N]NMFCQLAKTCPVQLWVDSTPPPGTRV	ALNNMFCQL,NMFCQLAKT,TYSPALNNM,YSPALNNMF,ALNNMFCQLA,TYSPALNNMF,CTYSPALNNM	BLCA,BRCA
TP53	c.396G>T	p.K132N	YGFRLGFLHSGTAKSVTCTYSPALN[p.K132N]NMFCQLAKTCPVQLWVDSTPPPGTRV	ALNNMFCQL,NMFCQLAKT,TYSPALNNM,YSPALNNMF,ALNNMFCQLA,TYSPALNNMF,CTYSPALNNM	OV
TP53	c.421T>G	p.C141G	SGTAKSVTCTYSPALNKMFCQLAKT[p.C141G]GPVQLWVDSTPPPGTRVRAMAIYKQS	CQLAKTGPV,KTGPVQLWV,AKTGPVQLW,QLAKTGPVQL,KMFCQLAKTG,LAKTGPVQLW	PRAD
TP53	c.422G>A	p.C141Y	SGTAKSVTCTYSPALNKMFCQLAKT[p.C141Y]YPVQLWVDSTPPPGTRVRAMAIYKQS	CQLAKTYPV,KTYPVQLWV,MFCQLAKTY,LAKTYPVQL,AKTYPVQLW,QLAKTYPVQL,KMFCQLAKTY,LAKTYPVQLW,YPVQLWVDST	BRCA
TP53	c.427G>A	p.V143M	TAKSVTCTYSPALNKMFCQLAKTCP[p.V143M]MQLWVDSTPPPGTRVRAMAIYKQSQH	KTCPMQLWV,CQLAKTCPM,AKTCPMQLW,MQLWVDSTP,QLAKTCPMQL,FCQLAKTCPM,LAKTCPMQLW,MQLWVDSTPP,CPMQLWVDST	HNSC
TP53	c.451C>A	p.P151T	YSPALNKMFCQLAKTCPVQLWVDST[p.P151T]TPPGTRVRAMAIYKQSQHMTEVVRRC	STTPPGTRV,VQLWVDSTT,STTPPGTRVR,TPPGTRVRAM,VQLWVDSTTP	HNSC
TP53	c.455delC	p.P152fs	SPALNKMFCQLAKTCPVQLWVDSTP[p.P152fs]RPAPASAPWPSTSSHST*	QLWVDSTPR,TPRPAPASA,RPAPASAPW,APWPSTSSH,WPSTSSHST,STPRPAPASA,TPRPAPASAP,APASAPWPST	STAD
TP53	c.461G>T	p.G154V	ALNKMFCQLAKTCPVQLWVDSTPPP[p.G154V]VTRVRAMAIYKQSQHMTEVVRRCPHH	WVDSTPPPV,VTRVRAMAI,DSTPPPVTR,STPPPVTRV,PPVTRVRAM,VTRVRAMAIY,DSTPPPVTRV,LWVDSTPPPV	LUAD
TP53	c.464C>A	p.T155N	LNKMFCQLAKTCPVQLWVDSTPPPG[p.T155N]NRVRAMAIYKQSQHMTEVVRRCPHHE	STPPPGNRV,PPGNRVRAM,GNRVRAMAI,NRVRAMAIY,GNRVRAMAIY,DSTPPPGNRV	GBM
TP53	c.469G>T	p.V157F	KMFCQLAKTCPVQLWVDSTPPPGTR[p.V157F]FRAMAIYKQSQHMTEVVRRCPHHERC	RFRAMAIYK,GTRFRAMAI,TRFRAMAIY,PPGTRFRAM,TRFRAMAIYK,GTRFRAMAIY,RFRAMAIYKQ,STPPPGTRFR	HNSC,LIHC,LUAD,LUSC,OV
TP53	c.473G>A	p.R158H	MFCQLAKTCPVQLWVDSTPPPGTRV[p.R158H]HAMAIYKQSQHMTEVVRRCPHHERCS	RVHAMAIYK,GTRVHAMAI,PPGTRVHAM,TRVHAMAIY,GTRVHAMAIY	GBM,LIHC
TP53	c.473G>T	p.R158L	MFCQLAKTCPVQLWVDSTPPPGTRV[p.R158L]LAMAIYKQSQHMTEVVRRCPHHERCS	RVLAMAIYK,GTRVLAMAI,TPPPGTRVL,PPGTRVLAM,TRVLAMAIY,GTRVLAMAIY	LUAD,LUSC
TP53	c.475G>C	p.A159P	FCQLAKTCPVQLWVDSTPPPGTRVR[p.A159P]PMAIYKQSQHMTEVVRRCPHHERCSD	RVRPMAIYK,GTRVRPMAI,PPGTRVRPM,TRVRPMAIY,GTRVRPMAIY,RVRPMAIYKQ	LUAD
TP53	c.476C>T	p.A159V	FCQLAKTCPVQLWVDSTPPPGTRVR[p.A159V]VMAIYKQSQHMTEVVRRCPHHERCSD	RVRVMAIYK,GTRVRVMAI,RVMAIYKQS,TRVRVMAIY,GTRVRVMAIY,RVRVMAIYKQ,VMAIYKQSQH	BLCA,OV
TP53	c.488A>G	p.Y163C	AKTCPVQLWVDSTPPPGTRVRAMAI[p.Y163C]CKQSQHMTEVVRRCPHHERCSDSDGL	RVRAMAICK,AICKQSQHM,GTRVRAMAIC,RVRAMAICKQ,MAICKQSQHM	BRCA,HNSC,LUAD,LUSC,OV
TP53	c.517G>A	p.V173M	DSTPPPGTRVRAMAIYKQSQHMTEV[p.V173M]MRRCPHHERCSDSDGLAPPQHLIRVE	MRRCPHHER,QSQHMTEVM,VMRRCPHHER,KQSQHMTEVM	BRCA,HNSC
TP53	c.517G>T	p.V173L	DSTPPPGTRVRAMAIYKQSQHMTEV[p.V173L]LRRCPHHERCSDSDGLAPPQHLIRVE	VLRRCPHHER,QSQHMTEVLR,KQSQHMTEVL	BRCA,HNSC
TP53	c.523C>G	p.R175G	TPPPGTRVRAMAIYKQSQHMTEVVR[p.R175G]GCPHHERCSDSDGLAPPQHLIRVEGN	TEVVRGCPH,VVRGCPHHER	LUSC
TP53	c.523C>T	p.R175C	TPPPGTRVRAMAIYKQSQHMTEVVR[p.R175C]CCPHHERCSDSDGLAPPQHLIRVEGN	TEVVRCCPH,VVRCCPHHER	CRC

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TP53	c.524G>A	p.R175H	TPPPGTRVRAMAIYKQSQHMTEVVR[p.R175H]HCPHHERCSDSDGLAPPQHLIRVEGN	TEVVRHCPH,VVRHCPHHER,SQHMTEVVRH	BLCA,BRCA,CLL,CRC,GBM,HNSC,LUAD,OV,PAAD,PRAD,STAD,UCS
TP53	c.527G>A	p.C176Y	PPPGTRVRAMAIYKQSQHMTEVVRR[p.C176Y]YPHHERCSDSDGLAPPQHLIRVEGNL	HMTEVVRRY,TEVVRRYPH,VVRRYPHHER,QHMTEVVRRY	OV
TP53	c.527G>T	p.C176F	PPPGTRVRAMAIYKQSQHMTEVVRR[p.C176F]FPHHERCSDSDGLAPPQHLIRVEGNL	HMTEVVRRF,TEVVRRFPH,VVRRFPHHER,QHMTEVVRRF	BRCA,LUAD,STAD
TP53	c.535C>T	p.H179Y	GTRVRAMAIYKQSQHMTEVVRRCPH[p.H179Y]YERCSDSDGLAPPQHLIRVEGNLRVE	VVRRCPHYE,EVVRRCPHY,VVRRCPHYER,TEVVRRCPHY,YERCSDSDGL	HNSC
TP53	c.536A>G	p.H179R	GTRVRAMAIYKQSQHMTEVVRRCPH[p.H179R]RERCSDSDGLAPPQHLIRVEGNLRVE	EVVRRCPHR,VVRRCPHRER,RERCSDSDGL	BRCA,GBM,HNSC,OV,UCS
TP53	c.536A>T	p.H179L	GTRVRAMAIYKQSQHMTEVVRRCPH[p.H179L]LERCSDSDGLAPPQHLIRVEGNLRVE	EVVRRCPHL,VVRRCPHLER,TEVVRRCPHL,LERCSDSDGL	LUSC
TP53	c.572_574delCTC	p.P191del	SQHMTEVVRRCPHHERCSDSDGLAP[p.P191del]QHLIRVEGNLRVEYLDDRNTFRHSVVVP	GLAPQHLIR,GLAPQHLIRV	OV
TP53	c.577C>T	p.H193Y	HMTEVVRRCPHHERCSDSDGLAPPQ[p.H193Y]YLIRVEGNLRVEYLDDRNTFRHSVVV	GLAPPQYLI,YLIRVEGNL,DSDGLAPPQY,GLAPPQYLIR,QYLIRVEGNL,YLIRVEGNLR	BRCA
TP53	c.578A>G	p.H193R	HMTEVVRRCPHHERCSDSDGLAPPQ[p.H193R]RLIRVEGNLRVEYLDDRNTFRHSVVV	GLAPPQRLI,RLIRVEGNL,RLIRVEGNLR	BRCA,LIHC,OV,UCS
TP53	c.578A>T	p.H193L	HMTEVVRRCPHHERCSDSDGLAPPQ[p.H193L]LLIRVEGNLRVEYLDDRNTFRHSVVV	GLAPPQLLI,LLIRVEGNL,GLAPPQLLIR,LLIRVEGNLR	BRCA,HNSC,LUSC
TP53	c.581T>G	p.L194R	MTEVVRRCPHHERCSDSDGLAPPQH[p.L194R]RIRVEGNLRVEYLDDRNTFRHSVVVP	GLAPPQHRI,RIRVEGNLR,APPQHRIRV,RIRVEGNLRV	BRCA,OV
TP53	c.584T>C	p.I195T	TEVVRRCPHHERCSDSDGLAPPQHL[p.I195T]TRVEGNLRVEYLDDRNTFRHSVVVPY	GLAPPQHLT,LTRVEGNLR,GLAPPQHLTR,LTRVEGNLRV,HLTRVEGNLR	BRCA,OV
TP53	c.587G>C	p.R196P	EVVRRCPHHERCSDSDGLAPPQHLI[p.R196P]PVEGNLRVEYLDDRNTFRHSVVVPYE	HLIPVEGNL,APPQHLIPV,IPVEGNLRV,HLIPVEGNLR,LAPPQHLIPV	HNSC
TP53	c.596G>T	p.G199V	RRCPHHERCSDSDGLAPPQHLIRVE[p.G199V]VNLRVEYLDDRNTFRHSVVVPYEPPE	HLIRVEVNL,LIRVEVNLR,EVNLRVEYL,VEVNLRVEY,LIRVEVNLRV,RVEVNLRVEY,HLIRVEVNLR,VEVNLRVEYL	BRCA
TP53	c.614A>G	p.Y205C	ERCSDSDGLAPPQHLIRVEGNLRVE[p.Y205C]CLDDRNTFRHSVVVPYEPPEVGSDCT	CLDDRNTFR,ECLDDRNTFR,VECLDDRNTF,VEGNLRVECL	OV
TP53	c.626_627delGA	p.R209fs	DSDGLAPPQHLIRVEGNLRVEYLDD[p.R209fs]KHFST*	YLDDKHFST,VEYLDDKHF,RVEYLDDKHF	BRCA
TP53	c.641A>G	p.H214R	APPQHLIRVEGNLRVEYLDDRNTFR[p.H214R]RSVVVPYEPPEVGSDCTTIHYNYMCN	NTFRRSVVV,FRRSVVVPY,TFRRSVVVPY,YLDDRNTFRR	LUSC
TP53	c.644G>T	p.S215I	PPQHLIRVEGNLRVEYLDDRNTFRH[p.S215I]IVVVPYEPPEVGSDCTTIHYNYMCNS	NTFRHIVVV,RNTFRHIVV,FRHIVVVPY,TFRHIVVVPY	LUAD
TP53	c.645T>G	p.S215R	PPQHLIRVEGNLRVEYLDDRNTFRH[p.S215R]RVVVPYEPPEVGSDCTTIHYNYMCNS	NTFRHRVVV,RHRVVVPYE,FRHRVVVPY,TFRHRVVVPY	OV

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TP53	c.646G>A	p.V216M	PQHLIRVEGNLRVEYLDDRNTFRHS[p.V216M]MVVPYEPPEVGSDCTTIHYNYMCNSS	NTFRHSMVV,DRNTFRHSM,FRHSMVVPY,MVVPYEPPEV,TFRHSMVVPY	BRCA,GBM,OV
TP53	c.659A>C	p.Y220S	IRVEGNLRVEYLDDRNTFRHSVVVP[p.Y220S]SEPPEVGSDCTTIHYNYMCNSSCMGG	VVPSEPPEV,VVVPSEPPEV	BRCA
TP53	c.659A>G	p.Y220C	IRVEGNLRVEYLDDRNTFRHSVVVP[p.Y220C]CEPPEVGSDCTTIHYNYMCNSSCMGG	VVPCEPPEV,VVVPCEPPEV	BRCA,GBM,HNSC,LUSC,OV,UCEC
TP53	c.701A>G	p.Y234C	RNTFRHSVVVPYEPPEVGSDCTTIH[p.Y234C]CNYMCNSSCMGGMNRRPILTIITLED	CTTIHCNYM,TTIHCNYMC,CNYMCNSSCM	BRCA,GBM,LUSC,OV
TP53	c.706T>G	p.Y236D	TFRHSVVVPYEPPEVGSDCTTIHYN[p.Y236D]DMCNSSCMGGMNRRPILTIITLEDSS	NDMCNSSCM	HNSC
TP53	c.707A>G	p.Y236C	TFRHSVVVPYEPPEVGSDCTTIHYN[p.Y236C]CMCNSSCMGGMNRRPILTIITLEDSS	YNCMCNSSCM	HNSC,OV
TP53	c.711G>A	p.M237I	FRHSVVVPYEPPEVGSDCTTIHYNY[p.M237I]ICNSSCMGGMNRRPILTIITLEDSSG	CTTIHYNYI,YNYICNSSCM	HNSC
TP53	c.711G>C	p.M237I	FRHSVVVPYEPPEVGSDCTTIHYNY[p.M237I]ICNSSCMGGMNRRPILTIITLEDSSG	CTTIHYNYI,YNYICNSSCM	LUAD
TP53	c.713G>A	p.C238Y	RHSVVVPYEPPEVGSDCTTIHYNYM[p.C238Y]YNSSCMGGMNRRPILTIITLEDSSGN	TTIHYNYMY,YMYNSSCMG,YNYMYNSSC,CTTIHYNYMY,YMYNSSCMGG,YNYMYNSSCM,IHYNYMYNSS,MYNSSCMGGM	BRCA,GBM
TP53	c.713G>T	p.C238F	RHSVVVPYEPPEVGSDCTTIHYNYM[p.C238F]FNSSCMGGMNRRPILTIITLEDSSGN	YMFNSSCMG,TTIHYNYMF,NYMFNSSCM,YNYMFNSSC,YMFNSSCMGG,CTTIHYNYMF,YNYMFNSSCM,IHYNYMFNSS,MFNSSCMGGM	BRCA,GBM,HNSC
TP53	c.722C>A	p.S241Y	VVVPYEPPEVGSDCTTIHYNYMCNS[p.S241Y]YCMGGMNRRPILTIITLEDSSGNLLG	NYMCNSYCM,HYNYMCNSY,SYCMGGMNR,NSYCMGGMNR,IHYNYMCNSY,SYCMGGMNRR,YNYMCNSYCM,MCNSYCMGGM	UCS
TP53	c.722C>T	p.S241F	VVVPYEPPEVGSDCTTIHYNYMCNS[p.S241F]FCMGGMNRRPILTIITLEDSSGNLLG	HYNYMCNSF,NYMCNSFCM,SFCMGGMNR,YMCNSFCMG,NSFCMGGMNR,IHYNYMCNSF,SFCMGGMNRR,YNYMCNSFCM	OV
TP53	c.723delC	p.S241fs	VVPYEPPEVGSDCTTIHYNYMCNSS[p.S241fs]AWAA*	YMCNSSAWA,NYMCNSSAW,YNYMCNSSA,YMCNSSAWAA,HYNYMCNSSA,YNYMCNSSAW	BRCA
TP53	c.725G>T	p.C242F	VVPYEPPEVGSDCTTIHYNYMCNSS[p.C242F]FMGGMNRRPILTIITLEDSSGNLLGR	SSFMGGMNR,YNYMCNSSF,NYMCNSSFM,SFMGGMNRR,YMCNSSFMG,FMGGMNRRPI,SSFMGGMNRR,HYNYMCNSSF,NSSFMGGMNR,YNYMCNSSFM,YMCNSSFMGG,MCNSSFMGGM	CLL,HNSC,LUSC
TP53	c.730G>T	p.G244C	PYEPPEVGSDCTTIHYNYMCNSSCM[p.G244C]CGMNRRPILTIITLEDSSGNLLGRNS	YMCNSSCMC,SSCMCGMNR,CGMNRRPIL,SSCMCGMNRR,NSSCMCGMNR,MCNSSCMCGM,CMCGMNRRPI	OV
TP53	c.731G>A	p.G244D	PYEPPEVGSDCTTIHYNYMCNSSCM[p.G244D]DGMNRRPILTIITLEDSSGNLLGRNS	SSCMDGMNR,DGMNRRPIL,NSSCMDGMNR,CMDGMNRRPI	CRC
TP53	c.733G>A	p.G245S	YEPPEVGSDCTTIHYNYMCNSSCMG[p.G245S]SMNRRPILTIITLEDSSGNLLGRNSF	SSCMGSMNR,GSMNRRPIL,MGSMNRRPI,CNSSCMGSM,SMNRRPILTI,SSCMGSMNRR,NSSCMGSMNR,MGSMNRRPIL,MCNSSCMGSM,CMGSMNRRPI	CRC,GBM,HNSC,OV,PRAD
TP53	c.734G>A	p.G245D	YEPPEVGSDCTTIHYNYMCNSSCMG[p.G245D]DMNRRPILTIITLEDSSGNLLGRNSF	SSCMGDMNR,NSSCMGDMNR,CMGDMNRRPI	OV
TP53	c.734G>T	p.G245V	YEPPEVGSDCTTIHYNYMCNSSCMG[p.G245V]VMNRRPILTIITLEDSSGNLLGRNSF	SSCMGVMNR,GVMNRRPIL,SCMGVMNRR,MGVMNRRPI,CNSSCMGVM,YMCNSSCMGV,VMNRRPILTI,SSCMGVMNRR,NSSCMGVMNR,MGVMNRRPIL,MCNSSCMGVM,CMGVMNRRPI	HNSC,LUSC,OV

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TP53	c.742C>T	p.R248W	PEVGSDCTTIHYNYMCNSSCMGGMN[p.R248W]WRPILTIITLEDSSGNLLGRNSFEVR	NWRPILTII,SSCMGGMNW,MGGMNWRPI,MNWRPILTI,CMGGMNWRPI,GMNWRPILTI,SSCMGGMNWR,MNWRPILTII,NSSCMGGMNW	BLCA,BRCA,CLL,CRC,GBM,HNSC,OV,PAAD,UCEC
TP53	c.743G>A	p.R248Q	PEVGSDCTTIHYNYMCNSSCMGGMN[p.R248Q]QRPILTIITLEDSSGNLLGRNSFEVR	MNQRPILTI,NQRPILTII,CMGGMNQRPI,GMNQRPILTI,SSCMGGMNQR,NQRPILTIIT	BLCA,BRCA,CLL,GBM,HNSC,OV,PRAD,STAD,UCEC,UCS
TP53	c.743G>C	p.R248P	PEVGSDCTTIHYNYMCNSSCMGGMN[p.R248P]PRPILTIITLEDSSGNLLGRNSFEVR	SCMGGMNPR,NPRPILTII,GMNPRPILTI,CMGGMNPRPI,SSCMGGMNPR,NPRPILTIIT	LUAD
TP53	c.745A>G	p.R249G	EVGSDCTTIHYNYMCNSSCMGGMNR[p.R249G]GPILTIITLEDSSGNLLGRNSFEVRV	GPILTIITL,MNRGPILTI,GMNRGPILTI,CMGGMNRGPI,MNRGPILTII	LUAD
TP53	c.746G>T	p.R249M	EVGSDCTTIHYNYMCNSSCMGGMNR[p.R249M]MPILTIITLEDSSGNLLGRNSFEVRV	MNRMPILTI,MPILTIITL,MGGMNRMPI,SCMGGMNRM,NRMPILTII,CMGGMNRMPI,GMNRMPILTI,RMPILTIITL,MNRMPILTII,SSCMGGMNRM,MPILTIITLE	LUAD
TP53	c.747G>T	p.R249S	EVGSDCTTIHYNYMCNSSCMGGMNR[p.R249S]SPILTIITLEDSSGNLLGRNSFEVRV	MNRSPILTI,SPILTIITL,MGGMNRSPI,GMNRSPILTI,CMGGMNRSPI,RSPILTIITL,MNRSPILTII	HNSC,LIHC,LUAD
TP53	c.749C>T	p.P250L	VGSDCTTIHYNYMCNSSCMGGMNRR[p.P250L]LILTIITLEDSSGNLLGRNSFEVRVC	RLILTIITL,GMNRRLILT,MNRRLILTI,GGMNRRLIL,GMNRRLILTI,MNRRLILTII,RRLILTIITL	OV
TP53	c.763A>T	p.I255F	TTIHYNYMCNSSCMGGMNRRPILTI[p.I255F]FTLEDSSGNLLGRNSFEVRVCACPGR	RPILTIFTL,NRRPILTIF,FTLEDSSGNL,MNRRPILTIF,RRPILTIFTL	LUAD
TP53	c.775G>T	p.D259Y	YNYMCNSSCMGGMNRRPILTIITLE[p.D259Y]YSSGNLLGRNSFEVRVCACPGRDRRT	ILTIITLEY,LEYSSGNLL,PILTIITLEY,EYSSGNLLGR,LEYSSGNLLG	OV
TP53	c.785G>T	p.G262V	MCNSSCMGGMNRRPILTIITLEDSS[p.G262V]VNLLGRNSFEVRVCACPGRDRRTEEE	IITLEDSSV,DSSVNLLGR,LEDSSVNLL,VNLLGRNSF,TIITLEDSSV,TLEDSSVNLL,SVNLLGRNSF	HNSC
TP53	c.796G>A	p.G266R	SCMGGMNRRPILTIITLEDSSGNLL[p.G266R]RRNSFEVRVCACPGRDRRTEEENLRK	LLRRNSFEV,DSSGNLLRR,GNLLRRNSF,NLLRRNSFEV,LLRRNSFEVR,SGNLLRRNSF	OV
TP53	c.797G>A	p.G266E	SCMGGMNRRPILTIITLEDSSGNLL[p.G266E]ERNSFEVRVCACPGRDRRTEEENLRK	LLERNSFEV,DSSGNLLER,GNLLERNSF,NLLERNSFEV,SGNLLERNSF,LERNSFEVRV	BRCA,HNSC
TP53	c.797G>T	p.G266V	SCMGGMNRRPILTIITLEDSSGNLL[p.G266V]VRNSFEVRVCACPGRDRRTEEENLRK	LLVRNSFEV,LVRNSFEVR,GNLLVRNSF,NLLVRNSFEV,LVRNSFEVRV,SGNLLVRNSF,LEDSSGNLLV	OV
TP53	c.800G>C	p.R267P	CMGGMNRRPILTIITLEDSSGNLLG[p.R267P]PNSFEVRVCACPGRDRRTEEENLRKK	LLGPNSFEV,GNLLGPNSF,NLLGPNSFEV,SGNLLGPNSF	LUSC
TP53	c.811G>A	p.E271K	MNRRPILTIITLEDSSGNLLGRNSF[p.E271K]KVRVCACPGRDRRTEEENLRKKGEPH	LLGRNSFKV,NLLGRNSFK,LGRNSFKVR,KVRVCACPG,NSFKVRVCA,SFKVRVCAC,NLLGRNSFKV,GNLLGRNSFK,KVRVCACPGR	BLCA,LUSC
TP53	c.814G>A	p.V272M	NRRPILTIITLEDSSGNLLGRNSFE[p.V272M]MRVCACPGRDRRTEEENLRKKGEPHH	LLGRNSFEM,LGRNSFEMR,NSFEMRVCA,FEMRVCACP,NLLGRNSFEM,EMRVCACPGR,FEMRVCACPG	BRCA,OV
TP53	c.817C>T	p.R273C	RRPILTIITLEDSSGNLLGRNSFEV[p.R273C]CVCACPGRDRRTEEENLRKKGEPHHE	NSFEVCVCA,EVCVCACPGR,FEVCVCACPG	BLCA,BRCA,CRC,HNSC,OV,STAD,UCEC

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TP53	c.818G>A	p.R273H	RRPILTIITLEDSSGNLLGRNSFEV[p.R273H]HVCACPGRDRRTEEENLRKKGEPHHE	NSFEVHVCA,LGRNSFEVH,EVHVCACPGR,HVCACPGRDR,FEVHVCACPG	BRCA,CLL,CRC,GBM,HNSC,LUAD,OV,STAD,UCEC,UCS
TP53	c.818G>T	p.R273L	RRPILTIITLEDSSGNLLGRNSFEV[p.R273L]LVCACPGRDRRTEEENLRKKGEPHHE	NSFEVLVCA,LGRNSFEVL,LLGRNSFEVL,EVLVCACPGR,FEVLVCACPG	LUAD,LUSC,OV
TP53	c.820G>T	p.V274F	RPILTIITLEDSSGNLLGRNSFEVR[p.V274F]FCACPGRDRRTEEENLRKKGEPHHEL	NSFEVRFCA,GRNSFEVRF,EVRFCACPGR,LGRNSFEVRF,FEVRFCACPG	LUAD
TP53	c.824G>A	p.C275Y	PILTIITLEDSSGNLLGRNSFEVRV[p.C275Y]YACPGRDRRTEEENLRKKGEPHHELP	RNSFEVRVY,YACPGRDRR,NSFEVRVYA,RVYACPGRDR,EVRVYACPGR,GRNSFEVRVY,FEVRVYACPG	OV
TP53	c.824G>T	p.C275F	PILTIITLEDSSGNLLGRNSFEVRV[p.C275F]FACPGRDRRTEEENLRKKGEPHHELP	FACPGRDRR,NSFEVRVFA,RNSFEVRVF,FEVRVFACP,RVFACPGRDR,EVRVFACPGR,VFACPGRDRR,GRNSFEVRVF,FEVRVFACPG	HNSC,LUAD
TP53	c.830G>T	p.C277F	LTIITLEDSSGNLLGRNSFEVRVCA[p.C277F]FPGRDRRTEEENLRKKGEPHHELPPG	CAFPGRDRR,SFEVRVCAF,EVRVCAFPGR,NSFEVRVCAF,FEVRVCAFPG	LUAD
TP53	c.832C>T	p.P278S	TIITLEDSSGNLLGRNSFEVRVCAC[p.P278S]SGRDRRTEEENLRKKGEPHHELPPGS	CACSGRDRR,FEVRVCACS,EVRVCACSGR,FEVRVCACSG	HNSC
TP53	c.841G>A	p.D281N	TLEDSSGNLLGRNSFEVRVCACPGR[p.D281N]NRRTEEENLRKKGEPHHELPPGSTKR	CACPGRNRR,RVCACPGRNR	LUAD
TP53	c.844C>T	p.R282W	LEDSSGNLLGRNSFEVRVCACPGRD[p.R282W]WRTEEENLRKKGEPHHELPPGSTKRA	CACPGRDWR,RDWRTEEENL	BRCA,CRC,GBM,HNSC,OV,STAD
TP53	c.853G>A	p.E285K	SSGNLLGRNSFEVRVCACPGRDRRT[p.E285K]KEENLRKKGEPHHELPPGSTKRALPN	RTKEENLRK,RTKEENLRKK	BLCA,CESC,HNSC,LUAD
TP53	c.856G>A	p.E286K	SGNLLGRNSFEVRVCACPGRDRRTE[p.E286K]KENLRKKGEPHHELPPGSTKRALPNN	RTEKENLRK,RTEKENLRKK	BRCA,STAD
TP53	c.945_946delTC	p.S315fs	KGEPHHELPPGSTKRALPNNTSSSP[p.S315fs]AKEETTGWRIFHPSDPWA*	KEETTGWRI,RIFHPSDPW,EETTGWRIF,RIFHPSDPWA,LPNNTSSSPA,KEETTGWRIF,WRIFHPSDPW,EETTGWRIFH,SPAKEETTGW	OV
TP53RK	c.520delC	p.L174fs	VLARMHDEDLIHGDLTTSNMLLKPP[p.L174fs]WNS*	SNMLLKPPW	STAD
TPO	c.1193G>C	p.S398T	AACAPEPGIPGETRGPCFLAGDGRA[p.S398T]TEVPSLTALHTLWLREHNRLAAALKA	FLAGDGRAT,GRATEVPSL,TEVPSLTAL,TEVPSLTALH	ACC
TPO	c.1672G>A	p.E558K	GGLDPLIRGLLARPAKLQVQDQLMN[p.E558K]KELTERLFVLSNSSTLDLASINLQRG	QVQDQLMNK,KELTERLFV,LMNKELTERL,QLMNKELTER,VQDQLMNKEL,MNKELTERLF,KELTERLFVL	LUAD
TPO	c.2476G>A	p.A826T	ADGAHPPCHASARCRNTKGGFQCLC[p.A826T]TDPYELGDDGRTCVDSGRLPRVTWIS	CLCTDPYEL,FQCLCTDPY,GFQCLCTDPY	CRC
TPPP	c.89G>A	p.R30K	AKPAKAANRTPPKSPGDPSKDRAAK[p.R30K]KLSLESEGAGEGAAASPELSALEEAF	KLSLESEGA,PSKDRAAKK,DRAAKKLSL	KIRP
TPR	c.6464C>T	p.S2155L	EDRTVPSTPTLVVPHRTDGFAEAIH[p.S2155L]LPQVAGVPRFRFGPPEDMPQTSSSHS	AEAIHLPQV,FAEAIHLPQV,AIHLPQVAGV,HLPQVAGVPR,LPQVAGVPRF,AEAIHLPQVA	CRC
TPRX1	c.598T>C	p.S200P	NPGPIPGPNPGPIPGPISGPIPGPI[p.S200P]PVPIPGPIPGPISGPISGPNPGPIPG	GPIPGPIPV,IPGPIPVPI,IPVPIPGPI	TGCT

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TPTE	c.1268C>T	p.S423L	AQVKHLYNWNLPPRRILFIKHFIIY[p.S423L]LIPRYVRDLKIQIEMEKKVVFSTISL	FIKHFIIYL,IIYLIPRYV,FIIYLIPRY,HFIIYLIPR,IYLIPRYVR,IKHFIIYLI,FIKHFIIYLI,FIIYLIPRYV,YLIPRYVRDL,IIYLIPRYVR,LIPRYVRDLK,LFIKHFIIYL,KHFIIYLIPR,HFIIYLIPRY	CRC,UCEC
TPTE	c.1623G>A	p.M541I	DNLHKQKARRIYPSDFAVEILFGEK[p.M541I]ITSSDVVAGSD*	VEILFGEKI,GEKITSSDV,GEKITSSDVV,VEILFGEKIT	LUSC
TPTE2	c.773G>A	p.R258Q	FPSSGRQSFYRNPIEEVVRFLDKKH[p.R258Q]QNHYRVYNLCSERAYDPKHFHNRVSR	KHQNHYRVY,QNHYRVYNL,KKHQNHYRV,FLDKKHQNHY,HQNHYRVYNL,KKHQNHYRVY	CRC
TRAF3	c.26C>T	p.S9F	MESSKKMD[p.S9F]FPGALQTNPPLKLHTDRSAGTPVFVP	MESSKKMDF,KKMDFPGAL,SSKKMDFPGA,SKKMDFPGAL	CESC
TRAF7	c.32G>A	p.R11H	MSSGKSARYN[p.R11H]HFSGGPSNLPTPDVTTGTRMETTFGP	KSARYNHFS,SARYNHFSG,GKSARYNHF,KSARYNHFSG,SARYNHFSGG,SGKSARYNHF,NHFSGGPSNL	DLBCL
TRAK1	c.1879G>A	p.D627N	DPRPGVVTKGFRTLDVDLDEVYCLN[p.D627N]NFEEDDTGDHISLPRLATSTPVQHPE	DEVYCLNNF	CRC
TRAM1	c.121G>C	p.E41Q	HEFVLQNHADIVSCVAMVFLLGLMF[p.E41Q]QITAKASIIFVTLQYNVTLPATEEQA	FLLGLMFQI,LMFQITAKA,FQITAKASI,GLMFQITAK,FLLGLMFQIT,GLMFQITAKA,FQITAKASII,LGLMFQITAK,VFLLGLMFQI,MFQITAKASI,LMFQITAKAS,QITAKASIIF	BLCA
TRAM1L1	c.1033delA	p.R345fs	LQRWVEDSNIQASCMKKKRSRSSKK[p.R345fs]EQKTEWEWKLQIE*	SKKEQKTEW,TEWEWKLQI,KEQKTEWEW,RSRSSKKEQK	STAD
TRANK1	c.2536G>A	p.E846K	YNISRRLSKLRVLPWSIHELYGDEI[p.E846K]KDFTQAELALLMKCINDPNSMFLTGD	LYGDEIKDF,IKDFTQAEL,DEIKDFTQA,EIKDFTQAEL,KDFTQAELAL,DEIKDFTQAE	UCEC
TRAPPC10	c.399_400insA	p.K133fs	WQNVLKAHSSVDWLIVIVENDAKKK[p.K133fs]KQNQHPSPNLYCGQNKK*	NLYCGQNKK,NQHPSPNLY,KQNQHPSPN,KQNQHPSPNL,QNQHPSPNLY	GBM
TRAPPC11	c.1703G>A	p.R568Q	MNESPDPEPDCDILAVKTAQKLWAD[p.R568Q]QISLAGSNIFTIGVQDFVPFVQCKAK	KLWADQISL,AQKLWADQI,KLWADQISLA,QISLAGSNIF,QKLWADQISL,DQISLAGSNI	CRC
TRDN	c.2190A>C	p.*730Y	PFTPADRPGESSGQANSPGQKQQGQ[p.*730Y]YTHMYDPYKCFKILKM*	YTHMYDPYK,MYDPYKCFK,QQGQYTHMY,KQQGQYTHM,HMYDPYKCF,QKQQGQYTH,GQYTHMYDP,YKCFKILKM,DPYKCFKIL,HMYDPYKCFK,MYDPYKCFKI,KQQGQYTHMY,GQYTHMYDPY,GQKQQGQYTH,QKQQGQYTHM,THMYDPYKCF,SPGQKQQGQY	KIRC
TRIM23	c.1187G>A	p.R396Q	QQQFTEVADHIQLDASIPVTFTKDN[p.R396Q]QVHIGPKMEIRVVTLGLDGAGKTTIL	FTKDNQVHI,NQVHIGPKM,KDNQVHIGPK	CRC
TRIM23	c.866G>A	p.R289Q	IVEDGIGMAHTEHVPGTAENARSCI[p.R289Q]QAYFYDLHETLCRQEEMALSVVDAHV	RSCIQAYFY,CIQAYFYDL,NARSCIQAY,ARSCIQAYF,IQAYFYDLH,ARSCIQAYFY,ENARSCIQAY,NARSCIQAYF,AENARSCIQA	CRC
TRIM4	c.1193G>T	p.R398L	NVFTSGKHYWEVESRDSLEVAVGVC[p.R398L]LEDVMGITDRSKMSPDVGIWAIYWSA	LEVAVGVCL	LUAD
TRIM42	c.379C>A	p.Q127K	TFHKGRLRSIHTSSKTALRTGSSDT[p.Q127K]KVDEVKSIPANSHLVNHLNCPMCSRL	ALRTGSSDTK	LUAD
TRIM48	c.278C>A	p.A93D	CFECIKTIQQRNLKTNIRLKKMASL[p.A93D]DRKASLWLFLSSEEQMCGIHRETKKM	RLKKMASLD,KMASLDRKA,RLKKMASLDR,MASLDRKASL,KKMASLDRKA,ASLDRKASLW,LDRKASLWLF	LUAD
TRIM61	c.294G>C	p.K98N	SLTEIAKQLQIRSKKRKRQEEKHVC[p.K98N]NKHNQVLTFFCQKDLELLCPRCSLST	NKHNQVLTF,RQEEKHVCNK,CNKHNQVLTF,NKHNQVLTFF	CESC
TRIM7	c.994C>A	p.L332I	MKNKVWNVSLKTFVLKGMLKKFKED[p.L332I]IRGELEKEEKVELTLDPDTANPRLIL	MLKKFKEDI,KFKEDIRGEL,MLKKFKEDIR	LUSC
TRIM9	c.1009C>A	p.R337S	FEACLVAQCDALIDALNRRKAQLLA[p.R337S]SVNKEHEHKLKVVRDQISHCTVKLRQ	AQLLASVNK,SVNKEHEHK,RKAQLLASV,KAQLLASVNK,ASVNKEHEHK,RRKAQLLASV	LUAD
TRIML1	c.1197C>A	p.H399Q	DLFSLIGLKIGDDYSLWVSSPLKGQ[p.H399Q]QVREPVCKVGVFLDYESGHIAFYNGT	LKGQQVREPV	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TRIO	c.1981C>T	p.R661W	QTGECDPEEIYQAAHQLEDRIQDFV[p.R661W]WRVEQRKILLDMSVSFHTHVKELWTW	RIQDFVWRV,FVWRVEQRK,DFVWRVEQR,WRVEQRKIL,DFVWRVEQRK,WRVEQRKILL	CRC
TRIOBP	c.3899A>G	p.H1300R	DLPPPRRLAQRQPGPQAQCSSGGRT[p.H1300R]RSPGRAEVERLFGQERRKSEAAGAFQ	GGRTRSPGR,RTRSPGRAE,GGRTRSPGRA,RTRSPGRAEV	ACC
TRIP11	c.1622delA	p.K541fs	DQLSKQQNEGDSIISKLKQDLNDEK[p.K541fs]REFINLKMIKWTLLKS*	KMIKWTLLK,EFINLKMIK,NLKMIKWTL,LKMIKWTLL,KREFINLKM,REFINLKMI,DEKREFINL,NLKMIKWTLL,EKREFINLKM,KMIKWTLLKS	STAD
TRIP12	c.5324T>C	p.L1775P	KLMAKAIMDFRLVDLPLGLPFYKWM[p.L1775P]PRQETSLTSHDLFDIDPVVARSVYHL	WMPRQETSL,KWMPRQETS,LPFYKWMPR,MPRQETSLT,YKWMPRQET,KWMPRQETSL,GLPFYKWMPR,MPRQETSLTS,YKWMPRQETS	MM
TRMT61A	c.731G>T	p.S244I	ALAARGFSELSTLEVLPQVYNVRTV[p.S244I]ILPPPDLGTGTDGPAGSDTSPFRSGT	VYNVRTVIL,QVYNVRTVI,PQVYNVRTVI,QVYNVRTVIL	TGCT
TRPA1	c.162G>T	p.K54N	TEDFKESLKVVFEGSAYGLQNFNKQ[p.K54N]NKLKRCDDMDTFFLHYAAAEGQIELM	NFNKQNKLKR,LQNFNKQNKL	CRC
TRPA1	c.2017delA	p.T673fs	DKSCRDYYIEYNFKYLQCPLEFTKK[p.T673fs]HLHRMLYMNRLQPSTQWYKITA*	YMNRLQPST,RLQPSTQWY,LQPSTQWYK,LHRMLYMNR,STQWYKITA,KKHLHRMLY,EFTKKHLHR,FTKKHLHRM,LEFTKKHLH,KHLHRMLYM,HRMLYMNRL,QPSTQWYKI,MLYMNRLQPS,HLHRMLYMNR,RLQPSTQWYK,LQPSTQWYKI,KKHLHRMLYM,FTKKHLHRML,TKKHLHRMLY,RMLYMNRLQP,YMNRLQPSTQ,MNRLQPSTQW,CPLEFTKKHL	STAD
TRPC5	c.1469C>T	p.S490L	PREEWEMWHPTLIAEALFAISNILS[p.S490L]LLRLISLFTANSHLGPLQISLGRMLL	FAISNILSL,AISNILSLL,ISNILSLLR,SLLRLISLF,LSLLRLISL,FAISNILSLL,ILSLLRLISL,LLRLISLFTA,AISNILSLLR,LFAISNILSL,LSLLRLISLF,ISNILSLLRL	CRC,UCEC
TRPM3	c.1285C>T	p.R429W	TRTQAQHLFIILMECMKKKELITVF[p.R429W]WMGSEGHQDIDLAILTALLKGANASA	KELITVFWM,WMGSEGHQDI,KKKELITVFW,KKELITVFWM,KELITVFWMG	UCEC
TRPM3	c.892G>T	p.G298W	QTMSNPMSKLTVLNSMHSHFILADN[p.G298W]WTTGKYGAEVKLRRQLEKHISLQKIN	FILADNWTT,LADNWTTGK,ADNWTTGKY,SHFILADNW,LADNWTTGKY,ILADNWTTGK,WTTGKYGAEV,HSHFILADNW	LUAD
TRPM6	c.2984G>A	p.R995H	IAKMTANMFYIVIIMAIVLLSFGVA[p.R995H]HKAILSPKEPPSWSLARDIVFEPYWM	LLSFGVAHK,SFGVAHKAI,AHKAILSPK,LSFGVAHKA,VLLSFGVAH,LLSFGVAHKA,VLLSFGVAHK,VAHKAILSPK,LSFGVAHKAI	CRC
TRPM7	c.2528G>A	p.R843Q	VRILDSNEGKNEMEIQMKSKKLPIT[p.R843Q]QKFYAFYHAPIVKFWFNTLAYLGFLM	ITQKFYAFY,KSKKLPITQ,KLPITQKFY,KKLPITQKF,TQKFYAFYH,QKFYAFYHA,LPITQKFYA,KLPITQKFYA,KSKKLPITQK,ITQKFYAFYH,TQKFYAFYHA,KKLPITQKFY,PITQKFYAFY,LPITQKFYAF,SKKLPITQKF,QKFYAFYHAP	CRC
TRPM7	c.5584C>T	p.R1862C	PQDEPSDLNLQPGNSTKESESTNSV[p.R1862C]CLML*	SESTNSVCL,KESESTNSVC,SESTNSVCLM	CRC
TRPM8	c.2295_2296insC	p.H765fs	VFYIAFLLLFAYVLLMDFHSVPHPP[p.H765fs]RAGPVLAGLCPLL*	VLAGLCPLL,HSVPHPPRA,HPPRAGPVL,RAGPVLAGL,DFHSVPHPPR,VPHPPRAGPV,GPVLAGLCPL	STAD
TRPS1	c.3373C>T	p.R1125W	IEKYQYPLFGLPFVHNDFQSEADWL[p.R1125W]WFWSKYKLSVPGNPHYLSHVPGLPNP	WLWFWSKYK,FQSEADWLW,SEADWLWFW,LWFWSKYKL,WLWFWSKYKL,EADWLWFWSK,DFQSEADWLW,FQSEADWLWF,WFWSKYKLSV,DWLWFWSKYK,ADWLWFWSKY,SEADWLWFWS	CRC
TRPV2	c.1865_1867delTGC	p.L627del	KFTIGMGELAFQEQLHFRGMVLLLL[p.L627del]AYVLLTYILLLNMLIALMSETVNSVATD	MVLLLLAYV,VLLLLAYVL,RGMVLLLLA,GMVLLLLAY,GMVLLLLAYV,MVLLLLAYVL,VLLLLAYVLL,RGMVLLLLAY	CLL
TRPV3	c.653C>A	p.A218E	FAEENDILGRFINAEYTEEAYEGQT[p.A218E]ELNIAIERRQGDIAALLIAAGADVNA	GQTELNIAI,ELNIAIERR,EAYEGQTEL,YEGQTELNI,AYEGQTELNI,QTELNIAIER,EEAYEGQTEL,YEGQTELNIA	KIRP
TRPV5	c.1475G>A	p.R492H	YFTRGFQMLGPFTIMIQKMIFGDLM[p.R492H]HFCWLMAVVILGFASAFYIIFQTEDP	LMHFCWLMA,MHFCWLMAV,KMIFGDLMH,MIFGDLMHF,DLMHFCWLM,GDLMHFCWL,MIFGDLMHFC,LMHFCWLMAV,KMIFGDLMHF,IFGDLMHFCW,HFCWLMAVVI,MHFCWLMAVV,GDLMHFCWLM	CRC

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TRRAP	c.10543C>T	p.R3515W	THYYIKIARFMPRVEIVQKHNTAAR[p.R3515W]WLYIRGHNGKIYPYLVMNDACLTESR	TAARWLYIR,AARWLYIRG,HNTAARWLY,NTAARWLYI,QKHNTAARW,KHNTAARWL,WLYIRGHNGK,NTAARWLYIR,AARWLYIRGH,RWLYIRGHNG,KHNTAARWLY,VQKHNTAARW,QKHNTAARWL	CRC
TRRAP	c.2917G>T	p.A973S	DCLKSANTEPYYRRQAWEVIKCFLV[p.A973S]SMMSLEDNKHALYQLLAHPNFTEKTI	SMMSLEDNK,CFLVSMMSL,VIKCFLVSM,IKCFLVSMM,VSMMSLEDNK,EVIKCFLVSM,KCFLVSMMSL,SMMSLEDNKH,WEVIKCFLVS	KICH
TSC1	c.1132G>T	p.G378C	CGMTTPPTSPGNVPPDLSHPYSKVF[p.G378C]CTTAGGKGTPLGTPATSPPPAPLCHS	KVFCTTAGG,YSKVFCTTA,SKVFCTTAG,KVFCTTAGGK,HPYSKVFCTT	LUAD
TSC22D2	c.1255G>A	p.A419T	AQPSSTGAAASPATAATLPVGTGQN[p.A419T]TSSVGAQLMGASSQPSEAMAPRTGPA	NTSSVGAQL,GQNTSSVGA,NTSSVGAQLM	ACC
TSG101	c.794A>G	p.K265R	WRMKEEMDRAQAELNALKRTEEDLK[p.K265R]RGHQKLEEMVTRLDQEVAEVDKNIEL	DLKRGHQKL,RGHQKLEEM	THCA
TSG101	c.826C>A	p.R276S	AELNALKRTEEDLKKGHQKLEEMVT[p.R276S]SLDQEVAEVDKNIELLKKKDEELSSA	KLEEMVTSL,SLDQEVAEV,MVTSLDQEV,EMVTSLDQEV,TSLDQEVAEV,QKLEEMVTSL	LUAD
TSHZ1	c.1503G>C	p.K501N	EDSLEKFEPSTLYPYLREEDLDDSP[p.K501N]NGGLDILKSLENTVSTAISKAQNGAP	SPNGGLDIL	LUAD
TSHZ1	c.2642G>T	p.R881M	QAQFASSLRETTEGKYIMSDLGPQE[p.R881M]MVHISKFTGLSMTTISHWLANVKYQL	MSDLGPQEM,QEMVHISKF,MSDLGPQEMV,IMSDLGPQEM,MVHISKFTGL,PQEMVHISKF,QEMVHISKFT	CRC
TSHZ2	c.664G>A	p.A222T	LYRQSSKMCGTVFTGASRFRCRQCS[p.A222T]TAYDTLVELTVHMNETGHYQDDNRKK	RFRCRQCST,RCRQCSTAY,CSTAYDTLV,TAYDTLVEL,RQCSTAYDT,STAYDTLVEL,RFRCRQCSTA,FRCRQCSTAY,RQCSTAYDTL	GBM
TSHZ3	c.2030G>T	p.G677V	EPIKMEASSDGGFRSQENSPSPPRD[p.G677V]VCKDGSPLAEPVENGKELVKPLASSL	RDVCKDGSPL	LUAD
TSKS	c.1537G>A	p.E513K	CPSCQRLHKKILELERQALAKHVRA[p.E513K]KALSSTLRLAQDEALRAKNLLLTDKM	ALAKHVRAK,LAKHVRAKA,HVRAKALSS,RAKALSSTL,KALSSTLRL,AKHVRAKAL,ALAKHVRAKA,QALAKHVRAK,HVRAKALSST,RAKALSSTLR,KALSSTLRLA,LAKHVRAKAL,VRAKALSSTL,AKALSSTLRL	BLCA
TSPAN4	c.274C>G	p.L92V	IGFVGCLGAIKENKCLLLTFFLLLL[p.L92V]VVFLLEATIAILFFAYTDKIDRYAQQ	LTFFLLLLV,FLLLLVVFL,LLLLVVFLL,LLVVFLLEA,FFLLLLVVF,LLTFFLLLLV,LTFFLLLLVV,FLLLLVVFLL,LLLVVFLLEA,TFFLLLVVF,FFLLLLVVFL	PRAD,TGCT
TSSK1B	c.901G>A	p.E301K	ARGSPSVAINKEGESSRGTEPLWTP[p.E301K]KPGSDKKSATKLEPEGEAQPQAQPET	GTEPLWTPK,RGTEPLWTPK	UCEC
TTBK2	c.249T>G	p.C83W	KQVLKMEVAVLKKLQGKDHVCRFIG[p.C83W]WGRNDRFNYVVMQLQGRNLADLRRSQ	WGRNDRFNY,VCRFIGWGR,FIGWGRNDR,IGWGRNDRF,HVCRFIGWGR,GWGRNDRFNY,RFIGWGRNDR,FIGWGRNDRF	KIRP
TTC21A	c.809C>A	p.S270Y	ESNIDACQILTVHELAREGNMTTVS[p.S270Y]YLKTQKATNHVRNLIKALETREPENP	NMTTVSYLK,TVSYLKTQK,EGNMTTVSY,GNMTTVSYL,GNMTTVSYLK,TTVSYLKTQK,REGNMTTVSY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TTF1	c.1007delA	p.K336fs	RPAVGLHGETAGIPAPAYKNKSKKK[p.K336fs]RKSPITRNLRQWPCLRASRVHTLKDHRWAVRLGLWKAVQLLKGSRNPTVQRRSLRKGSLRLSKGHECLVMIFQCPVRTLRAHSLIQ*	TLKDHRWAV,GLWKAVQLL,LVMIFQCPV,SLRKGSLRL,RLSKGHECL,RASRVHTLK,TVQRRSLRK,WAVRLGLWK,LWKAVQLLK,RSLRKGSLR,RWAVRLGLW,IFQCPVRTL,RTLRAHSLI,KNKSKKKRK,KKRKSPITR,KSPITRNLR,RNLRQWPCL,CLRASRVHT,RVHTLKDHR,HTLKDHRWA,AVRLGLWKA,GSRNPTVQR,NLRQWPCLR,QWPCLRASR,PTVQRRSLR,VMIFQCPVR,FQCPVRTLR,WPCLRASRV,NPTVQRRSL,SKKKRKSPI,LRASRVHTL,RKSPITRNL,RQWPCLRAS,HRWAVRLGL,SKGHECLVM,GHECLVMIF,VRTLRAHSL,CPVRTLRAH,KDHRWAVRL,RLSKGHECLV,CLVMIFQCPV,MIFQCPVRTL,CLRASRVHTL,LLKGSRNPTV,GLWKAVQLLK,RWAVRLGLWK,LVMIFQCPVR,KSKKKRKSPI,KKKRKSPITR,KRKSPITRNL,ITRNLRQWPC,RNLRQWPCLR,RQWPCLRASR,HTLKDHRWAV,TLKDHRWAVR,AVRLGLWKAV,GSRNPTVQRR,RSLRKGSLRL,SLRKGSLRLS,RTLRAHSLIQ,IFQCPVRTLR,LSKGHECLVM,RVHTLKDHRW,HRWAVRLGLW,LRLSKGHECL,KGHECLVMIF,FQCPVRTLRA,SPITRNLRQW	STAD
TTF1	c.1589A>G	p.Q530R	IKDRATSTIKRMYRDDLERFKEFKA[p.Q530R]RGVAIKFGKFSVKENKQLEKNVEDFL	RGVAIKFGK,RFKEFKARG,KARGVAIKF,EFKARGVAI,KEFKARGVA,RFKEFKARGV,EFKARGVAIK,KARGVAIKFG,KEFKARGVAI,FKARGVAIKF,RGVAIKFGKF	TGCT
TTF2	c.2281C>A	p.R761S	LDEAHNVKNPRVQTSIAVCKLQACA[p.R761S]SWAVTGTPIQNNLLDMYSLLKFLRCS	KLQACASWA,LQACASWAV,CKLQACASW,SWAVTGTPI,KLQACASWAV,LQACASWAVT,ASWAVTGTPI	LUAD
TTI1	c.2120G>A	p.R707H	CGYDSLQHLINQNSDYLVNGISLNL[p.R707H]HHLALHPHTPKVLEVMLRNSDANLLP	SLNLHHLAL,GISLNLHHL,LHHLALHPH,GISLNLHHLA,ISLNLHHLAL	STAD
TTLL11	c.367_368insAGGCCA	p.122_123insKA	SELAARWEAEAVAAAKAAAKAEAEA[p.122_123insKA]KATAETVAEQVRVDAGAAGEPECKAGEEQPK	AAKAEAEAK,EAKATAETV,AEAEAKATA,AKATAETVA,AEAKATAET,AAAKAEAEAK,AEAKATAETV	ACC
TTLL7	c.2252G>A	p.R751H	LIKLDSVKQRKVLDIVKTSIRTVLP[p.R751H]HIWKVPDVEEVNLYRIFNRVFNRLLW	TVLPHIWKV,SIRTVLPHI,RTVLPHIWK,TSIRTVLPH,KTSIRTVLPH,RTVLPHIWKV,TSIRTVLPHI,SIRTVLPHIW,LPHIWKVPDV	UCEC
TUBA1C	c.436C>T	p.L146F	EDGVVGLNYSCGNLGRRVNGELQLG[p.L146F]FLAIIN*	LQLGFLAII,ELQLGFLAI,VNGELQLGF,GELQLGFLA,RVNGELQLGF,GELQLGFLAI	ACC,TGCT
TUBA3C	c.526_527insC	p.Q176fs	SLLMERLSVDYGKKSKLEFAIYPAP[p.Q176fs]PGLHGRGGALQLHPDHPHDPGTF*	AIYPAPPGL,GLHGRGGAL,HGRGGALQL,LQLHPDHPH,FAIYPAPPGL,AIYPAPPGLH,LEFAIYPAPP,LHGRGGALQL	LUAD
TUBA3D	c.728G>A	p.R243Q	DIERPTYTNLNRLIGQIVSSITASL[p.R243Q]QFDGALNVDLTEFQTNLVPYPRIHFP	LQFDGALNV,SSITASLQF,ASLQFDGAL,SLQFDGALNV,ITASLQFDGA,VSSITASLQF,LQFDGALNVD	CRC
TUBBPS	c.304G>A	p.V102M	TYHGDSHLQLERINVHHHEASGGRY[p.V102M]MPRAVLVDLEPGTMDSVRSGPFGQVL	ASGGRYMPR,RYMPRAVLV,GGRYMPRAV,MPRAVLVDL,HEASGGRYM,GRYMPRAVL,YMPRAVLVDL,EASGGRYMPR,HHEASGGRYM	GBM
TUBBP5	c.356G>A	p.R119H	HEASGGRYVPRAVLVDLEPGTMDSV[p.R119H]HSGPFGQVLRPDNFIFGELRARTGVR	MDSVHSGPF,HSGPFGQVL,SVHSGPFGQV,HSGPFGQVLR,TMDSVHSGPF,VHSGPFGQVL	UCS
TUBD1	c.599C>T	p.A200V	YGTGEVIVQNYNSILTLSHLYRSSD[p.A200V]VLLLHENDAIHKICAKLMNIKQISFS	HLYRSSDVL,RSSDVLLLH,LYRSSDVLL,YRSSDVLLL,HLYRSSDVLL,VLLLHENDAI,LYRSSDVLLL,SHLYRSSDVL	BRCA
TUFT1	c.1018G>A	p.A340T	KSQQRKVRQMIEQLQNSKAVIQSKD[p.A340T]TTIQELKEKIAYLEAENLEMHDRMEH	TTIQELKEK,SKDTTIQEL,AVIQSKDTTI	CRC
TUFT1	c.303G>C	p.L101F	HSAGHSLASELVESHDGHEEIIKVY[p.L101F]FKGRSGDKMIHEKNINQLKSEVQYIQ	IIKVYFKGR,KVYFKGRSG,YFKGRSGDK,FKGRSGDKM,HEEIIKVYF,VYFKGRSGDK,EIIKVYFKGR	CESC
TWISTNB	c.918T>A	p.H306Q	KKKHQEVQDQDPVFQGSDSSGYQSD[p.H306Q]QKKKKKKRKHSEEAEFTPPLKCSPKR	SSGYQSDQK	CLL
TXNDC15	c.1028G>A	p.R343Q	LIKSVDWLLVFSLFFLISFIMYATI[p.R343Q]QTESIRWLIPGQEQEHVE*	FIMYATIQT,IQTESIRWL,QTESIRWLI,YATIQTESI,IMYATIQTE,IQTESIRWLI,IMYATIQTES,MYATIQTESI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TXNL1	c.700C>T	p.R234C	AERSEPTQALELTEDDIKEDGIVPL[p.R234C]CYVKFQNVNSVTIFVQSNQGEEETTR	GIVPLCYVK,IVPLCYVKF,DGIVPLCYV,KEDGIVPLCY,GIVPLCYVKF	UCEC
TYRP1	c.1054_1057delACAA	p.T352fs	PEPQDVAQCLEVGLFDTPPFYSNST[p.T352fs]VSETQWKVTVTPRESMTLLFEVFTIWLIYS*	TVSETQWKV,ESMTLLFEV,TLLFEVFTI,STVSETQWK,SMTLLFEVF,EVFTIWLIY,QWKVTVTPR,MTLLFEVFT,TPRESMTLL,SETQWKVTV,TQWKVTVTP,LLFEVFTIW,FEVFTIWLI,MTLLFEVFTI,LLFEVFTIWL,STVSETQWKV,TQWKVTVTPR,ESMTLLFEVF,TLLFEVFTIW,LFEVFTIWLI,KVTVTPRESM,EVFTIWLIYS,TPRESMTLLF,RESMTLLFEV,FEVFTIWLIY,SETQWKVTVT,TPPFYSNSTV	GBM
U2AF1	c.101C>A	p.S34Y	FGTEKDKVNCSFYFKIGACRHGDRC[p.S34Y]YRLHNKPTFSQTIALLNIYRNPQNSS	YRLHNKPTF,CYRLHNKPTF,GDRCYRLHNK,GACRHGDRCY	LAML
U2AF1	c.101C>T	p.S34F	FGTEKDKVNCSFYFKIGACRHGDRC[p.S34F]FRLHNKPTFSQTIALLNIYRNPQNSS	FRLHNKPTF,CFRLHNKPTF,ACRHGDRCFR,GDRCFRLHNK,GACRHGDRCF	CESC,LAML,LUAD,UCS
UBC	c.2051delG	p.G684fs	EDGRTLSDYNIQKESTLHLVLRLRG[p.G684fs]VSKFPLLRFQQISLHFPFNKVVAF	SLHFPFNKV,HLVLRLRGV,LLRFQQISL,VLRLRGVSK,GVSKFPLLR,ISLHFPFNK,RFQQISLHF,QQISLHFPF,RLRGVSKFP,RGVSKFPLL,FPLLRFQQI,FPFNKVVAF,LRLRGVSKF,LRGVSKFPL,VSKFPLLRF,LHFPFNKVV,RLRGVSKFPL,SLHFPFNKVV,LVLRLRGVSK,QISLHFPFNK,KFPLLRFQQI,FQQISLHFPF,HFPFNKVVAF,RGVSKFPLLR,ISLHFPFNKV,VLRLRGVSKF,GVSKFPLLRF,LRFQQISLHF,LHFPFNKVVA,FPLLRFQQIS	STAD
UBC	c.572T>C	p.I191T	TLEVEPSDTIENVKAKIQDKEGIPP[p.I191T]TSRGSSLQASSWKMAVLFLTTTSRRS	TSRGSSLQA,PPTSRGSSL,IPPTSRGSSL,IQDKEGIPPT	PRAD
UBE2J2	c.577G>T	p.G193W	KQKQKAQDELSSRPQTLPLPDVVPD[p.G193W]WETHLVQNGIQLLNGHAPGAVPNLAG	VPDWETHLV,VVPDWETHLV,DVVPDWETHL,WETHLVQNGI,LPLPDVVPDW	LUAD
UBE2M	c.392G>A	p.G131D	LEGNVCLNILREDWKPVLTINSIIY[p.G131D]DLQYLFLEPNPEDPLNKEAAEVLQNN	NSIIYDLQY,SIIYDLQYL,TINSIIYDL,IIYDLQYLF,IYDLQYLFL,IIYDLQYLFL,SIIYDLQYLF,INSIIYDLQY,LTINSIIYDL,NSIIYDLQYL	TGCT
UBE2NL	c.257G>T	p.R86I	EEYPMAAPKVRFMTKIYHPNVDKLE[p.R86I]IISLDILKDKWSPALQIRTVLLSIQA	EIISLDILK,HPNVDKLEI,LEIISLDIL,HPNVDKLEII	CRC
UBE2O	c.3354_3355insG	p.R1118fs	YENSRCYNEMALIRVVQSMTQLVRR[p.R1118fs]APRGL*	SMTQLVRRA,TQLVRRAPR,LVRRAPRGL,MTQLVRRAPR	KIRC
UBIAD1	c.289G>A	p.A97T	AYRSHGVLDPRLLVGCAVAVLAVHG[p.A97T]TGNLVNTYYDFSKGIDHKKSDDRTLV	GTGNLVNTY,AVHGTGNLV,TGNLVNTYY,GTGNLVNTYY,VLAVHGTGNL,HGTGNLVNTY,LAVHGTGNLV	CRC
UBOX5	c.1250C>T	p.S417L	LPTTSEHTAKKMKATNEPSLTHMDC[p.S417L]LTGPLSHEQKLSQSLEIALASTLGSM	HMDCLTGPL,LTGPLSHEQK,THMDCLTGPL	BLCA
UBQLN2	c.1568delC	p.A523fs	PIGPIVPFTPIGPIGPIGPTGPAAP[p.A523fs]LAPPALVAPRGLLCPALHLVKPRVLHQNLDPTSSSFSKWCRPWLEQMLHSCRIQKSDFSNNWNSSTQWGS*	GLLCPALHL,LLCPALHLV,ALHLVKPRV,ALVAPRGLL,VLHQNLDPT,MLHSCRIQK,SSSFSKWCR,SFSKWCRPW,APRGLLCPA,KPRVLHQNL,EQMLHSCRI,NLDPTSSSF,WCRPWLEQM,QKSDFSNNW,NNWNSSTQW,APLAPPALV,GLLCPALHLV,LLCPALHLVK,QMLHSCRIQK,TSSSFSKWCR,SFSKWCRPWL,KWCRPWLEQM,LAPPALVAPR,GPAAPLAPPA,APLAPPALVA,APRGLLCPAL,IQKSDFSNNW,RGLLCPALHL,HQNLDPTSSS,QNLDPTSSSF,SSFSKWCRPW,LEQMLHSCRI,HSCRIQKSDF,SNNWNSSTQW,DPTSSSFSKW	STAD
UBR1	c.4939G>T	p.G1647W	KHPVLCLFCGAILCSQNICCQEIVN[p.G1647W]WEEVGACIFHALHCGAGVCIFLKIRE	WEEVGACIF,QEIVNWEEV,WEEVGACIFH	LUAD
UBR4	c.8406delC	p.P2802fs	TAENVNNGNPSPLEALLAGAEGFPP[p.P2802fs]CWTSHLMQMTRPWLN*	LMQMTRPWL,TSHLMQMTR,CWTSHLMQM,FPPCWTSHL,HLMQMTRPW,AEGFPPCWT,HLMQMTRPWL,WTSHLMQMTR,GFPPCWTSHL,FPPCWTSHLM,SHLMQMTRPW,AEGFPPCWTS	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
UBR5	c.6360delA	p.K2120fs	EVLPTKMSYAANLKNVMNMQNRQKK[p.K2120fs]KGKNSPCCQKKLRVQNQGHLLMILLHN*	KNSPCCQKK,KLRVQNQGH,RVQNQGHLL,VQNQGHLLM,LRVQNQGHL,NQGHLLMIL,MQNRQKKKGK,KGKNSPCCQK,KLRVQNQGHL,RVQNQGHLLM,LRVQNQGHLL,VQNQGHLLMI,NQGHLLMILL	KICH
UBR5	c.7551G>T	p.R2517S	LDDTDDGDDNAPLFYQPGKRGFYTP[p.R2517S]SPGKNTEARLNCFRNIGRILGLCLLQ	GFYTPSPGK,RGFYTPSPG,RGFYTPSPGK,SPGKNTEARL	TGCT
UBXN7	c.827C>T	p.A276V	LDQVTGFLGEHGQLDGLSSSPPKKC[p.A276V]VRSESLIDASEDSQLEAAIRASLQET	KKCVRSESL	CLL
UGP2	c.784G>C	p.D262H	ASFYNSGLLDTFIGEGKEYIFVSNI[p.D262H]HNLGATVDLYILNHLMNPPNGKRCEF	NIHNLGATV,IFVSNIHNL,YIFVSNIHNL,FVSNIHNLGA,HNLGATVDLY,KEYIFVSNIH	BLCA
UGT1A1	c.10A>G	p.T4A	MAR[p.T4A]AGWTSPIPLCVSLLLTCGFAEAGKLL	ARAGWTSPI,AGWTSPIPL,MARAGWTSPI,RAGWTSPIPL	KIRP
UGT2A1	c.290delA	p.N97fs	EIYRVPFGKERIEGVIKDFVLTWLE[p.N97fs]IDHLLQPFGDSIRRWPK*	LLQPFGDSI,DFVLTWLEI,TWLEIDHLL,LEIDHLLQP,VLTWLEIDHL,HLLQPFGDSI,LEIDHLLQPF,KDFVLTWLEI,QPFGDSIRRW	CRC
UGT2B11	c.1340G>T	p.R447I	STDLLNALKTVINDPLYKENIMKLS[p.R447I]IIQHDQPVKPLDRAVFWIEFVMPHKG	KENIMKLSI,IMKLSIIQH,YKENIMKLSI,KENIMKLSII	TGCT
UGT2B28	c.866C>A	p.P289H	FQFPHPFLPNIDFVGGLHCKPAKPL[p.P289H]HKEMEEFVQSSGENGVVVFSLGSVIS	HCKPAKPLHK,KPAKPLHKEM	GBM
UGT2B7	c.642G>A	p.M214I	FPPSYVPVVMSELTDQMTFMERVKN[p.M214I]IIYVLYFDFWFEIFDMKKWDQFYSEV	RVKNIIYVL,TFMERVKNI,KNIIYVLYF,IIYVLYFDF,VKNIIYVLY,MERVKNIIY,FMERVKNII,FMERVKNIIY,RVKNIIYVLY,TFMERVKNII,NIIYVLYFDF,IIYVLYFDFW,MTFMERVKNI,MERVKNIIYV,VKNIIYVLYF	LUAD
UGT8	c.304G>A	p.E102K	FNSTTSDAFLQSKMRNIFSGRLTAI[p.E102K]KLFDILDHYTKNCDLMVGNHALIQGL	KLFDILDHY,FSGRLTAIK,SGRLTAIKL,TAIKLFDIL,GRLTAIKLF,RLTAIKLFDI,KLFDILDHYT,IFSGRLTAIK,SGRLTAIKLF,IKLFDILDHY	CRC,UCEC
UHRF1BP1	c.3990delC	p.I1330fs	EIPVVVPMQIELLNSSITLKDDIPP[p.I1330fs]SIQHLQAPSPSLWPWNMLC*	HLQAPSPSL,SLWPWNMLC,IQHLQAPSP,LQAPSPSLW,APSPSLWPW,SPSLWPWNM,TLKDDIPPSI,SPSLWPWNML,IQHLQAPSPS,QHLQAPSPSL,HLQAPSPSLW,IPPSIQHLQA	STAD
UMODL1	c.1677G>A	p.M559I	CQCRTTRDATPSRAGRACEGDLVSP[p.M559I]IGGGLSAATGVTVPGLGTGTAALGLE	LVSPIGGGL,SPIGGGLSA,CEGDLVSPI,SPIGGGLSAA	TGCT
UNC93A	c.1334_1335TC>CG	p.V445A	LTMVAYGLVECVESKNPIRPHAPGQ[p.V445A]ANQAEDEEIQTKM*	RPHAPGQAN	TGCT
UNC93B1	c.1492G>A	p.V498M	YHWWQAVAIFTVYLGSSLHMKAKLA[p.V498M]MLLVTLVAAAVSYLRMEQKLRRGVAP	KLAMLLVTL,LAMLLVTLV,AMLLVTLVA,MLLVTLVAA,HMKAKLAML,KAKLAMLLV,LHMKAKLAM,MKAKLAMLL,AKLAMLLVT,KLAMLLVTLV,AMLLVTLVAA,MLLVTLVAAA,HMKAKLAMLL,KAKLAMLLVT,SLHMKAKLAM,LHMKAKLAML,MKAKLAMLLV,AKLAMLLVTL,LAMLLVTLVA	CESC
UPK2	c.145delC	p.P49fs	DFNISSLSGLLSPALTESLLVALPP[p.P49fs]VTSQEAMPH*	SLLVALPPV,ALPPVTSQEA,ESLLVALPPV,LPPVTSQEAM	STAD
UPK3A	c.816_817insC	p.G272fs	QITQEAVPKSLGASESSYTSVNRGP[p.G272fs]ATGQG*	YTSVNRGPA	KIRC
UQCRFS1	c.16T>G	p.S6A	MLSVA[p.S6A]ARSGPFAPVLSATSRGVAGALRPLVQ	SVAARSGPF,ARSGPFAPV,SVAARSGPFA,AARSGPFAPV,LSVAARSGPF,ARSGPFAPVL	ACC
UQCRFS1	c.247A>G	p.I83V	QAVRRPLVASVGLNVPASVCYSHTD[p.I83V]VKVPDFSEYRRLEVLDSTKSSRESSE	VKVPDFSEY,SVCYSHTDVK,DVKVPDFSEY,SHTDVKVPDF	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
URGCP	c.1916_1917insG	p.G639fs	HFLREMGQFYEAESCLVEAGRLPAG[p.G639fs]PEAFCPLPRLGLGAAADRAASGANRWEHAEHARPLGHRAPEGAARPTGETVKAGGSVNRRGARHGQVHTPQHHVWAAVCHREELRSSRGLHAAHHSG*	HVWAAVCHR,RLPAGPEAF,HARPLGHRA,AARPTGETV,RSSRGLHAA,SSRGLHAAH,AVCHREELR,EAFCPLPRL,ETVKAGGSV,QVHTPQHHV,HTPQHHVWA,LPRLGLGAA,RPLGHRAPE,APEGAARPT,TPQHHVWAA,RAASGANRW,AEHARPLGH,RGARHGQVH,GQVHTPQHH,EELRSSRGL,GQVHTPQHHV,AGRLPAGPEA,AARPTGETVK,TVKAGGSVNR,RSSRGLHAAH,SSRGLHAAHH,HTPQHHVWAA,LPRLGLGAAA,RPLGHRAPEG,TPQHHVWAAV,ELRSSRGLHA,GRLPAGPEAF,WEHAEHARPL,QVHTPQHHVW,WAAVCHREEL,REELRSSRGL,LRSSRGLHAA,PEAFCPLPRL,GETVKAGGSV,CPLPRLGLGA	KICH
URI1	c.39_40insC	p.S13fs	MEAPTVETPPDPSPP[p.S13fs]FGPGPCPGSVARPGCGAAARGAGKGGH*	GAAARGAGK,VARPGCGAA,SVARPGCGA,TPPDPSPPF,VARPGCGAAA,CGAAARGAGK,SVARPGCGAA	HNSC
USF1	c.155G>A	p.R52Q	DPTSVAIASIQSAATFPDPNVKYVF[p.R52Q]QTENGGQVMYRVIQVSEGQLDGQTEG	FQTENGGQV,QTENGGQVMY,FQTENGGQVM	UCEC
USH2A	c.11156G>A	p.R3719H	NSTTVELYWSLPEKPNGLVSQYQLS[p.R3719H]HNGNLLFLGGSEEQNFTDKNLEPNSR	YQLSHNGNL,QLSHNGNLL,LSHNGNLLF,SQYQLSHNG,SHNGNLLFL,YQLSHNGNLL,QYQLSHNGNL,QLSHNGNLLF,SQYQLSHNGN,LSHNGNLLFL	GBM
USH2A	c.7107C>A	p.F2369L	KAHVRWEAPFRPNGLLTHSVLFTGI[p.F2369L]LYVDPVGNNYTLLNVTKVMYSGEETN	VLFTGILYV,SVLFTGILY,TGILYVDPV,HSVLFTGIL,HSVLFTGILY,SVLFTGILYV,FTGILYVDPV,LYVDPVGNNY	CRC
USP11	c.856G>A	p.A286T	VLDAALETGQLIIMETRKKDGTWPS[p.A286T]TQLHVMNNNMSEEDEDFKGQPGICGL	GTWPSTQLH,TWPSTQLHV,WPSTQLHVM,TWPSTQLHVM,TQLHVMNNNM	CRC
USP15	c.2344delA	p.K782fs	KKRYFDENAAEDFEKHESVEYKPPK[p.K782fs]NPL*	VEYKPPKNPL	STAD
USP16	c.1364G>A	p.R455Q	DIPSGTSKHLQKKAKKQAKKQAKNQ[p.R455Q]QRQQKIQGKVLHLNDICTIDHPEDSE	QAKNQQRQQK,QQRQQKIQGK,AKNQQRQQKI	UCEC
USP25	c.2618G>A	p.R873H	FKAIKLEYARLVKLAQEDTPPETDY[p.R873H]HLHHVVVYFIQNQAPKKIIEKTLLEQ	ETDYHLHHV,HLHHVVVYF,YHLHHVVVY,TDYHLHHVV,ETDYHLHHVV,HLHHVVVYFI,YHLHHVVVYF,DTPPETDYHL,TDYHLHHVVV	UCEC
USP25	c.3356G>A	p.R1119Q	EPPKLPSYSTHELCERFARIMLSLS[p.R1119Q]QTPADGR*	MLSLSQTPA,RIMLSLSQT,IMLSLSQTP,IMLSLSQTPA	CRC
USP26	c.2582G>A	p.R861Q	TLKSGHYICDAYDFEKQIWFTYDDM[p.R861Q]QVLGIQEAQMQEDRRCTGYIFFYMHN	FTYDDMQVL,MQVLGIQEA,TYDDMQVLGI,MQVLGIQEAQ	CRC
USP29	c.243C>A	p.F81L	NIRSVVLRHCKKRQSHLRLTLKNNV[p.F81L]LLFIDKLSYRDAKQLNMFLDIIHQNK	LLFIDKLSY,TLKNNVLLF,RLTLKNNVL,LKNNVLLFI,TLKNNVLLFI,LLFIDKLSYR,LTLKNNVLLF,KNNVLLFIDK,VLLFIDKLSY,LRLTLKNNVL,RLTLKNNVLL	CRC
USP31	c.1171G>A	p.D391N	LTEMYYDGFHRSFCDTDDLETVHES[p.D391N]NCIFAFETPEIFRPEGILSQRGIHLN	ETVHESNCI,TVHESNCIF,HESNCIFAF,TVHESNCIFA,ESNCIFAFET,VHESNCIFAF	CRC
USP33	c.107G>A	p.R36Q	LTLKVLPHFESLGKQEKIPNKMSAF[p.R36Q]QNHCPHLDSVGEITKEDLIQKSLGTC	KMSAFQNHC,SAFQNHCPH,MSAFQNHCPH,SAFQNHCPHL	UCEC
USP4	c.775C>G	p.L259V	STAPSRNFTTSPKSSASPYSSVSAS[p.L259V]VIANGDSTSTCGMHSSGVSRGGSGFS	YSSVSASVI,PYSSVSASVI,SPYSSVSASV,YSSVSASVIA	CESC
USP40	c.2552C>T	p.S851L	DSYTLKEAELKMGSSLGLCLGKAPS[p.S851L]LSQLFLFFAMGSDVQPGTEMEIVVEE	KAPSLSQLF,PSLSQLFLF,SLSQLFLFF,APSLSQLFL,GKAPSLSQL,SLSQLFLFFA,PSLSQLFLFF,KAPSLSQLFL,LGKAPSLSQL,GKAPSLSQLF,APSLSQLFLF,LSQLFLFFAM	CRC
USP42	c.2336G>C	p.R779P	SPAAESLEEPDAAAGLSSTKKAPPP[p.R779P]PDPGTPATKEGAWEAMAVAPEEPPPS	STKKAPPPP,STKKAPPPPD	ACC
USP46	c.410A>G	p.Q137R	LFDNYMQQDAHEFLNYLLNTIADIL[p.Q137R]REEKKQEKQNGKLKNGNMNEPAENNK	TIADILREEK,ILREEKKQEK,LLNTIADILR	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
UTP14A	c.442G>A	p.V148I	EEIERIHREVAFNKTAQVLSKWDPV[p.V148I]ILKNRQAEQLVFPLEKEEPAIAPIEH	VLSKWDPVI,VLSKWDPVIL,ILKNRQAEQL,LSKWDPVILK	CRC
UTP3	c.226_228delGAG	p.E81del	SRAALAKGWNEVQSGDEEDGEEEEE[p.E81del]VLALDMDDEDDEDGGNAGEEEEEENADD	GEEEEEVLAL	PRAD
UTS2R	c.866C>A	p.A289E	VLLFWACFLPFWLWQLLAQYHQAPL[p.A289E]EPRTARIVNYLTTCLTYGNSCANPFL	LEPRTARIV,APLEPRTARI,AQYHQAPLEP,HQAPLEPRTA,EPRTARIVNY	KIRP
UXS1	c.298G>C	p.V100L	QKYPPVKFLSEKDRKRILITGGAGF[p.V100L]LGSHLTDKLMMDGHEVTVVDNFFTGR	LITGGAGFL,ILITGGAGFL,FLGSHLTDKL	OV
VARS	c.151_152CC>AG	p.P51S	EAGEGPGWGGAHPRICLQPPPTSRT[p.P51S]SFPPPRLPALEQGPGGLWVWGATAVAQ	TSRTSFPPP,RTSFPPPRL,TSRTSFPPPR,SFPPPRLPAL,TSFPPPRLPA,QPPPTSRTSF	ACC
VASH1	c.7delG	p.G3fs	MPGG[p.G3fs]RRWLGVAAAVPLQRPLRPPPPLGSGVWRPAKEPQPREMRSQKRKGKRTCETEASPSLSTGVGYLWMRPPGKGCGNTWPRSTPMERRWRNGSVGPQTCPRSPYRVCLRSSRLHLSLSAWKLCSATSESCSTITQGHSSLKLRRADL*	SLSTGVGYL,HLSLSAWKL,LSAWKLCSA,ATSESCSTI,YLWMRPPGK,ITQGHSSLK,VAAAVPLQR,GSGVWRPAK,SVGPQTCPR,QTCPRSPYR,RWLGVAAAV,GGRRWLGVA,AVPLQRPLR,RSQKRKGKR,RWRNGSVGP,RSPYRVCLR,RVCLRSSRL,CLRSSRLHL,RSSRLHLSL,SSRLHLSLS,TGVGYLWMR,NTWPRSTPM,RPLRPPPPL,CPRSPYRVC,ERRWRNGSV,SLKLRRADL,RLHLSLSAW,GRRWLGVAA,RRWLGVAAA,LGVAAAVPL,AAVPLQRPL,LQRPLRPPP,AKEPQPREM,CETEASPSL,LSTGVGYLW,RSTPMERRW,RRWRNGSVG,PQTCPRSPY,SRLHLSLSA,TQGHSSLKL,TEASPSLST,WLGVAAAVPL,SLSAWKLCSA,RLHLSLSAWK,TITQGHSSLK,GVAAAVPLQR,STGVGYLWMR,GSVGPQTCPR,GGRRWLGVAA,LGSGVWRPAK,EMRSQKRKGK,KGKRTCETEA,GYLWMRPPGK,RSTPMERRWR,RWRNGSVGPQ,RVCLRSSRLH,CLRSSRLHLS,RSSRLHLSLS,SSRLHLSLSA,TWPRSTPMER,EASPSLSTGV,QTCPRSPYRV,STITQGHSSL,MPGGRRWLGV,RPPPPLGSGV,CPRSPYRVCL,MERRWRNGSV,SPSLSTGVGY,RRWLGVAAAV,AAAVPLQRPL,LQRPLRPPPP,SLSTGVGYLW,LSTGVGYLWM,GNTWPRSTPM,GPQTCPRSPY,YRVCLRSSRL,LRSSRLHLSL,SRLHLSLSAW,LHLSLSAWKL,SATSESCSTI	STAD
VAV3	c.2053G>A	p.E685K	CVPKPVDYSCQPWYAGAMERLQAET[p.E685K]KLINRVNSTYLVRHRTKESGEYAISI	RLQAETKLI,KLINRVNST,AETKLINRV,KLINRVNSTY,AMERLQAETK,MERLQAETKL	CRC
VCAN	c.3374G>A	p.R1125H	HSVSYPPGAVTEHKVKTDEVVTLTP[p.R1125H]HIGPKVSLSPGPEQKYETEGSSTTGF	TLTPHIGPK,EVVTLTPHI,LTPHIGPKV,DEVVTLTPH,TLTPHIGPKV,VTLTPHIGPK,TPHIGPKVSL,DEVVTLTPHI	CRC
VCAN	c.3923C>G	p.S1308C	SSPPATQPTRPPTVEDKEAFGPQAL[p.S1308C]CTPQPPASTKFHPDINVYIIEVRENK	ALCTPQPPA,CTPQPPASTK,KEAFGPQALC	CESC
VEZF1	c.1063_1064insACA	p.355_356insN	ETSNQKQQQQQQQQQQQQQQQQQQQH[p.355_356insN]NVTSWPGKQVETLRLWEEAVKARKKEAA	HNVTSWPGK,QQQQQHNVT,QQQQHNVTS,QQQHNVTSW,NVTSWPGKQV,QQQQQQQHNV,QQQQQQHNVT,QQQQHNVTSW,QQHNVTSWPG	STAD
VHL	c.115G>A	p.G39S	GAEEAGVEEYGPEEDGGEESGAEES[p.G39S]SPEESGPEELGAEEEMEAGRPRPVLR	SPEESGPEEL	KIRC
VHL	c.134C>T	p.P45L	VEEYGPEEDGGEESGAEESGPEESG[p.P45L]LEELGAEEEMEAGRPRPVLRSVNSRE	PEESGLEEL,LEELGAEEEM,EESGPEESGL	KIRC
VHL	c.194C>T	p.S65L	PEESGPEELGAEEEMEAGRPRPVLR[p.S65L]LVNSREPSQVIFCNRSPRVVLPVWLN	RPRPVLRLV,PVLRLVNSR,LVNSREPSQV,AGRPRPVLRL,RPRPVLRLVN	KIRC
VHL	c.221T>A	p.V74D	GAEEEMEAGRPRPVLRSVNSREPSQ[p.V74D]DIFCNRSPRVVLPVWLNFDGEPQPYP	PSQDIFCNR,DIFCNRSPR,SREPSQDIF,DIFCNRSPRV,NSREPSQDIF	KIRC

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VHL	c.232A>G	p.N78D	EMEAGRPRPVLRSVNSREPSQVIFC[p.N78D]DRSPRVVLPVWLNFDGEPQPYPTLPP	VIFCDRSPR,VIFCDRSPRV,QVIFCDRSPR	KIRC
VHL	c.236G>C	p.R79P	MEAGRPRPVLRSVNSREPSQVIFCN[p.R79P]PSPRVVLPVWLNFDGEPQPYPTLPPG	VIFCNPSPR,SQVIFCNPS,VIFCNPSPRV,QVIFCNPSPR,NPSPRVVLPV,SQVIFCNPSP,FCNPSPRVVL	KIRC
VHL	c.245G>C	p.R82P	GRPRPVLRSVNSREPSQVIFCNRSP[p.R82P]PVVLPVWLNFDGEPQPYPTLPPGTGR	RSPPVVLPV,SPPVVLPVW,VIFCNRSPPV,RSPPVVLPVW	KIRC
VHL	c.263G>T	p.W88L	LRSVNSREPSQVIFCNRSPRVVLPV[p.W88L]LLNFDGEPQPYPTLPPGTGRRIHSYR	VVLPVLLNF,SPRVVLPVL,RVVLPVLLNF,SPRVVLPVLL,RSPRVVLPVL	KIRC
VHL	c.266T>A	p.L89H	RSVNSREPSQVIFCNRSPRVVLPVW[p.L89H]HNFDGEPQPYPTLPPGTGRRIHSYRG	VVLPVWHNF,RVVLPVWHNF,HNFDGEPQPY	KIRC
VHL	c.266T>C	p.L89P	RSVNSREPSQVIFCNRSPRVVLPVW[p.L89P]PNFDGEPQPYPTLPPGTGRRIHSYRG	VVLPVWPNF,WPNFDGEPQ,RVVLPVWPNF	KIRC
VHL	c.320G>C	p.R107P	RVVLPVWLNFDGEPQPYPTLPPGTG[p.R107P]PRIHSYRGHLWLFRDAGTHDGLLVNQ	GTGPRIHSY,TLPPGTGPR,TGPRIHSYR,LPPGTGPRI,TLPPGTGPRI,GTGPRIHSYR	KIRC
VHL	c.332G>A	p.S111N	PVWLNFDGEPQPYPTLPPGTGRRIH[p.S111N]NYRGHLWLFRDAGTHDGLLVNQTELF	NYRGHLWLF,TGRRIHNYR,RIHNYRGHL,GTGRRIHNY,IHNYRGHLW,HNYRGHLWL,GTGRRIHNYR,HNYRGHLWLF,RIHNYRGHLW,NYRGHLWLFR,RRIHNYRGHL,IHNYRGHLWL	KIRC
VHL	c.333C>A	p.S111R	PVWLNFDGEPQPYPTLPPGTGRRIH[p.S111R]RYRGHLWLFRDAGTHDGLLVNQTELF	RYRGHLWLF,TGRRIHRYR,RIHRYRGHL,GTGRRIHRY,IHRYRGHLW,HRYRGHLWL,GTGRRIHRYR,HRYRGHLWLF,RIHRYRGHLW,RYRGHLWLFR,RRIHRYRGHL,IHRYRGHLWL	KIRC
VHL	c.343C>A	p.H115N	NFDGEPQPYPTLPPGTGRRIHSYRG[p.H115N]NLWLFRDAGTHDGLLVNQTELFVPSL	SYRGNLWLF,RIHSYRGNL,HSYRGNLWL,IHSYRGNLW,HSYRGNLWLF,RIHSYRGNLW,SYRGNLWLFR,RRIHSYRGNL,IHSYRGNLWL	KIRC
VHL	c.347delT	p.L116fs	DGEPQPYPTLPPGTGRRIHSYRGHL[p.L116fs]GSSEMQGHTMGFWLTKLNYLCHLSMLTDSLFLPISHCQCIL*	LTDSLFLPI,TMGFWLTKL,YLCHLSMLT,SMLTDSLFL,HLSMLTDSL,SLFLPISHC,FLPISHCQC,HTMGFWLTK,FWLTKLNYL,NYLCHLSML,RGHLGSSEM,GFWLTKLNY,EMQGHTMGF,LSMLTDSLF,LNYLCHLSM,SSEMQGHTM,SEMQGHTMG,MQGHTMGFW,TKLNYLCHL,LPISHCQCI,KLNYLCHLSM,MLTDSLFLPI,FLPISHCQCI,HTMGFWLTKL,GFWLTKLNYL,RIHSYRGHLG,LTKLNYLCHL,MGFWLTKLNY,LPISHCQCIL,SEMQGHTMGF,HLSMLTDSLF,HSYRGHLGSS,YRGHLGSSEM,GSSEMQGHTM,MQGHTMGFWL,LNYLCHLSML,CHLSMLTDSL,LSMLTDSLFL	KIRC
VHL	c.361G>T	p.D121Y	QPYPTLPPGTGRRIHSYRGHLWLFR[p.D121Y]YAGTHDGLLVNQTELFVPSLNVDGQP	RYAGTHDGL,RGHLWLFRY,WLFRYAGTH,RYAGTHDGLL,RGHLWLFRYA,YRGHLWLFRY,FRYAGTHDGL	KIRC
VHL	c.367delG	p.G123fs	PTLPPGTGRRIHSYRGHLWLFRDAG[p.G123fs]HTMGFWLTKLNYLCHLSMLTDSLFLPISHCQCIL*	LTDSLFLPI,TMGFWLTKL,YLCHLSMLT,SMLTDSLFL,WLFRDAGHT,HLSMLTDSL,SLFLPISHC,FLPISHCQC,HTMGFWLTK,FWLTKLNYL,NYLCHLSML,GFWLTKLNY,LSMLTDSLF,LFRDAGHTM,LNYLCHLSM,RDAGHTMGF,TKLNYLCHL,LPISHCQCI,WLFRDAGHTM,KLNYLCHLSM,MLTDSLFLPI,FLPISHCQCI,HTMGFWLTKL,GFWLTKLNYL,LTKLNYLCHL,MGFWLTKLNY,LPISHCQCIL,HLSMLTDSLF,FRDAGHTMGF,RDAGHTMGFW,LNYLCHLSML,CHLSMLTDSL,LSMLTDSLFL	KIRC
VHL	c.383T>A	p.L128H	PGTGRRIHSYRGHLWLFRDAGTHDG[p.L128H]HLVNQTELFVPSLNVDGQPIFANITL	HLVNQTELF,GHLVNQTEL,HLVNQTELFV,GHLVNQTELF	KIRC
VHL	c.405A>T	p.L135F	HSYRGHLWLFRDAGTHDGLLVNQTE[p.L135F]FFVPSLNVDGQPIFANITLPVYTLKE	LVNQTEFFV,EFFVPSLNV,GLLVNQTEF,LLVNQTEFF,NQTEFFVPS,LLVNQTEFFV,NQTEFFVPSL,GLLVNQTEFF,TEFFVPSLNV	KIRC
VHL	c.452T>C	p.I151T	DGLLVNQTELFVPSLNVDGQPIFAN[p.I151T]TTLPVYTLKERCLQVVRSLVKPENYR	FANTTLPVY,TTLPVYTLK,IFANTTLPV,NTTLPVYTL,QPIFANTTL,PIFANTTLPV,NTTLPVYTLK,IFANTTLPVY,GQPIFANTTL	KIRC

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VHL	c.458T>C	p.L153P	LLVNQTELFVPSLNVDGQPIFANIT[p.L153P]PPVYTLKERCLQVVRSLVKPENYRRL	IFANITPPV,ITPPVYTLK,FANITPPVY,NITPPVYTL,PIFANITPPV,NITPPVYTLK,IFANITPPVY,ANITPPVYTL	KIRC
VHL	c.472C>G	p.L158V	TELFVPSLNVDGQPIFANITLPVYT[p.L158V]VKERCLQVVRSLVKPENYRRLDIVRS	NITLPVYTV,ITLPVYTVK,TVKERCLQV,YTVKERCLQV,NITLPVYTVK,TVKERCLQVV	KIRC
VHL	c.473T>C	p.L158P	TELFVPSLNVDGQPIFANITLPVYT[p.L158P]PKERCLQVVRSLVKPENYRRLDIVRS	ITLPVYTPK,TPKERCLQV,NITLPVYTPK,YTPKERCLQV,TPKERCLQVV	KIRC
VHL	c.492delG	p.Q164fs	LNVDGQPIFANITLPVYTLKERCLQ[p.Q164fs]LSGA*	TLKERCLQL,KERCLQLSGA	KIRC
VHL	c.506T>C	p.L169P	GQPIFANITLPVYTLKERCLQVVRS[p.L169P]PVKPENYRRLDIVRSLYEDLEDHPNV	CLQVVRSPV,LQVVRSPVK,RSPVKPENY,PVKPENYRR,CLQVVRSPVK,VRSPVKPENY	KIRC
VHL	c.551T>C	p.L184P	KERCLQVVRSLVKPENYRRLDIVRS[p.L184P]PYEDLEDHPNVQKDLERLTQERIAHQ	RLDIVRSPY,SPYEDLEDH,RRLDIVRSPY	KIRC
VHL	c.563T>C	p.L188P	LQVVRSLVKPENYRRLDIVRSLYED[p.L188P]PEDHPNVQKDLERLTQERIAHQRMGD	YEDPEDHPNV	KIRC
VLDLR	c.692G>A	p.R231H	IPISWVCDDDADCSDQSDESLEQCG[p.R231H]HQPVIHTKCPASEIQCGSGECIHKKW	LEQCGHQPV,EQCGHQPVI,SLEQCGHQPV,CGHQPVIHTK,LEQCGHQPVI	BRCA
VMP1	c.1105G>C	p.E369Q	AQRQKLHHKSEMGTPQGENWLSWMF[p.E369Q]QKLVVVMVCYFILSIINSMAQSYAKR	WLSWMFQKL,WMFQKLVVV,FQKLVVVMV,NWLSWMFQK,SWMFQKLVV,MFQKLVVVM,WLSWMFQKLV,WMFQKLVVVM,NWLSWMFQKL,SWMFQKLVVV,MFQKLVVVMV,ENWLSWMFQK,LSWMFQKLVV,QKLVVVMVCY	LUAD
VPRBP	c.2405G>A	p.R802Q	ARLQKADVVAQSRISFPEKELLLLI[p.R802Q]QNHLISKGLGETATVLTKEADLPMTA	LLLLIQNHL,LLLIQNHLI,LIQNHLISK,KELLLLIQN,LLLLIQNHLI,IQNHLISKGL,LLIQNHLISK	UCEC
VPRBP	c.2817delA	p.K939fs	CNGRKIRVLRQKSDHGAYSQSPAIK[p.K939fs]NSWTDIFLPHLRWTV*	WTDIFLPHL,FLPHLRWTV,AIKNSWTDI,SWTDIFLPH,IKNSWTDIF,WTDIFLPHLR,SWTDIFLPHL,IFLPHLRWTV,AIKNSWTDIF,SQSPAIKNSW,IKNSWTDIFL	STAD
VPS13A	c.8647delT	p.F2883fs	ILGLDVLGNPFGLIREFSEGVEAFF[p.F2883fs]MNLTREPSRVLKSLWKEWH*	NLTREPSRV,LTREPSRVL,EAFFMNLTR,MNLTREPSR,EPSRVLKSL,SEGVEAFFM,FMNLTREPS,VLKSLWKEW,VEAFFMNLT,FSEGVEAFFM,LTREPSRVLK,RVLKSLWKEW,PSRVLKSLWK,FMNLTREPSR,EGVEAFFMNL,REPSRVLKSL,EPSRVLKSLW	STAD
VPS13B	c.2075G>A	p.R692Q	IMGEKNSSNFMNTTNFQSLRPLPSI[p.R692Q]QILVDKINLEHSVPMYAEQLVHVVSS	RPLPSIQIL,SLRPLPSIQI,RPLPSIQILV,IQILVDKINL	UCEC
VPS13B	c.7723G>T	p.G2575W	AQADCKLLECRNVTMQSVVKPFSIF[p.G2575W]WQMAVSSDVVEKLLDCTVIVDSVFVN	FSIFWQMAV,WQMAVSSDV,KPFSIFWQM,WQMAVSSDVV,FSIFWQMAVS,VKPFSIFWQM,KPFSIFWQMA	LUAD
VPS13C	c.4075G>T	p.D1359Y	SWYHKVPVVEIKGHLDSMNVSLNQE[p.D1359Y]YLNLLFRILTENLCEGTEDLDKVKPR	SLNQEYLNL,YLNLLFRIL,EYLNLLFRI,MNVSLNQEY,NVSLNQEYL,NQEYLNLLF,SLNQEYLNLL,YLNLLFRILT,EYLNLLFRIL,SMNVSLNQEY,MNVSLNQEYL,LNQEYLNLLF,QEYLNLLFRI	CRC
VWA2	c.950G>A	p.G317D	RTTCPGPCDSQPCQNGGTCVPEGLD[p.G317D]DYQCLCPLAFGGEANCALKLSLECRV	DDYQCLCPL,DYQCLCPLAF	TGCT
VWA3A	c.2863G>A	p.V955I	LEKVLRRYVQRLQWLLSGSRRLFGT[p.V955I]ILESKVCILLDTSGSMGPYLQQVKTE	RLFGTILES,ILESKVCIL,GSRRLFGTI,SRRLFGTIL,ILESKVCILL,RLFGTILESK,GSRRLFGTIL	BRCA
VWA3B	c.1670G>T	p.R557L	QFIQEQLKYKSKFNFVKFDGQAVAW[p.R557L]LEQLAEVNEDNLEQAQSWIRDIKIGS	QAVAWLEQL,VAWLEQLAEV,GQAVAWLEQL	LUAD
VWA7	c.2375T>G	p.V792G	FSLTSNLSRAHLELNESAWGRLWLE[p.V792G]GPDSAAPDSVVMVTVTAGGREANPVP	RLWLEGPDSA	TGCT

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VWF	c.5160A>T	p.K1720N	LLDGSSSFPASYFDEMKSFAKAFIS[p.K1720N]NANIGPRLTQVSVLQYGSITTIDVPW	FAKAFISNA,ISNANIGPR,KAFISNANI,KSFAKAFISN,SFAKAFISNA,FISNANIGPR,AKAFISNANI,ISNANIGPRL	BRCA
WAPAL	c.1564delA	p.R522fs	GFDDLSESEDDEDDDCQVERKTSKK[p.R522fs]ELKQLHHPPCSLPQKAMIIPRTVSLVLTMQRTCLVCLKV*	MIIPRTVSL,IIPRTVSLV,LTMQRTCLV,QLHHPPCSL,SLPQKAMII,MQRTCLVCL,VSLVLTMQR,KAMIIPRTV,RTVSLVLTM,IPRTVSLVL,KQLHHPPCSL,AMIIPRTVSL,MIIPRTVSLV,VLTMQRTCLV,MQRTCLVCLK,TVSLVLTMQR,VERKTSKKEL,TMQRTCLVCL,KELKQLHHPP	STAD
WASF3	c.913_914insC	p.P305fs	EHEYRPPSASARHMALNRPQQPPPP[p.P305fs]ASPSGPRGVPGLCTDGSSRLRDAPSADN*	SSRLRDAPS,RPQQPPPPA,GLCTDGSSRL,SSRLRDAPSA,RPQQPPPPAS,SPSGPRGVPG	STAD
WASH3P	c.523G>A	p.G175S	APREVVDPSGGRATLLESIRQAGGI[p.G175S]SKAKLRSMKERKLEKKQQKEQEQVRA	RQAGGISKA,ISKAKLRSM,SIRQAGGISK,RQAGGISKAK,ISKAKLRSMK	GBM,KIRC,PRAD,SKCM
WASH3P	c.559C>G	p.L187V	ATLLESIRQAGGIGKAKLRSMKERK[p.L187V]VEKKQQKEQEQVRATSQGGHLMSDLF	SMKERKVEK,RSMKERKVEK,SMKERKVEKK,KLRSMKERKV	PRAD,TGCT
WBP1	c.412_413insC	p.P138fs	LRFLSTFKPPAYEDVVHRPGTPPPP[p.P138fs]LYCGPRPPLDCFQ*	LYCGPRPPL,RPGTPPPPL,GPRPPLDCF	STAD
WBSCR17	c.682C>T	p.R228C	LEEYVHKRYPGLVKVVRNQKREGLI[p.R228C]CARIEGWKVATGQVTGFFDAHVEFTA	REGLICARI,LICARIEGWK	CRC
WDFY3	c.5525delT	p.L1842fs	FIFGVPASSGTVVSSIHNVCTEAVF[p.L1842fs]YYWECSAAC*	CTEAVFYYW,YYWECSAAC,EAVFYYWEC,FYYWECSAA,AVFYYWECSA,HNVCTEAVFY,TEAVFYYWEC	STAD
WDR17	c.832C>T	p.P278S	SESLSCITTFNLPSAAASVQCLAWV[p.P278S]SSAPGMFITGDSQVGVLRIWNVSRTT	AWVSSAPGM,WVSSAPGMF,WVSSAPGMFI,AWVSSAPGMF,LAWVSSAPGM,VQCLAWVSSA	CESC
WDR3	c.2521G>A	p.E841K	KSSELEESLLVLPFSYVPDILKLFN[p.E841K]KFIQLGSDVELICRCLFFLLRIHFGQ	KLFNKFIQL,LKLFNKFIQL	CRC
WDR34	c.178T>G	p.W60G	PGPLQDETLGVASVPSQWRAVQGIR[p.W60G]GETKSCQTASIATASASAQARNHVDA	GETKSCQTA,AVQGIRGETK	ACC
WDR5	c.642delC	p.N214fs	DGLCRIWDTASGQCLKTLIDDDNPP[p.N214fs]CLL*	TLIDDDNPPC	STAD
WDR59	c.2509C>A	p.R837S	EHLSSPWGESSPEELRFGSLTYSDP[p.R837S]SERERDQHDKNKRLLDPANTQQFDDF	LTYSDPSER	LUAD
WDR59	c.479delA	p.N160fs	IKDTRKPTVALSAVAGASQVKWNKK[p.N160fs]MLTALPPAMTAMCGYGIRGNPVQQWNI*	KMLTALPPA,MLTALPPAM,ALPPAMTAM,KWNKKMLTA,PAMTAMCGY,TAMCGYGIR,MTAMCGYGI,WNKKMLTAL,SQVKWNKKM,KKMLTALPP,KMLTALPPAM,AMTAMCGYGI,MLTALPPAMT,ALPPAMTAMC,MTAMCGYGIR,KWNKKMLTAL,LTALPPAMTA,TALPPAMTAM,SQVKWNKKML,VKWNKKMLTA,KKMLTALPPA,PPAMTAMCGY	STAD
WDR60	c.1235delA	p.Q412fs	DGDDDESSNEPESREKLEELPLAQK[p.Q412fs]RKYKKFKELLMQKMKGLASYL*	LLMQKMKGL,KMKGLASYL,KYKKFKELL,LAQKRKYKK,KFKELLMQK,QKMKGLASY,RKYKKFKEL,MQKMKGLAS,AQKRKYKKF,YKKFKELLM,FKELLMQKM,LPLAQKRKY,LLMQKMKGLA,KYKKFKELLM,AQKRKYKKFK,KFKELLMQKM,MQKMKGLASY,LAQKRKYKKF,RKYKKFKELL,QKMKGLASYL	STAD
WDR7	c.784delG	p.G262fs	RVFDAGDYSLLCSGPSENGQTWTGG[p.G262fs]TLSHQIKSSFGQKMGKVIFTNYLPVAFQLVIHSAVMWGRQLKI*	FTNYLPVAF,VIFTNYLPV,YLPVAFQLV,FQLVIHSAV,VMWGRQLKI,QIKSSFGQK,SSFGQKMGK,AVMWGRQLK,NYLPVAFQL,MGKVIFTNY,LPVAFQLVI,LSHQIKSSF,QLVIHSAVM,GQTWTGGTL,HQIKSSFGQ,IKSSFGQKM,GQKMGKVIF,GKVIFTNYL,LVIHSAVMW,SAVMWGRQL,KVIFTNYLPV,VIFTNYLPVA,YLPVAFQLVI,HQIKSSFGQK,KSSFGQKMGK,KMGKVIFTNY,VIHSAVMWGR,SAVMWGRQLK,IFTNYLPVAF,NYLPVAFQLV,MGKVIFTNYL,AVMWGRQLKI,WTGGTLSHQI,SSFGQKMGKV,TLSHQIKSSF,FQLVIHSAVM,FGQKMGKVIF,VAFQLVIHSA,HSAVMWGRQL,LPVAFQLVIH	STAD

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WDR73	c.944_961delATGGAACACGGAGCCAAG	p.DGTRSQ315del	CLAISGFDGTVQVYDATSWDGTRSQ[p.DGTRSQ315del]VEPLFTHRGHIFLDGNGMDPAPLVTTHTWHPCRPRTLLSATND	TSWDGTRSQV	KIRC
WDR75	c.860C>A	p.P287Q	SLLSGGRESVLVEWRDATEKNKEFL[p.P287Q]QRLGATIEHISVSPAGDLFCTSHSDN	FLQRLGATI,KEFLQRLGA,EFLQRLGATI,KEFLQRLGAT,LQRLGATIEH	LUAD
WDR78	c.330T>A	p.N110K	NQSRMAVSKTVLIPPELKTVEKPNP[p.N110K]KIKTTQVFDINGTDVTPRPLYHPDPL	KTVEKPNPK,KIKTTQVFD,NPKIKTTQV,PKIKTTQVF,KIKTTQVFDI,NPKIKTTQVF	CLL
WDR88	c.298G>T	p.G100W	KHQVPEKLIWGDQDPLSKIPFKILS[p.G100W]WHEHAVSTCHFCVDDTKLLSGSYDCT	KILSWHEHA,ILSWHEHAV,KIPFKILSW,FKILSWHEH,KILSWHEHAV,SKIPFKILSW,FKILSWHEHA	LUAD
WDTC1	c.861_862insG	p.M287fs	RLRVLVATYVTFSPNGTELLVNMGG[p.M287fs]GTGLFV*	NMGGGTGLF,VNMGGGTGL,NMGGGTGLFV,VNMGGGTGLF	STAD
WHSC1L1	c.1254_1255insA	p.K418fs	YIDKQPEEALSQAKKSVASKTEVKK[p.K418fs]NPTTKICAEYSARTDQCRGGGLLTLKY*	PTTKICAEY,KICAEYSAR,RGGGLLTLK,GGGLLTLKY,CRGGGLLTL,TTKICAEYSA,RGGGLLTLKY,EYSARTDQCR,NPTTKICAEY,AEYSARTDQC	STAD
WNK4	c.1816delG	p.G606fs	CETDGYLSSSGFLDASDPALQPPGG[p.G606fs]CHPAWLSPISACPRLLPYPFHVLALEVTFPPGTAMPQMQLQALAMWEKGWDK*	RLLPYPFHV,LLPYPFHVL,AMPQMQLQA,AMWEKGWDK,SACPRLLPY,LQALAMWEK,PYPFHVLAL,HVLALEVTF,MQLQALAMW,EVTFPPGTA,SPISACPRL,CPRLLPYPF,MPQMQLQAL,VTFPPGTAM,QMQLQALAM,HPAWLSPIS,LPYPFHVLA,LEVTFPPGT,ISACPRLLPY,RLLPYPFHVL,LLPYPFHVLA,AMPQMQLQAL,QLQALAMWEK,LAMWEKGWDK,WLSPISACPR,YPFHVLALEV,EVTFPPGTAM,HPAWLSPISA,SPISACPRLL,LPYPFHVLAL,FPPGTAMPQM,MPQMQLQALA,LQPPGGCHPA,FHVLALEVTF,LEVTFPPGTA,PQMQLQALAM,QMQLQALAMW,QPPGGCHPAW,QALAMWEKGW	STAD
WNT1	c.500delG	p.W167fs	SEGSIESCTCDYRRRGPGGPDWHWG[p.W167fs]AAATTLTSAASSAGSSWTPGRRGGTCASS*	TLTSAASSA,GPDWHWGAA,WHWGAAATT,HWGAAATTL,AASSAGSSW,SAGSSWTPGR,TTLTSAASSA,GPDWHWGAAA,SAASSAGSSW,WHWGAAATTL,AAATTLTSAA	STAD
WNT11	c.1031G>A	p.C344Y	NPYTDRVVERCHCKYHWCCYVTCRR[p.C344Y]YERTVERYVCK*	CCYVTCRRY,RYERTVERY,YVTCRRYER,YERTVERYV,RRYERTVERY,CYVTCRRYER,YERTVERYVC	OV
WNT16	c.494delG	p.W165fs	GNMTECSCDTTLQNGGSASEGWHWG[p.W165fs]AAPMMSSMACGSAESS*	MMSSMACGS,SMACGSAES,MSSMACGSA,APMMSSMAC,GAAPMMSSM,SEGWHWGAA,GWHWGAAPM,WHWGAAPMM,MMSSMACGSA,SASEGWHWGA,EGWHWGAAPM,WGAAPMMSSM,GWHWGAAPMM,SMACGSAESS	STAD
WNT5B	c.979A>G	p.K327E	RLCNKTSEGMDGCELMCCGRGYNQF[p.K327E]ESVQVERCHCKFHWCCFVRCKKCTEI	RGYNQFESV,QFESVQVER,NQFESVQVE,NQFESVQVER	TGCT
WT1	c.1142_1143insCGGTC	p.S381fs	HTHGVFRGIQDVRRVPGVAPTLVRS[p.S381fs]GRHLRPVRNAPSCVLTQAAIRDILSCPTYRCTAGSTLVRNHTSVTSRTVNEGFLVQTSSKDTKGDIQV*	TLVRNHTSV,CTAGSTLVR,LVRSGRHLR,RSGRHLRPV,SGRHLRPVR,LVRNHTSVT,RNHTSVTSR,HTSVTSRTV,GFLVQTSSK,RDILSCPTY,CVLTQAAIR,DILSCPTYR,RPVRNAPSC,TLVRSGRHL,VRNAPSCVL,TQAAIRDIL,YRCTAGSTL,TSRTVNEGF,LVQTSSKDTK,TYRCTAGSTL,RSGRHLRPVR,HLRPVRNAPS,STLVRNHTSV,TSRTVNEGFL,TLVRSGRHLR,RPVRNAPSCV,APSCVLTQAA,IRDILSCPTY,VTSRTVNEGF	LAML
WWP2	c.1373G>C	p.G458A	EDPRTQGMIQEPALPPGWEMKYTSE[p.G458A]AVRYFVDHNTRTTTFKDPRPGFESGT	EMKYTSEAV,KYTSEAVRY,YTSEAVRYF,TSEAVRYFV,WEMKYTSEA,YTSEAVRYFV,KYTSEAVRYF,MKYTSEAVRY,EMKYTSEAVR,WEMKYTSEAV,SEAVRYFVDH	KIRC
XAB2	c.2344G>A	p.E782K	SDLAPGQSGMDDMKLLEQRAEQLAA[p.E782K]KAERDQPLRAQSKILFVRSDASREEL	EQLAAKAER,AKAERDQPL,EQRAEQLAAK	BLCA
XDH	c.1228C>T	p.P410S	MDHTFFPGYRKTLLSPEEILLSIEI[p.P410S]SYSREGEYFSAFKQASRREDDIAKVT	ISYSREGEY,LSIEISYSR,SYSREGEYF,ILLSIEISY,IEISYSREG,ISYSREGEYF,LLSIEISYSR,EILLSIEISY,EEILLSIEIS	TGCT
XIRP2	c.7315G>A	p.D2439N	GKTGVLPPPTLPKPKLPKHIKDNKN[p.D2439N]NFSPKVELATSLSDMECKITTSKDQK	KDNKNNFSPK,KHIKDNKNNF	SKCM
XIRP2	c.9023T>A	p.V3008E	IPGWLISEDKREYAVHIAMENNLEK[p.V3008E]EKEEITHIKTQAEDMLVSYENIIQTA	KEKEEITHI	CLL

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XKR6	c.803G>A	p.R268Q	SVIHLLQMGQVWRYIRTMYLGIQSQ[p.R268Q]QRKEHQRRFYWAMMYEYADVNMLRLL	MYLGIQSQQR,QQRKEHQRRF	CRC
XPO1	c.1711G>A	p.E571K	QYPRFLRAHWKFLKTVVNKLFEFMH[p.E571K]KTHDGVQDMACDTFIKIAQKCRRHFV	KLFEFMHKT,FMHKTHDGV,KTHDGVQDM,KLFEFMHKTH,VNKLFEFMHK,KTHDGVQDMA,EFMHKTHDGV,FMHKTHDGVQ,HKTHDGVQDM	BRCA,CLL
XPOT	c.1621C>T	p.R541W	EPQHIPCVLMAFLDHRGLRHSSAKV[p.R541W]WSRTAYLFSRFVKSLNKQMNPFIEDI	KVWSRTAYL,HSSAKVWSR,VWSRTAYLF,SAKVWSRTA,WSRTAYLFS,AKVWSRTAY,LRHSSAKVW,KVWSRTAYLF,SAKVWSRTAY,WSRTAYLFSR,GLRHSSAKVW,AKVWSRTAYL	CRC
XYLB	c.260C>T	p.S87F	TSPVLMWVQALDIILEKMKASGFDF[p.S87F]FQVLALSGAGQQHGSIYWKAGAQQAL	FQVLALSGA,MKASGFDFF,SGFDFFQVL,FDFFQVLAL,KASGFDFFQV,KMKASGFDFF,FQVLALSGAG	BLCA
XYLT2	c.1578delC	p.Y526fs	RKFESTVNQEVLEILDFHLYGSYPP[p.Y526fs]ARQPSRPTGRTPTTRLMAPVGSVMSCSLLTQPSPASACTMPPLLHPQWAPHSAGLSPGACRPACTCISMTTISRATW*	HLYGSYPPA,RLMAPVGSV,SLLTQPSPA,LMAPVGSVM,CISMTTISR,RTPTTRLMA,TTRLMAPVG,ASACTMPPL,ISMTTISRA,LYGSYPPAR,PTTRLMAPV,HSAGLSPGA,RPTGRTPTT,HPQWAPHSA,SPGACRPAC,RPACTCISM,LLHPQWAPH,GSVMSCSLL,MTTISRATW,MPPLLHPQW,RLMAPVGSVM,LLTQPSPASA,GLSPGACRPA,HLYGSYPPAR,TMPPLLHPQW,TGRTPTTRLM,ASACTMPPLL,SYPPARQPSR,TCISMTTISR,TPTTRLMAPV,QPSPASACTM,HPQWAPHSAG,APHSAGLSPG,RPACTCISMT,FHLYGSYPPA,PQWAPHSAGL,SMTTISRATW,MPPLLHPQWA	STAD
YBX1	c.749C>T	p.P250L	GAGEQGRPVRQNMYRGYRPRFRRGP[p.P250L]LRQRQPREDGNEEDKENQGDETQGQQ	RFRRGPLRQ,RPRFRRGPL,RPRFRRGPLR,RFRRGPLRQR	KIRP
YBX2	c.677delC	p.P226fs	SAGTGPGSKGERAEDSGQRPRRWCP[p.P226fs]HPSSTDGGLCEAPGLPTSSSL*	RWCPHPSST,HPSSTDGGL,CEAPGLPTS,GQRPRRWCPH,RPRRWCPHPS,APGLPTSSSL,RRWCPHPSST,CEAPGLPTSS	STAD
YIF1A	c.391delC	p.R131fs	LGLLVFPYTHQNWEVQYSRDAPLPP[p.R131fs]GKTSTPLTSISPRWPSLLTCSWLGWHWAFRKGSPRRCWACVQAQRWCGW*	KTSTPLTSI,SISPRWPSL,LGWHWAFRK,WLGWHWAFR,ISPRWPSLL,SWLGWHWAF,AFRKGSPRR,KGSPRRCWA,TPLTSISPR,WAFRKGSPR,CWACVQAQR,PPGKTSTPL,SPRWPSLLT,SPRRCWACV,LLTCSWLGW,RKGSPRRCW,VQAQRWCGW,WPSLLTCSW,WACVQAQRW,SISPRWPSLL,WLGWHWAFRK,STPLTSISPR,SWLGWHWAFR,RWPSLLTCSW,SLLTCSWLGW,CSWLGWHWAF,CWACVQAQRW,TSISPRWPSL,HWAFRKGSPR,WAFRKGSPRR,APLPPGKTST,LPPGKTSTPL,SPRWPSLLTC,WPSLLTCSWL,GKTSTPLTSI,TPLTSISPRW	STAD
YLPM1	c.3533delA	p.E1178fs	RGLGRSDFGRDRGPFRPEPGDGGEK[p.E1178fs]CIHITGMSLLGLHGTMEKSEGMKSFH*	LGLHGTMEK,TMEKSEGMK,CIHITGMSL,IHITGMSLL,SLLGLHGTM,EKSEGMKSF,CIHITGMSLL,HITGMSLLGL,GMSLLGLHGT,LLGLHGTMEK,GTMEKSEGMK,MEKSEGMKSF,MSLLGLHGTM,GEKCIHITGM,KCIHITGMSL	STAD
YTHDC2	c.1900G>A	p.E634K	IMHLLYNICHSCDAGAVLIFLPGYD[p.E634K]KIVGLRDRILFDDKRFADSTHRYQVF	FLPGYDKIV,LIFLPGYDK,IFLPGYDKI,VLIFLPGYDK,LPGYDKIVGL	CRC
YTHDC2	c.553G>A	p.E185K	NREMSKTSGRLNNGIPQIPVKRGES[p.E185K]KFDSFRQSLPVFEKQEEIVKIIKENK	RGESKFDSF,IPVKRGESKF,KRGESKFDSF,SKFDSFRQSL	UCEC
ZAR1	c.126G>C	p.Q42H	CPPCSYRYPYPAATKGKGAAGGSWQ[p.Q42H]HRGRGCLPASSPCSAGAASLSFPGCG	WQHRGRGCL,WQHRGRGCLP	ACC
ZBBX	c.1787G>T	p.R596I	TKSSLLLQEIACRSKPITKQYQGLE[p.R596I]IFFIFDTNERLNLLPSHRLECNNSST	YQGLEIFFI,KQYQGLEIF,QYQGLEIFF,QGLEIFFIF,TKQYQGLEI,LEIFFIFDT,KQYQGLEIFF,QYQGLEIFFI,YQGLEIFFIF,ITKQYQGLEI,IFFIFDTNER,TKQYQGLEIF	CRC
ZBBX	c.453_455delAGA	p.E151del	KPKINGKVCGQCENKAALLVCLECG[p.E151del]DYCSGCFAKVHQKGALKLHRTTLLQAKS	LVCLECGDY,LLVCLECGDY	STAD
ZBED4	c.1154C>T	p.S385L	PSLLPPEGELSSVSSSPVKPVRESP[p.S385L]LASSSPDRLTEDLQSHLNPGDGLMED	RESPLASSS,RESPLASSSP	CESC

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ZBTB20	c.2075delC	p.P692fs	CKKKFSHKTLLERHVALHSASNGTP[p.P692fs]LQAHPQVPALAPQAWWPARRGPLTSAPSAQQSLTKSSSSTTT*	APQAWWPAR,HSASNGTPL,LAPQAWWPA,TPLQAHPQV,WPARRGPLT,WWPARRGPL,LQAHPQVPA,QAHPQVPAL,VPALAPQAW,LQAHPQVPAL,ALAPQAWWPA,AWWPARRGPL,LAPQAWWPAR,APQAWWPARR,WPARRGPLTS,LHSASNGTPL,TSAPSAQQSL,AQQSLTKSSS,VPALAPQAWW	STAD
ZBTB24	c.1819C>A	p.L607I	QNMTADQAANLTLLTQQPEQLQNLI[p.L607I]ISAQQEQTEHIQSLNMIESQMGP5QT	QLQNLIISA,LQNLIISAQ,EQLQNLIISA,QPEQLQNLII	CRC
ZBTB40	c.786_787insA	p.L262fs	QLNFLLENEGVFSDALMVTQDVLKK[p.L262fs]TRNVFRN*	VLKKTRNVF,VLKKTRNVFR,VTQDVLKKTR	STAD
ZBTB7C	c.1025_1026insG	p.G342fs	ELPPPPPPPFPNDFFKDMFPDLPGG[p.G342fs]ASGTHQGGERLRCLSQLPECHPPGRPLPTLAPGRRAQAEAQGLSAVPHLPQSHHGGREAAAAHEDPYRGEAIHVHHLRGPLHQAGQAENPHAEAHRGAALPVHPLQRQVRAQLRPQEPHAHPHGRAALPVRVLLQELHAL*	VLLQELHAL,HLRGPLHQA,RLRCLSQLP,HVHHLRGPL,QLRPQEPHA,HAHPHGRAA,HGRAALPVR,AALPVRVLL,RVLLQELHA,AAAAHEDPY,EAIHVHHLR,HPPGRPLPT,RPLPTLAPG,HAEAHRGAA,HPLQRQVRA,LQRQVRAQL,RAALPVRVL,SQLPECHPP,RAQAEAQGL,AEAQGLSAV,AQGLSAVPH,SHHGGREAA,GEAIHVHHL,AENPHAEAH,AEAHRGAAL,AHRGAALPV,GAALPVHPL,RQVRAQLRP,AQLRPQEPH,FPDLPGGAS,DPYRGEAIH,DMFPDLPGGA,TLAPGRRAQA,AQAEAQGLSA,GQAENPHAEA,AAAAHEDPYR,AALPVHPLQR,RLRCLSQLPE,HVHHLRGPLH,LQRQVRAQLR,HAHPHGRAAL,HGRAALPVRV,RAALPVRVLL,RVLLQELHAL,HLPQSHHGGR,EAHRGAALPV,HPPGRPLPTL,APGRRAQAEA,HAEAHRGAAL,LPVHPLQRQV,RPQEPHAHPH,HPHGRAALPV,LPVRVLLQEL,EAAAAHEDPY,HQGGERLRCL,GERLRCLSQL,SQLPECHPPG,RRAQAEAQGL,AQGLSAVPHL,HEDPYRGEAI,IHVHHLRGPL,HQAGQAENPH,AHRGAALPVH,RGAALPVHPL,RQVRAQLRPQ,AQLRPQEPHA,GRAALPVRVL,FPDLPGGASG,AEAQGLSAVP,DPYRGEAIHV	STAD
ZBTB7C	c.460delG	p.D154fs	ILNAARMLEIQCIVNVCLEIMEPGG[p.D154fs]TGGRRMTRRTMTTTKMMMMRRTKRRRRKRRRMTMMTRRTLLTKKTCLTPRTSAATKALPRQTISQRRPIQTPPGTSLTPSRLAVLAIWG*	TMMTRRTLL,SLTPSRLAV,CLTPRTSAA,KMMMMRRTK,MMMMRRTKR,MMMRRTKRR,MTRRTLLTK,GTGGRRMTR,TTTKMMMMR,TTKMMMMRR,SAATKALPR,RMTRRTMTT,MTRRTMTTT,TRRTMTTTK,RTMTTTKMM,MMRRTKRRR,RTKRRRRKR,RRRMTMMTR,MTMMTRRTL,RTSAATKAL,MTTTKMMMM,QTISQRRPI,RRKRRRMTM,TLLTKKTCL,IQTPPGTSL,RRTMTTTKM,TMTTTKMMM,RKRRRMTMM,TKALPRQTI,SQRRPIQTP,SRLAVLAIW,TMMTRRTLLT,CLTPRTSAAT,SLTPSRLAVL,MTRRTMTTTK,KMMMMRRTKR,MMMMRRTKRR,MMMRRTKRRR,MMTRRTLLTK,MTRRTLLTKK,MTTTKMMMMR,TTTKMMMMRR,LTPRTSAATK,TSAATKALPR,RTMTTTKMMM,MMRRTKRRRR,MRRTKRRRRK,RTKRRRRKRR,RRRKRRRMTM,KRRRMTMMTR,RRRMTMMTRR,RMTMMTRRTL,MTMMTRRTLL,RTLLTKKTCL,LTKKTCLTPR,KTCLTPRTSA,ATKALPRQTI,RQTISQRRPI,TPRTSAATKA,TPSRLAVLAI,RRKRRRMTMM,RMTRRTMTTT,TRRTMTTTKM,RRTMTTTKMM,TMTTTKMMMM,SQRRPIQTPP,IQTPPGTSLT	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZBTB7C	c.469delG	p.E157fs	AARMLEIQCIVNVCLEIMEPGGDGG[p.E157fs]RRMTRRTMTTTKMMMMRRTKRRRRKRRRMTMMTRRTLLTKKTCLTPRTSAATKALPRQTISQRRPIQTPPGTSLTPSRLAVLAIWG*	TMMTRRTLL,SLTPSRLAV,CLTPRTSAA,KMMMMMRRTK,MMMMRRTKR,MMMRRTKRR,MTRRTLLTK,TTTKMMMMR,TTKMMMMRR,SAATKALPR,RMTRRTMTT,MTRRTMTTT,TRRTMTTTK,RTMTTTKMM,MMRRTKRRR,RTKRRRRKR,RRRMTMMTR,MTMMTRRTL,RTSAATKAL,MTTTKMMMM,QTISQRRPI,RRKRRRMTM,TLLTKKTCL,IQTPPGTSL,RRTMTTTKM,TMTTTKMMM,RKRRRMTMM,TKALPRQTI,SQRRPIQTP,SRLAVLAIW,TMMTRRTLLT,CLTPRTSAAT,SLTPSRLAVL,MTRRTMTTTK,KMMMMRRTKR,MMMMRRTKRR,MMMRRTKRRR,MMTRRTLLTK,MTRRTLLTKK,MTTTKMMMMR,TTTKMMMMRR,LTPRTSAATK,TSAATKALPR,RTMTTTKMMM,MMRRTKRRRR,MRRTKRRRRK,RTKRRRRKRR,RRRKRRRMTM,KRRRMTMMTR,RRRMTMMTRR,RMTMMTRRTL,MTMMTRRTLL,RTLLTKKTCL,LTKKTCLTPR,KTCLTPRTSA,ATKALPRQTI,RQTISQRRPI,TPRTSAATKA,TPSRLAVLAI,RRKRRRMTMM,RMTRRTMTTT,TRRTMTTTKM,RRTMTTTKMM,TMTTTKMMMM,SQRRPIQTPP,IQTPPGTSLT	STAD
ZC3H12D	c.1213C>T	p.P405S	SAGGRVPGPLSLPSPESQFSPGDLP[p.P405S]SPPGLQLQPRGEHRPRDLHGDLLSPR	LPSPPGLQL,SQFSPGDLPS	ACC
ZC3H13	c.3018delA	p.K1006fs	NIETTSEDGQVFSPKKGQKKKSIEK[p.K1006fs]NVKNPKVILIFLMKKQPSKVRRKEAHGLPL*	LMKKQPSKV,KVILIFLMK,VILIFLMKK,FLMKKQPSK,KNPKVILIF,KQPSKVRRK,KVRRKEAHG,RKEAHGLPL,FLMKKQPSKV,KVILIFLMKK,SIEKNVKNPK,IFLMKKQPSK,LMKKQPSKVR,KVRRKEAHGL,RRKEAHGLPL,QPSKVRRKEA,VKNPKVILIF,NPKVILIFLM,IEKNVKNPKV	STAD
ZC3H18	c.2102_2103insC	p.T701fs	PVPEPTKPGDPREARRKERPARTPP[p.T701fs]QEADAKRQRQWQW*	AKRQRQWQW,RTPPQEADAK,RPARTPPQEA	STAD
ZC3H18	c.2473delC	p.P825fs	PKSAKPPAGGKSSQQPSTPQQAPPG[p.P825fs]SPSRAHLWPTRRSS*	RAHLWPTRR,QQAPPGSPS,PSRAHLWPTR,RAHLWPTRRS,SPSRAHLWPT	STAD
ZC3H4	c.2392G>A	p.E798K	IQQKQQEEEERARRLAESSKQDREN[p.E798K]KEGDTGNWYSSDEDEGGSSVTSILKT	SSKQDRENK,KEGDTGNWY	BLCA
ZC3H7A	c.1724G>C	p.C575S	NGKINLTVFKLLQEHLGEFIFLCEK[p.C575S]SFDHKPRMISKRNKDNSTACSHPVTK	KSFDHKPRM,FIFLCEKSF,EFIFLCEKSF,KSFDHKPRMI,GEFIFLCEKS	TGCT
ZCCHC6	c.2811A>T	p.K937N	GKHVERALLVELNKISLKEENVCEE[p.K937N]NNSPVDQSDFFYEFSKLIFTKGKSPT	NVCEENNSPV	KIRC
ZCRB1	c.228A>T	p.L76F	KGVAFILFLDKDSAQNCTRAINNKQ[p.L76F]FFGRVIKASIAIDNGRAAEFIRRRNY	KQFFGRVIK,RAINNKQFF,INNKQFFGR,NKQFFGRVI,AINNKQFFGR,FFGRVIKAS,RAINNKQFFG,KQFFGRVIKA,CTRAINNKQF	CLL
ZCWPW2	c.430G>A	p.D144N	DRFKGKYVTYDPDGNVEEYHIEFLG[p.D144N]NPHSRSWIKATFVGHYSITLKPEKCK	EFLGNPHSR,LGNPHSRSW,IEFLGNPHS,YHIEFLGNPH,FLGNPHSRSW	CRC
ZDHHC11	c.750C>G	p.H250Q	PVQVQTLIVVIIGMLVLLLDFLGLV[p.H250Q]QLGQLLIFHIYLKAKKMTTFEYLINN	GLVQLGQLL,VQLGQLLIF,LDFLGLVQL,LLDFLGLVQL,FLGLVQLGQL,QLGQLLIFHI,GLVQLGQLLI,LVQLGQLLIF	TGCT
ZDHHC4	c.899G>A	p.R300H	LFVLYLAATNQTTNEWYRGDWAWCQ[p.R300H]HCPLVAWPPSAEPQVHRNIHSHGLRS	WAWCQHCPL,CQHCPLVAW,WAWCQHCPLV	GBM
ZDHHC5	c.1947_1949delAGA	p.E651del	PTAPYLGRSMSYSSQKAQPGVSETE[p.E651del]VALQPLLTPKDEVQLKTTYSKSNGQPKS	ETEVALQPL,TEVALQPLL,AQPGVSETEV,ETEVALQPLL,SETEVALQPL,TEVALQPLLT	STAD
ZDHHC7	c.948delC	p.P316fs	LKSEKPTWERRLRWEGMKSVFGGPP[p.P316fs]HSSG*	KSVFGGPPH,MKSVFGGPPH	STAD
ZEB2	c.3280G>A	p.E1094K	SYSQHMNHRYSYCKREAEEREAAER[p.E1094K]KAREKGHLEPTELLMNRAYLQSITPQ	KAREKGHLE,KAREKGHLEP	CESC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZEB2	c.467G>A	p.R156H	NNGTVKNANCTSDFEEYFAKRKLEE[p.R156H]HDGHAVSIEEYLQRSDTAIIYPEAPE	LEEHDGHAV,EEHDGHAVS,KLEEHDGHAV,EEHDGHAVSI	CRC
ZFAND2B	c.446T>C	p.I149T	IKHRHPLDHDCSGEGHPTSRAGLAA[p.I149T]TSRAQAVASTSTVPSPSQTMPSCTSP	TSRAGLAAT,RAGLAATSR,ATSRAQAVA,GLAATSRAQA,TSRAQAVAST,LAATSRAQAV	KIRC
ZFC3H1	c.1155delA	p.K385fs	KKLGEDEEELSELQLRLLALQSASK[p.K385fs]NGNKKNSR*	QSASKNGNK,LQSASKNGNK	STAD
ZFHX3	c.2287delG	p.E763fs	KGNLSIHMQSDKHLNNMQNLQNGGG[p.E763fs]SRSSATLPGRRRRRWLRRRRQPISVAPAGPPRRPNQKPNPPGGARCVIMRPTWPGTSAFT*	RQPISVAPA,RSSATLPGR,SSATLPGRR,SVAPAGPPR,ATLPGRRRR,RRRRRWLRR,RRRRQPISV,IMRPTWPGT,TLPGRRRRR,WLRRRRQPI,RPNQKPNPP,RPTWPGTSA,LQNGGGSRS,RRRQPISVA,RCVIMRPTW,PTWPGTSAF,QPISVAPAG,RSSATLPGRR,ISVAPAGPPR,SVAPAGPPRR,RWLRRRRQPI,GSRSSATLPG,ATLPGRRRRR,RRRRRWLRRR,RRRRQPISVA,AGPPRRPNQK,IMRPTWPGTS,LPGRRRRRWL,RPNQKPNPPG,RPTWPGTSAF,WLRRRRQPIS,LRRRRQPISV,LQNGGGSRSS,RRQPISVAPA	STAD
ZFHX3	c.2330_2332delTGG	p.V777del	NNMQNLQNGGGEQVFSHTAGAAAAA[p.V777del]AAAAAAANISSSCGAPSPTKPKTKPTWR	HTAGAAAAAA	PAAD
ZFHX3	c.5677_5678delAG	p.R1893fs	LQPSQHPEKKNKLVIKEKEKESQRE[p.R1893fs]GQRRGGRGQHRSEGNTARCLEGQREERVGTRGWF*	TARCLEGQR,SEGNTARCL,EERVGTRGW,NTARCLEGQR,GQRRGGRGQH,GQHRSEGNTA,REERVGTRGW,EERVGTRGWF	STAD,UCEC
ZFHX4	c.1224_1225insG	p.L408fs	ASTSSSAEQPLGITQMPKAEVNLGG[p.L408fs]AV*	AEVNLGGAV	STAD
ZFHX4	c.2433G>T	p.L811F	MTSEKHMHNMMLLQQNMKQIQHNLH[p.L811F]FGLAPAEAELYQYYLAQNIGLTGMKL	IQHNLHFGL,NLHFGLAPA,KQIQHNLHF,MKQIQHNLHF,KQIQHNLHFG,IQHNLHFGLA,LHFGLAPAEA	LUAD
ZFHX4	c.4988C>A	p.T1663N	IAANVNSPGQGMLDSMSLAAVNSKD[p.T1663N]NHLDAKELNKKQTPDLISAQPAHHPP	NSKDNHLDAK	LUAD
ZFHX4	c.7533C>A	p.H2511Q	LPPQLLQYQCDQCTVAFPTLELWQE[p.H2511Q]QQHMHFLAAQNQFLHSPFLERPMDMP	QQHMHFLAA,ELWQEQQHM,WQEQQHMHF,QEQQHMHFL,LWQEQQHMHF,LELWQEQQHM,WQEQQHMHFL,EQQHMHFLAA,QQHMHFLAAQ,QEQQHMHFLA	LUAD
ZFP14	c.1156C>T	p.R386C	SIHTGEKPYECKECGKTFRLRQQLV[p.R386C]CHQRIHTREKPYECMECWKTFSSYSQ	RLRQQLVCH,QQLVCHQRI,RQQLVCHQRI,LVCHQRIHTR,QQLVCHQRIH	CRC
ZFP14	c.50A>T	p.Q17L	MAHGSVTFRDVAIDFS[p.Q17L]LEEWEFLDPAQRDLYRDVMWENYSNF	DFSLEEWEF,RDVAIDFSL,VAIDFSLEEW,IDFSLEEWEF,LEEWEFLDPA	LUAD
ZFP2	c.449G>T	p.R150I	TGEKPYKCNVCGKHFIERSSLTVHQ[p.R150I]IIHTGEKPYKCNECGKAFSQSMNLTV	RSSLTVHQI,SSLTVHQII,RSSLTVHQII	CRC
ZFP3	c.818G>T	p.R273I	TGEKPYECNECGKTFRVSSQLIQHQ[p.R273I]IIHTEERYHECNECGKAFKHSSGLIR	QIIHTEERY,HQIIHTEER,IQHQIIHTE,HQIIHTEERY	CRC
ZFP36L2	c.718G>A	p.D240N	IHNADERRPAPSGGASGDLRAFGTR[p.D240N]NALHLGFPREPRPKLHHSLSFSGFPS	RAFGTRNAL,GTRNALHLG,NALHLGFPR,TRNALHLGF,RAFGTRNALH,GTRNALHLGF,RNALHLGFPR,LRAFGTRNAL	LUSC
ZFP42	c.679G>A	p.V227I	RAALRKHLLIHGPRDHVCAECGKAF[p.V227I]IESSKLKRHFLVHTGEKPFRCTFEGC	AFIESSKLK,KAFIESSKL,KAFIESSKLK,CGKAFIESSK,AFIESSKLKR,GKAFIESSKL,IESSKLKRHF,AECGKAFIES	GBM
ZFP42	c.791C>T	p.T264M	HTGEKPFRCTFEGCGKRFSLDFNLR[p.T264M]MHVRIHTGEKRFVCPFQGCNRRFIQS	RMHVRIHTG,DFNLRMHVR,FSLDFNLRM,SLDFNLRMHV,RFSLDFNLRM,RMHVRIHTGE,NLRMHVRIHT	GBM
ZFP90	c.1772_1773insA	p.R591fs	IQHERTHTGEKPYECNECGRAFRKK[p.R591fs]NQPA*	AFRKKNQPA,RAFRKKNQPA	PRAD

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ZFPM1	c.1330_1331delGA	p.E444fs	GLAPTPSPGLDRKALAEATNGEARA[p.E444fs]ASGPEWRQQRAPGGPQEHQGGGGGGAGGGPHPGPRRAWAPGPVADAVAAQPRPGQGQGRAVQPHAGLQPGARRAGPGRGPVPSAVRVRARRGAPRLGDPGQDVRAGAQPAAAGRGRGRRRRADRALPRGPQGRYVLRVRDHLQQRQQLLRAQAPLLFRPPCARGRACRAQAQGAPRPGPRAPRPARRTRRAALVPGPRSARGGGWGRGHARGRRGRPGQRGQPEPG*	QLLRAQAPL,RLGDPGQDV,LLRAQAPLL,ALVPGPRSA,RAQAPLLFR,LLFRPPCAR,RAQAQGAPR,RAALVPGPR,RAWAPGPVA,QGRAVQPHA,GARRAGPGR,RAGPGRGPV,SAVRVRARR,AVRVRARRG,RVRARRGAP,RARRGAPRL,RAGAQPAAA,AGRGRGRRR,RGRGRRRRA,RGRRRRADR,RALPRGPQG,QGRYVLRVR,RVRDHLQQR,CARGRACRA,RGRACRAQA,RTRRAALVP,SARGGGWGR,RGHARGRRG,RGRRGRPGQ,SGPEWRQQR,HAGLQPGAR,LVPGPRSAR,HPGPRRAWA,GPRRAWAPG,APGPVADAV,RPGQGQGRA,RAVQPHAGL,VPSAVRVRA,RRRRADRAL,RPPCARGRA,APRPGPRAP,RPARRTRRA,ARRTRRAAL,RPGQRGQPE,HLQQRQQLL,ARAASGPEW,RRAWAPGPV,GQGRAVQPH,RQQLLRAQA,LRAQAPLLF,GPVADAVAA,LPRGPQGRY,QLLRAQAPLL,RVRARRGAPR,RSARGGGWGR,RYVLRVRDHL,AVRVRARRGA,RARRGAPRLG,AGRGRGRRRR,RGRRRRADRA,RRRADRALPR,RALPRGPQGR,RVRDHLQQRQ,LLRAQAPLLF,LFRPPCARGR,RGRACRAQAQ,RAPRPARRTR,RTRRAALVPG,RGHARGRRGR,RGRRGRPGQR,ALPRGPQGRY,HAGLQPGARR,HLQQRQQLLR,WAPGPVADAV,GPHPGPRRAW,RPGQGQGRAV,LPRGPQGRYV,RPPCARGRAC,RPGPRAPRPA,RPARRTRRAA,PARRTRRAAL,GPRSARGGGW,QQLLRAQAPL,RQQRAPGGPQ,RRAWAPGPVA,GQGRAVQPHA,RRAGPGRGPV,VRARRGAPRL,RDHLQQRQQL,LQQRQQLLRA,RQQLLRAQAP,AQAPLLFRPP,AQAQGAPRPG	ACC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZFPM1	c.1335delT	p.P445Sfs	APTPSPGLDRKALAEATNGEARAEP[p.P445fs]WPRMEAAASPRRPPGASRWRRWRSRRPPSWAPESLGPRPRRGRRRRAAPPRPGSRPSCPAPRRAPARCPASWAWPGPCSFRSTCSGPTRRPPPRRSWPRCPSWCTAGCSRARARAPAARRPGSSPGPPRALRASSARSPSATSTTTTCTSASTVQAAVRPRTRLPRAGPRRPPARPARPPASPPNPTRRARPRAPERARRGLGARPRPRTARAAGAARAARARVAPWTTRRTTPAARCARPATSASAATRPTPCTSGTTAPRATTRRRADRPRPRDPLGRPRPRPPLPPRLCARADAASSTSCTRPAPRPPRRPATPPRPSRRGPEAEAEAAPASPLRARPAPRPTAPST*	RMEAAASPR,RVAPWTTRR,STCSGPTRR,RALRASSAR,TVQAAVRPR,ATSASAATR,CTSGTTAPR,TTAPRATTR,TSCTRPAPR,WAWPGPCSF,RSWPRCPSW,ASRWRRWRS,RWRRWRSRR,RWRSRRRPP,RSRRRPPSW,RPRRGRRRR,RGRRRRAAP,RRRRAAPPR,RSTCSGPTR,PTRRPPPRR,RARARAPAA,RARAPAARR,ALRASSARS,RASSARSPS,ASSARSPSA,AVRPRTRLP,RPRTRLPRA,RTRLPRAGP,RLPRAGPRR,RAGPRRPPA,PARPARPPA,PTRRARPRA,RARPRAPER,RARRGLGAR,GARPRPRTA,RPRPRTARA,RTARAAGAA,TARAAGAAR,AAGAARAAR,AARAARARV,AARARVAPW,RARVAPWTT,TTRRTTPAA,RTTPAARCA,AARCARPAT,ATRPTPCTS,ATTRRRADR,RPRPPLPPR,CTRPAPRPP,RPAPRPPRR,PLRARPAPR,RARPAPRPT,EARAEPWPR,GASRWRRWR,ESLGPRPRR,SWCTAGCSR,CTAGCSRAR,QAAVRPRTR,TTPAARCAR,EAAPASPLR,TTCTSASTV,CTSASTVQA,SASTVQAAV,WTTRRTTPA,EPWPRMEAA,WPRMEAAAS,SPRRPPGAS,CPAPRRAPA,APARCPASW,APAARRPGS,RPARPPASP,APERARRGL,RPRTARAAG,RAAGAARAA,APWTTRRTT,RPATSASAA,RPTPCTSGT,RPRPRPPLP,APRPPRRPA,RPATPPRPS,RPSRRGPEA,RPAPRPTAP,APRPTAPST,ARAEPWPRM,RRAPARCPA,ARCPASWAW,AAVRPRTRL,AEAAPASPL,CPASWAWPG,AEAEAAPAS,AEPWPRMEA,LPPRLCARA,STVQAAVRPR,RTARAAGAAR,RTTPAARCAR,GTTAPRATTR,TTAPRATTRR,STSCTRPAPR,SWAWPGPCSF,RMEAAASPRR,AASPRRPPGA,ASRWRRWRSR,RWRRWRSRRR,RWRSRRRPPS,RSRRRPPSWA,RGRRRRAAPP,RAAPPRPGSR,GSRPSCPAPR,SFRSTCSGPT,RSTCSGPTRR,SGPTRRPPPR,RSWPRCPSWC,CSRARARAPA,RARARAPAAR,RARAPAARRP,AARRPGSSPG,RALRASSARS,RASSARSPSA,AVRPRTRLPR,RTRLPRAGPR,RAGPRRPPAR,RARPRAPERA,RPRAPERARR,RARRGLGARP,RGLGARPRPR,GARPRPRTAR,TARAAGAARA,RAAGAARAAR,AARAARARVA,AARARVAPWT,RARVAPWTTR,TTRRTTPAAR,AARCARPATS,CARPATSASA,ATRPTPCTSG,RATTRRRADR,TTRRRADRPR,RRRADRPRPR,RPRPRDPLGR,RPRDPLGRPR,LGRPRPRPPL,RPRPPLPPRL,CTRPAPRPPR,RARPAPRPTA,SWAPESLGPR,CPAPRRAPAR,WAWPGPCSFR,RPPPRRSWPR,TAGCSRARAR,SASTVQAAVR,DAASSTSCTR,SPLRARPAPR,CTAGCSRARA,TTTCTSASTV,CTSASTVQAA,TSASTVQAAV,WTTRRTTPAA,CTSGTTAPRA,EAEAAPASPL,EAAPASPLRA,WPRMEAAASP,RPPSWAPESL,RPRRGRRRRA,RPGSRPSCPA,RPSCPAPRRA,APARCPASWA,WPRCPSWCTA,APAARRPGSS,PPRALRASSA,RPRTRLPRAG,LPRAGPRRPP,GPRRPPARPA,RPARPPASPP,RPRPRTARAA,RPRTARAAGA,APWTTRRTTP,TPAARCARPA,RPATSASAAT,RPTPCTSGTT,APRATTRRRA,RPRPRPPLPP,RPPLPPRLCA,APRPPRRPAT,RPAPRPTAPS,WRSRRRPPSW,RAPARCPASW,RRSWPRCPSW,ARAAGAARAA,RAARARVAPW,EPWPRMEAAA,AEPWPRMEAA,AEAEAAPASP,PEAEAEAAPA	ACC
ZFR2	c.319T>A	p.Y107N	TTMATYQDSYSYGQSAAARSYEDRP[p.Y107N]NFQSAALQSGRMTAADSGQPGTQEAC	RSYEDRPNF,RPNFQSAAL,ARSYEDRPNF,YEDRPNFQSA	KIRC
ZFYVE1	c.797G>A	p.R266Q	GATVNLSQRTRLLLKVLAISDLVIY[p.R266Q]QTHADRLHNDLFKFLGDASEAYLKHF	IYQTHADRL,VIYQTHADR,YQTHADRLH,AISDLVIYQT,LVIYQTHADR,VIYQTHADRL	UCEC
ZFYVE9	c.3441G>C	p.M1147I	VVQGLVVDMEVRKTSIKIPSNRYNE[p.M1147I]IMKAMNKSNEHVLAGGACFNEKADSH	SNRYNEIMK,IPSNRYNEI,RYNEIMKAM,IPSNRYNEIM,NRYNEIMKAM	CESC
ZHX3	c.747C>A	p.N249K	EVREGDHSFINGAVPVSQASASSAK[p.N249K]KPHAANGPLIGTVPVLPAGIAQFLSL	QASASSAKK,ASSAKKPHA,KPHAANGPL,SQASASSAKK,KPHAANGPLI,KKPHAANGPL	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZIC1	c.335C>A	p.A112E	GSYSSAAFNSTRDFLFRNRGFGDAA[p.A112E]EAASAQHSLFAASAGGFGGPHGHTDA	EAASAQHSL,AEAASAQHS,EAASAQHSLF,RGFGDAAEAA,AEAASAQHSL	LUAD
ZIC4	c.914C>T	p.S305L	GEKPFRCEFEGCERRFANSSDRKKH[p.S305L]LHVHTSDKPYTCKVRGCDKCYTHPSS	HLHVHTSDK,KKHLHVHTS,KHLHVHTSDK,LHVHTSDKPY	CRC
ZIM3	c.1054G>A	p.D352N	RIHTGEKPYKCSICEKAFSQKSNVI[p.D352N]NHEKIHTGKRAYECDLCGNTFIQKKN	KSNVINHEK,SQKSNVINH,KSNVINHEKI,INHEKIHTGK	CRC
ZIM3	c.1150delA	p.I384fs	GKRAYECDLCGNTFIQKKNLIQHKK[p.I384fs]SILGKSPMNVTDVEKPSFRSQTFIAIRKLIAERGPIDVVNVEKPSSGN*	ILGKSPMNV,FIAIRKLIA,KLIAERGPI,SQTFIAIRK,RSQTFIAIR,TFIAIRKLI,QHKKSILGK,KSILGKSPM,SFRSQTFIA,AIRKLIAER,KPSFRSQTF,NLIQHKKSI,LIQHKKSIL,FRSQTFIAI,AERGPIDVV,SILGKSPMNV,LIAERGPIDV,IQHKKSILGK,RSQTFIAIRK,SFRSQTFIAI,IAIRKLIAER,QTFIAIRKLI,KPSFRSQTFI,NLIQHKKSIL,KKSILGKSPM,SQTFIAIRKL,RKLIAERGPI,NVTDVEKPSF	STAD
ZKSCAN1	c.1621_1622delAG	p.R541fs	KCTKCGKAFTRSSTLTLHHRIHARE[p.R541fs]SL*	HRIHARESL,HHRIHARESL	UCEC
ZKSCAN3	c.598_599AA>GC	p.K200A	VGSQPLQDRVLQVPVLAHGGCCRED[p.K200A]AVVASRLTPESQGLLKVEDVALTLTPE	REDAVVASRL	TGCT
ZKSCAN4	c.956G>A	p.R319Q	IPTHAEAGEQEGRLQRKQKNAIGSR[p.R319Q]QHYCHECGKSFAQSSGLTKHRRIHTG	NAIGSRQHY,RQHYCHECG,RQHYCHECGK,KNAIGSRQHY	CRC
ZKSCAN5	c.39delC	p.D13fs	MIMTESREVIDLDP[p.D13fs]QLRLPRSRKTFS*	QLRLPRSRK,EVIDLDPQL,RLPRSRKTF,EVIDLDPQLR,DLDPQLRLPR,REVIDLDPQL,LRLPRSRKTF	STAD
ZMIZ1	c.3144delC	p.D1048fs	MPEPSLDLLPELTNPDELLSYLDPP[p.D1048fs]TCRAIVTMTSCLYLRTTEGHPVGAIPPHSASYPTYPTHFSTWEPVPSDRPAPEPRAVGRGALPRCSPLRTEG*	IVTMTSCLY,YLDPPTCRA,AIVTMTSCL,TMTSCLYLR,AVGRGALPR,SYPTYPTHF,TYPTHFSTW,VTMTSCLYL,AIPPHSASY,SYLDPPTCR,SASYPTYPT,RPAPEPRAV,EPRAVGRGA,GALPRCSPL,RAIVTMTSC,ASYPTYPTH,THFSTWEPV,HPVGAIPPH,YPTYPTHFS,EPVPSDRPA,TEGHPVGAI,YLDPPTCRAI,YLRTTEGHPV,VTMTSCLYLR,LSYLDPPTCR,AIVTMTSCLY,STWEPVPSDR,RAVGRGALPR,ASYPTYPTHF,PTYPTHFSTW,RAIVTMTSCL,RTTEGHPVGA,RGALPRCSPL,GALPRCSPLR,GAIPPHSASY,HSASYPTYPT,YPTYPTHFST,RPAPEPRAVG,EPRAVGRGAL,PPHSASYPTY,WEPVPSDRPA	PRAD
ZMIZ2	c.457_501delGTGGCTGCTGCGGCAGCCACTGCCACCGCCACAGCCACAGCCACC	p.VAAAAATATATATATA T153del	LGLPSHAARPSTDFTQAAAAAAVAA[p.VAAAAATATATATAT153del]LQEKQSQELSQYGAMGAGQSFNSQFLQHGGPRGPSVPAGMNPTGIGGVMGPSGLSPLAMNPTRAAGMTPL	AAAAAVAAL,AAVAALQEK,AAAVAALQEK,AAAAAAVAAL	PAAD
ZMYM4	c.1033delA	p.K345fs	SSGMNKMLPSVPATAVRVSCSGCKK[p.K345fs]SSRRGKLLIRGKGLLSYSAPHCASLDIQFHLPAHRLLSPRKLVQVAQKTF*	LLIRGKGLL,YSAPHCASL,KSSRRGKLL,SSRRGKLLI,RGKLLIRGK,RGKGLLSYS,AHRLLSPRK,RLLSPRKLV,IRGKGLLSY,CSGCKKSSR,IQFHLPAHR,PAHRLLSPR,APHCASLDI,LPAHRLLSP,SPRKLVQVA,LVQVAQKTF,GLLSYSAPH,HCASLDIQF,ASLDIQFHL,LDIQFHLPA,FHLPAHRLL,SLDIQFHLPA,IQFHLPAHRL,LLSPRKLVQV,LLSYSAPHCA,SYSAPHCASL,GCKKSSRRGK,KSSRRGKLLI,SSRRGKLLIR,RGKGLLSYSA,PAHRLLSPRK,LIRGKGLLSY,DIQFHLPAHR,LPAHRLLSPR,KLVQVAQKTF,KKSSRRGKLL,LDIQFHLPAH	STAD
ZMYM4	c.1100C>T	p.T367I	SGCKKILQKGQTAYQRKGSTQLFCS[p.T367I]ILCLTGYTVPPARPPPPLTKKTCSSC	CSILCLTGY,QLFCSILCL,ILCLTGYTV,GSTQLFCSI,TQLFCSILCL,QLFCSILCLT,SILCLTGYTV,KGSTQLFCSI,GSTQLFCSIL,FCSILCLTGY	TGCT
ZMYM4	c.4337G>A	p.R1446Q	TYLRFFPPLQKQESEPDKLTVGKRK[p.R1446Q]QNEDDEVPVGVEMAENTDNPLRCPVR	KQNEDDEVPV	CRC
ZNF117	c.554G>T	p.R185I	TGEKPYKCKECGKAFNQTSHLIRHK[p.R185I]IIHTEEKPYKCEECGKAFNQSSTLTT	QTSHLIRHKI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZNF124	c.1015delA	p.T339fs	GEKPYECQKCGKAFSRASTLWKHKK[p.T339fs]LILEKSPINVKKCKGFNHYSFCQKHEQSHT*	KLILEKSPI,ILEKSPINV,KHKKLILEK,KGFNHYSFC,FNHYSFCQK,KKCKGFNHY,LWKHKKLIL,CKGFNHYSF,LILEKSPINV,ILEKSPINVK,GFNHYSFCQK,KSPINVKKCK,TLWKHKKLIL,KKLILEKSPI,VKKCKGFNHY,KCKGFNHYSF	STAD
ZNF154	c.1223C>A	p.T408N	RPYECSECGKSFTQNSGLIKHRRVH[p.T408N]NGEKPYECTECGKSFSHNSSLIKHQR	HRRVHNGEK,KHRRVHNGEK,RRVHNGEKPY	LUAD
ZNF16	c.1354C>T	p.R452W	HTGEKPYKCSDCGKAFSQSSSLIQH[p.R452W]WRIHTGEKPHVCNVCGKAFSYSSVLR	QSSSLIQHW,QSSSLIQHWR,SQSSSLIQHW	CESC
ZNF167	c.2048G>T	p.R683I	TGEKPYECNECGKVFSYSSSLMVHQ[p.R683I]ITHTGEKPYKCNDCGKAFSDSSQLIV	LMVHQITHT,SLMVHQITH,SLMVHQITHT,YSSSLMVHQI	CRC
ZNF174	c.1057C>A	p.P353T	CDDCGKSFTWNSELKRHKRVHTGER[p.P353T]TYTCGECGNCFGRQSTLKLHQRIHTG	RVHTGERTY,RVHTGERTYT,KRVHTGERTY	TGCT
ZNF180	c.1202G>T	p.R401I	TGEKPYECSECGKSFSRSSHLVSHQ[p.R401I]ITHTGEKPYRCNQCGKSFSQSYVLVV	HLVSHQITH,HLVSHQITHT,ITHTGEKPYR,RSSHLVSHQI	CRC
ZNF180	c.1706G>T	p.R569I	TGEKPYECSECGKSFNRSSHLVMHQ[p.R569I]IIHTGEKPYECNQCGKSFSQSYVLVV	SHLVMHQII,RSSHLVMHQI,SSHLVMHQII	UCEC
ZNF180	c.1874G>T	p.R625I	TGEKPYECSQCGKSFRQSSCLTQHQ[p.R625I]ITHTGEKPFECNQCGKTFSLSARLIV	ITHTGEKPF,TQHQITHTG,QITHTGEKPF	UCEC
ZNF19	c.1046G>T	p.R349I	TGEKPYSCKVCGQAFNFHTKLTRHQ[p.R349I]IIHSEEKPFDCVDCGKAFSAQEQLKR	HTKLTRHQI,HQIIHSEEK,TKLTRHQII,IIHSEEKPF,HTKLTRHQII,RHQIIHSEEK,QIIHSEEKPF	CRC
ZNF195	c.176G>A	p.R59Q	LENYRNLFSVGLTVCKPGLITCLEQ[p.R59Q]QKEPWNVKRQEAADGHPEMGFHHATQ	QQKEPWNVK,QQKEPWNVKR,LEQQKEPWNV	UCEC
ZNF205	c.1150C>T	p.R384C	TGEKPYTCPACRKSFSHHSTLIQHQ[p.R384C]CIHTGEKPYVCDRCAKRFTRRSDLVT	HQCIHTGEK,IQHQCIHTG,CIHTGEKPYV,QCIHTGEKPY	CRC
ZNF223	c.67G>T	p.G23W	MTMSKEAVTFKDVAVVFTEEEL[p.G23W]WLLDLAQRKLYRDVMLENFRNLLSVG	FTEEELWLL,EELWLLDLA,EEELWLLDL,VVFTEEELW,WLLDLAQRKL,VFTEEELWLL,ELWLLDLAQR,TEEELWLLDL,EELWLLDLAQ,EEELWLLDLA	LUAD
ZNF23	c.366delT	p.F122fs	NIKKEKSNTIDGTVKDETSPVEECF[p.F122fs]LVKVQTHISVIPSLESSPLGVQDWGNPSALIQNS*	FLVKVQTHI,KVQTHISVI,SLESSPLGV,IPSLESSPL,VKVQTHISV,THISVIPSL,VQDWGNPSA,QDWGNPSAL,VEECFLVKV,SPVEECFLV,VQDWGNPSAL,VIPSLESSPL,CFLVKVQTHI,LVKVQTHISV,QTHISVIPSL,ETSPVEECFL,TSPVEECFLV,VKVQTHISVI	STAD
ZNF236	c.4229C>T	p.T1410M	NITLQIDPSILQQTLQQGNLLAQQL[p.T1410M]MGEPGLAPQNSSLQTSDSTVPASVVI	QLMGEPGLA,AQQLMGEPG,QQLMGEPGL,LMGEPGLAP,AQQLMGEPGL	STAD
ZNF236	c.4439C>T	p.S1480L	GPLSEQDSVLTTNSSGTQDLTQVMT[p.S1480L]LQGLVSPSGGPHEITLTINNSSLSQV	TQVMTLQGL,QVMTLQGLV,TQVMTLQGLV,MTLQGLVSPS,TQDLTQVMTL	CRC
ZNF248	c.1703G>T	p.R568I	TGEKPYECNACGKTFSQRSVLTKHQ[p.R568I]IIHTRVKALSTS*	HQIIHTRVK,SVLTKHQII,IIHTRVKAL,RSVLTKHQI,LTKHQIIHTR,KHQIIHTRVK,RSVLTKHQII,HQIIHTRVKA	CRC
ZNF254	c.537G>T	p.K179N	FQCDKYLKVFYKFLNSNRPKIRHTE[p.K179N]NKSFKCKKRVKLFCMLSHKTQHKSIY	KIRHTENKS,RHTENKSFK,IRHTENKSF,HTENKSFKCK,RPKIRHTENK,KIRHTENKSF	UCEC
ZNF257	c.1175G>T	p.R392I	TKEKPYKCEECGKAFNRSSHLTKHK[p.R392I]IIHTREKAYKCDEYCKAFNWSSALTT	IIHTREKAY,IIHTREKAYK,KIIHTREKAY,RSSHLTKHKI	UCEC
ZNF259	c.521G>T	p.R174I	LITRAISGLEQDQPARRANKDATAE[p.R174I]IIDEFIVKLKELKQVASPFTLIIDDP	IIDEFIVKL,ATAEIIDEF,AEIIDEFIV,ATAEIIDEFI,IIDEFIVKLK,EIIDEFIVKL,RANKDATAEI	CRC
ZNF263	c.1529G>T	p.R510I	TGEKPYKCPECGEIFAHSSNLLRHQ[p.R510I]IIHTGERPYKCPECGKSFSRSSHLVI	SNLLRHQII	UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZNF266	c.1031G>A	p.R344Q	TAKDPFECKICGKSFRNSSCLSDHF[p.R344Q]QIHTGIKPYKCKDCGKAFTQNSDLTK	HFQIHTGIK,FQIHTGIKP,CLSDHFQIHT,QIHTGIKPYK,FQIHTGIKPY	CRC
ZNF266	c.1535G>A	p.R512Q	TGEKPYKCKQCGKSFSYSNSFQLHE[p.R512Q]QTHTGEKPYECKECGKAFSSSSSFRN	FQLHEQTHT,EQTHTGEKPY,FQLHEQTHTG	CRC
ZNF268	c.2700_2702delCTT	p.F901del	NSQLIVHQRTHSGEKPYGCNECGKT[p.F901del]SQKSILSAHQRTHTGEKPCKCTECGKAF	KTSQKSILS,KTSQKSILSA	BRCA
ZNF273	c.957T>A	p.N319K	DCGKVFSVFSVLTKHKIIHTGTKPY[p.N319K]KCEECGKGFSIFSTLTKHKIIHTGEK	IIHTGTKPYK	KIRC
ZNF280B	c.1087G>A	p.E363K	SWENHTTCQHCHRQFPTPFQLQCHI[p.E363K]KNVHTAQEPSTVCKICELSFETDQVL	QLQCHIKNV,LQCHIKNVH,CHIKNVHTA,FQLQCHIKNV	CRC
ZNF280B	c.1198G>A	p.E400K	CKICELSFETDQVLLQHMKDHHKPG[p.E400K]KMPYVCQVCHYRSSVFADVETHFRTC	HHKPGKMPY,GKMPYVCQV,HMKDHHKPGK,MKDHHKPGKM,GKMPYVCQVC	GBM
ZNF283	c.1175G>A	p.R392Q	KIHTGKKPYECKICGKAFCWGYQLT[p.R392Q]QHQIFHTGEKPYECKECGKAFNCGSS	GYQLTQHQI,YQLTQHQIF,TQHQIFHTG,GYQLTQHQIF,WGYQLTQHQI,YQLTQHQIFH	CRC
ZNF32	c.185C>T	p.S62L	EATGSSSWDIQNSFRREKLEQKSPD[p.S62L]LKTLQEDSPGVRQRVYECQECGKSFR	KLEQKSPDLK	CRC
ZNF322	c.318G>T	p.K106N	VQSSDLTSHQRIHNYEKPYKCSKCE[p.K106N]NSFWHHLVLSGHQRTHAGKKFYTCDI	ENSFWHHLV,NSFWHHLVL,KCSKCENSF,CENSFWHHL,YKCSKCENSF,CENSFWHHLV	LUAD
ZNF333	c.1661G>A	p.R554Q	TGEKLYECATCGQVLSRLSTLKSHM[p.R554Q]QTHTGEKPYVCQECGRAFSEPSSLRK	HMQTHTGEK,KSHMQTHTG,SHMQTHTGEK,MQTHTGEKPY,QTHTGEKPYV	UCEC
ZNF334	c.1278delA	p.K426fs	ECKECGKTFFCQSALTAHQRIHTGE[p.K426fs]NPMNVVNVRKPSFVNLPSMCIEEVIQERSPMNAVNVENFYVRNQPSLHIR*	AVNVENFYV,FVNLPSMCI,FYVRNQPSL,RIHTGENPM,HTGENPMNV,EVIQERSPM,NAVNVENFY,VVNVRKPSF,VRKPSFVNL,PSFVNLPSM,QERSPMNAV,MNAVNVENF,VRNQPSLHI,LPSMCIEEV,NLPSMCIEEV,VVNVRKPSFV,AVNVENFYVR,SFVNLPSMCI,NVRKPSFVNL,YVRNQPSLHI,MNAVNVENFY,HTGENPMNVV,NAVNVENFYV,KPSFVNLPSM,NFYVRNQPSL,QRIHTGENPM,GENPMNVVNV,NVVNVRKPSF,EEVIQERSPM,IQERSPMNAV,PMNAVNVENF,LPSMCIEEVI	STAD
ZNF354B	c.1205G>T	p.R402I	TGEKPFKCSECGRAFSQSASLIQHE[p.R402I]IIHTGEKPYRCNECGKGFTSISRLNR	SASLIQHEI,IQHEIIHTG,SLIQHEIIHT,QSASLIQHEI	UCEC
ZNF354B	c.1825G>A	p.D609N	GKLFSQRSSLTNHYKIHIEEDSLKA[p.D609N]NLHV*	EEDSLKANL,IEEDSLKANL	UCEC
ZNF358	c.389delC	p.T130fs	DPNSDTLSPGDPKVDPISSGLTATP[p.T130fs]RSWPPAPRCSPPPPARPGPSPARIAGEPSAAAPG*	RIAGEPSAA,SSGLTATPR,ATPRSWPPA,RPGPSPARI,GLTATPRSW,ARIAGEPSA,RIAGEPSAAA,ISSGLTATPR,PARPGPSPAR,TPRSWPPAPR,APRCSPPPPA,RPGPSPARIA,SGLTATPRSW,ARIAGEPSAA	STAD
ZNF382	c.558T>A	p.H186Q	FGDSTGWEKSLLNTKHEKIHPAVNL[p.H186Q]QKQTERVLSGKQELIQHQKVQAPEQP	NLQKQTERV,LQKQTERVL,KIHPAVNLQK	CLL
ZNF385D	c.677C>G	p.T226S	KRLLYCSLCKVAVNSASQLEAHNSG[p.T226S]SKHKTMLEARNGSGTIKAFPRAGVKG	SKHKTMLEA,GSKHKTMLEA,SQLEAHNSGS,LEAHNSGSKH	LUAD
ZNF43	c.752delA	p.N251fs	GEKPYTCEECGKVFNWSSRLTTHKK[p.N251fs]IILDTNSTNVKNVAKLLTSPQSLPIR*	ILDTNSTNV,KLLTSPQSL,LLTSPQSLL,IILDTNSTNV,KLLTSPQSLL,ILDTNSTNVK,SSRLTTHKKI,DTNSTNVKNV,LTSPQSLPI,RLTTHKKIIL,AKLLTSPQSL	STAD
ZNF43	c.838C>T	p.R280C	YKLYKCEECGKAFNKSSILTTHKII[p.R280C]CTGEKFYKCKECAKAFNQSSNLTEHK	IICTGEKFY,KIICTGEKF,IICTGEKFYK,CTGEKFYKCK,THKIICTGEK,KIICTGEKFY,HKIICTGEKF	UCEC
ZNF434	c.916C>T	p.R306C	QNSQIYRAMAEGLWEQGFLRTPEQC[p.R306C]CTKFKSLQLSYRKVRRGRVPEPCIFY	RTPEQCCTK,CTKFKSLQL,TPEQCCTKF,RTPEQCCTKF	CRC

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ZNF439	c.785G>T	p.R262I	TGEKPYECKQCGKSFSYSATHRIHE[p.R262I]ITHIGEKPYECQECGKAFHSPRSCHR	ITHIGEKPY,HRIHEITHI,YSATHRIHEI	CRC
ZNF442	c.926G>A	p.R309Q	ERTHTGEKPYKCKRCGRAFSVSSSL[p.R309Q]QIHERTHTGEKPYECKQCGKAFHHLG	SSSLQIHER,FSVSSSLQI,VSSSLQIHER,RAFSVSSSLQ,FSVSSSLQIH	UCEC
ZNF443	c.902G>T	p.R301I	TGEKPYKCKQCSKAFPDSSSCLIHE[p.R301I]ITHTGEKPYTCKQCGKAFSVSGSLQR	CLIHEITHT,SSSCLIHEI,DSSSCLIHEI,EITHTGEKPY	CRC
ZNF445	c.2044C>A	p.L682M	ECREGFRQSPDCSQPQGAPAVEKTF[p.L682M]MCQQCGKTFTRKKTLVDHQRIHTGEK	TFMCQQCGK,KTFMCQQCG,APAVEKTFM,MCQQCGKTF,KTFMCQQCGK,FMCQQCGKTF	CRC
ZNF454	c.1127G>T	p.R376I	TGEKPFECNECGKAFRVNSSLTEHQ[p.R376I]IIHTGEKPYKCNECGKAFRDNSSFAR	SSLTEHQII,TEHQIIHTG,SLTEHQIIHT	UCEC
ZNF454	c.569G>T	p.S190I	SDQSQGFQPSKNAFECSECGKVFSK[p.S190I]ISTLNKHQKIHNEKNANQKIHIKEKR	KVFSKISTL,FSKISTLNK,ISTLNKHQK,VFSKISTLNK,KISTLNKHQK,GKVFSKISTL,SECGKVFSKI	LUAD
ZNF462	c.1948T>A	p.S650T	FCDNLPKFEGQPSSLPLENETDSHP[p.S650T]TSSNTVKKSQTSILGLSSKNNFVAKA	PTSSNTVKK,DSHPTSSNTV,LENETDSHPT	KIRC
ZNF470	c.1922G>T	p.R641I	TGEKPYECNVCGKAFSHRKSLTLHQ[p.R641I]IIHTGEKPYECKECSKAFSQVAHLTL	KSLTLHQII,RKSLTLHQI,KSLTLHQIIH,RKSLTLHQII	CRC
ZNF471	c.845G>T	p.R282I	TGEKLFECKECRKAFKQSEHLIQHQ[p.R282I]IIHTGEKPYKCKECRKAFRQPAHLAQ	SEHLIQHQI,SEHLIQHQII	CRC
ZNF48	c.704G>A	p.R235H	HQRTHTGEKPYKCGICGKGFGDSSA[p.R235H]HIKHQRTHRGEQPPRPVVPRRQPSRA	SSAHIKHQR,HIKHQRTHR,KGFGDSSAH,AHIKHQRTH,DSSAHIKHQR,KGFGDSSAHI	LUSC
ZNF48	c.739delC	p.P247fs	ICGKGFGDSSARIKHQRTHRGEQPP[p.P247fs]DQWCPDGSHLGQPRQLPRDRRPRTSHISALIAARGLCSAAAS*	RTSHISALI,HISALIAAR,RPRTSHISA,AARGLCSAA,LPRDRRPRT,SHISALIAA,LIAARGLCSA,RQLPRDRRPR,RTSHISALIA,TSHISALIAA,AARGLCSAAA,HLGQPRQLPR,SHISALIAAR,LPRDRRPRTS,RPRTSHISAL,DQWCPDGSHL,IAARGLCSAA	STAD
ZNF484	c.412C>T	p.R138C	SILEELWKDDEHTRKCGENQNKPLS[p.R138C]CVVFINKKTLANDSIFEYKDIGEIVH	NQNKPLSCV,LSCVVFINK,NKPLSCVVF,KPLSCVVFI,NQNKPLSCVV,PLSCVVFINK,LSCVVFINKK,QNKPLSCVVF	CRC
ZNF485	c.1121G>T	p.R374I	SGNKPYQCRDCGKAFTKSSTLTGHQ[p.R374I]IIHTGEKPYHCKKCGKAFRHSSGLVE	KSSTLTGHQI	UCEC
ZNF488	c.617G>A	p.R206Q	PAGESADALGELSGLLNTTDLACWG[p.R206Q]QLSTPKLLVGDLWNLQALPQNAPLCS	QLSTPKLLV,GQLSTPKLL,CWGQLSTPKL,GQLSTPKLLV	UCEC
ZNF491	c.1028G>A	p.R343Q	ERTHTGEKPDGCKQCGKAFRSAKYI[p.R343Q]QIHGRTHTGEKPYECKQCGKAFHCVS	SAKYIQIHG,RSAKYIQIH,FRSAKYIQI,IQIHGRTHT,AFRSAKYIQI,SAKYIQIHGR,IQIHGRTHTG	CRC
ZNF492	c.1175C>A	p.P392H	CEVCSKAFSRFSHLTTHKRIHTGEK[p.P392H]HYKCEECGKAFNLSSQLTTHKIIHTG	RIHTGEKHY,RIHTGEKHYK,KRIHTGEKHY	LUAD
ZNF514	c.242T>G	p.V81G	PGEEGTTNSFLKARPRDLMTFEDVA[p.V81G]GEFSQWEWGQLNPAQKDLYREVMLEN	MTFEDVAGE,MTFEDVAGEF,VAGEFSQWEW	KIRP
ZNF519	c.1291C>T	p.H431Y	CKECGKAFNRASHLTQHQRIHTGEK[p.H431Y]YFKCKECGKAFNRGSHLTRHQRIHTG	YFKCKECGK,QRIHTGEKY,RIHTGEKYF,RIHTGEKYFK,HTGEKYFKCK,KYFKCKECGK,HQRIHTGEKY,QRIHTGEKYF	KIRC
ZNF521	c.1918G>T	p.G640C	TSLKMMQAVGGAPARPTGEYICNQC[p.G640C]CAKYTSLDSFQTHLKTHLDTVLPKLT	ICNQCCAKY,GEYICNQCC,YICNQCCAKY,CAKYTSLDSF,NQCCAKYTSL,GEYICNQCCA	LUAD
ZNF521	c.809C>A	p.P270H	TQKCSQCEEGFDFPEDLQKHIAECH[p.P270H]HECSPNEDRAALQCVYCHELFVEETS	LQKHIAECHH	LUAD

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ZNF528	c.836G>A	p.R279Q	SNLSQHQRIHTGEKPYKCHECDKVF[p.R279Q]QSSSKLAQHQRIHTGEKPYKCHECDK	KVFQSSSKL,FQSSSKLAQ,KVFQSSSKLA,FQSSSKLAQH,HECDKVFQSS	CRC
ZNF534	c.1749T>A	p.N583K	TGEKPYSCNECGKVFSRNSHLARHR[p.N583K]KIHTGEKPHSCNECGKVFSRNSHLAR	RKIHTGEKPH	GBM
ZNF536	c.1987G>T	p.G663W	RVFRTYHQVVVHSRVHKRDRKGEED[p.G663W]WLHVGLDERRGSGSDQESQSVSRSTT	EEDWLHVGL,DWLHVGLDER,GEEDWLHVGL	LUAD
ZNF536	c.556G>T	p.G186C	PYCDHRAAQKGNLKIHLRTHKLGNL[p.G186C]CKGRGRVREENRLLHELEERAILRDK	RTHKLGNLC,RTHKLGNLCK,NLCKGRGRVR	LUAD
ZNF559	c.850G>A	p.E284K	PSSSHLRECVRIYGGERPYTHKEYV[p.E284K]KTFSHSTALFVHMQTQDGEKFYECKA	KTFSHSTAL,THKEYVKTF,KEYVKTFSH,VKTFSHSTA,YVKTFSHSTA,KTFSHSTALF,YTHKEYVKTF,RPYTHKEYVK,VKTFSHSTAL,KEYVKTFSHS	UCEC
ZNF563	c.622delT	p.W208fs	NLRRHMVVQGGNRPYKCKLCGKAFF[p.W208fs]GPVYYVCMKELTLERNRMNVSSVLKPFLFTVPIEDMRECTLGRNRMNVSSVLKPCLIPVPI*	AFFGPVYYV,VLKPFLFTV,KAFFGPVYY,CMKELTLER,FFGPVYYVC,VYYVCMKEL,SSVLKPFLF,CGKAFFGPV,GKAFFGPVY,FTVPIEDMR,KPFLFTVPI,NVSSVLKPF,KAFFGPVYYV,SVLKPFLFTV,FLFTVPIEDM,FFGPVYYVCM,YYVCMKELTL,VSSVLKPFLF,CGKAFFGPVY,GKAFFGPVYY,NVSSVLKPFL,MNVSSVLKPF,KELTLERNRM,LKPFLFTVPI	GBM
ZNF563	c.78G>T	p.K26N	MDAVAFEDVAVNFTQEEWALLGPSQ[p.K26N]NNLYRYVMQETIRNLDCIRMIWEEQN	PSQNNLYRY,LLGPSQNNL,SQNNLYRYV,LGPSQNNLY,QNNLYRYVM,ALLGPSQNNL,LLGPSQNNLY,SQNNLYRYVM,GPSQNNLYRY	CRC
ZNF573	c.1049G>T	p.R350I	TGKKPYECKECGKGYTTASYFLLHQ[p.R350I]IIHKGGKPYECKECKKTFTLYRNLTR	FLLHQIIHK,SYFLLHQII,HQIIHKGGK,IIHKGGKPY,ASYFLLHQI,QIIHKGGKPY,TASYFLLHQI,ASYFLLHQII	CRC
ZNF578	c.931G>A	p.G311S	PYKCNECGKSFSYKSSLTCHRRCHT[p.G311S]SEKPYKCNECGKSFSYKSSLTCHHRC	CHRRCHTSEK	CLL
ZNF583	c.1031G>T	p.R344I	TGERPFECIECGKAFSNGSFLAQHQ[p.R344I]IIHTGEKPYVCNVCGKAFSHRGYLIV	SFLAQHQII,GSFLAQHQI,FLAQHQIIH,FLAQHQIIHT,GSFLAQHQII	CRC
ZNF585A	c.1473G>T	p.E491D	YMCNKCGKAFTNRSNLITHQKTHTG[p.E491D]DKSYICSKCGKAFTQRSDLITHQRIH	HQKTHTGDK,KTHTGDKSY,KTHTGDKSYI,QKTHTGDKSY	CRC
ZNF585A	c.1912G>A	p.E638K	KSFTSKSQLLVHQPVHTGEKPYVCA[p.E638K]KCGKAFSGRSNLSKHQKTHTGEKPYI	VCAKCGKAF,KPYVCAKCGK,YVCAKCGKAF,GEKPYVCAKC	CRC
ZNF592	c.1498C>A	p.P500T	PGSQTGKKQQSTALQASTLAPANLL[p.P500T]TKAVHLANLNLVPHSVAASVTAKSSV	LLTKAVHLA,NLLTKAVHL,TKAVHLANL,NLLTKAVHLA,TLAPANLLTK,LTKAVHLANL,APANLLTKAV	TGCT
ZNF592	c.970A>C	p.K324Q	VTKEDQPGHTKDLSGPTKESSKGSP[p.K324Q]QMPKSPKSPRSPLEATRKSIKPSDSP	SSKGSPQMPK,QMPKSPKSPR,KESSKGSPQM	TGCT
ZNF594	c.860G>T	p.R287I	TGEKPYECYDCGQMFSQSSHLVPHQ[p.R287I]IIHTGEKPLKCNECEKAFRQHSHLTE	HLVPHQIIH,IIHTGEKPLK,SSHLVPHQII	UCEC
ZNF598	c.74A>G	p.E25G	MAAAGGAEGRRADMEAEAAAAPER[p.E25G]GGGSCVLCCGDLEATALGRCDHPVCY	AEAAAAPERG	ACC,KIRP
ZNF608	c.1393delG	p.A465fs	SAAAAPGSEASFTESRGLQNKNRGG[p.A465fs]PMGKGGGAASMPADEGHPQIVLLRISKPALPPPTKGKTSLQWSWT*	QIVLLRISK,KNRGGPMGK,LLRISKPAL,KPALPPPTK,GPMGKGGGA,PPTKGKTSL,GKGGGAASM,TKGKTSLQW,GKTSLQWSW,DEGHPQIVL,MPADEGHPQ,HPQIVLLRI,VLLRISKPAL,ISKPALPPPT,EGHPQIVLLR,MPADEGHPQI,GPMGKGGGAA,MGKGGGAASM,LQNKNRGGPM,KGKTSLQWSW,DEGHPQIVLL	STAD
ZNF611	c.1169G>T	p.R390I	TGEKPYKCEECDKVFSRKSTIETHK[p.R390I]IIHTGEKPYRCKVCDTAFTWHSQLAR	RKSTIETHKI	UCEC

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ZNF625	c.704G>A	p.R235Q	TGEKPYECSECGKAFHSSTCLHAHK[p.R235Q]KTHTGEKPYECKQCGKAFVSFNSVRY	STCLHAHKK,SSTCLHAHKK,AHKKTHTGEK	CRC
ZNF626	c.1418A>G	p.K473R	TGEKFYKCEECGKAFKCSSNLTTHK[p.K473R]RIHTGERPYKCEECGKAFNQSSILTT	CSSNLTTHKR	LUSC
ZNF638	c.1198G>A	p.D400N	SQADIPIRSPFGIVKASWLPKFSHA[p.D400N]NAQKMKRLPTPSMMNDYYAASPRIFP	KFSHANAQK,HANAQKMKR,FSHANAQKM,WLPKFSHANA,FSHANAQKMK,KFSHANAQKM	LIHC
ZNF644	c.61G>T	p.G21W	MRSFLQQDVNKTKSRLNVLN[p.G21W]WLANNMDDLKINTDITGAKEELLDDN	RLNVLNWLA,WLANNMDDL,VLNWLANNM,KSRLNVLNW,SRLNVLNWL,WLANNMDDLK,KSRLNVLNWL,NVLNWLANNM,TKSRLNVLNW	LUAD
ZNF645	c.460C>T	p.R154C	SLQAHIKRRHKRARKQVTSASLEKV[p.R154C]CPHIAPPQTEISDIPKRLQDRDHLSY	SLEKVCPHI,LEKVCPHIA	UCEC
ZNF649	c.593G>T	p.R198I	NIEKAHECTDCGKAFLKKSQLTEHK[p.R198I]IIHTGKKPHVCSLCGKAFYKKYRLTE	SQLTEHKII,IIHTGKKPHV,KKSQLTEHKI,SQLTEHKIIH	UCEC
ZNF652	c.981G>T	p.K327N	VSCNKSFKKLWSLHEHIKIVHGYAE[p.K327N]NKFSCEICEKKFYTMAHVRKHMVAHT	IVHGYAENK,AENKFSCEI,KIVHGYAENK,IVHGYAENKF,AENKFSCEIC	CRC
ZNF674	c.1214G>T	p.R405I	TKENIYECSKCGKSFRGKSHLSVHQ[p.R405I]IIHTGEKPYECSICGKTFSGKSHLSV	SHLSVHQII,KSHLSVHQI,KSHLSVHQII,GKSHLSVHQI	UCEC
ZNF675	c.659G>T	p.R220I	TKVNFCKCEECEKAVNQSSKLTKHK[p.R220I]IIYTCEKLYKCQECDRTFNQFSNLTE	KLTKHKIIY,IIYTCEKLY,SSKLTKHKI,IIYTCEKLYK,SSKLTKHKII,KHKIIYTCEK,KIIYTCEKLY,SKLTKHKIIY,HKIIYTCEKL	UCEC
ZNF676	c.127C>A	p.P43T	PDLIIFLEQGKEPWNMKRHEMVEEP[p.P43T]TVICSHFSQEFWPEQGIEDSFQKMIL	HEMVEEPTV,EPTVICSHF,HEMVEEPTVI,EEPTVICSHF	LUSC
ZNF677	c.1352G>T	p.R451I	PGEKPHKCNVCGRAFIQSSSLVEHQ[p.R451I]IIHTGEKPYKCNKCDKAFIKRSHLWG	SSLVEHQII,VEHQIIHTG,SLVEHQIIHT	CRC
ZNF677	c.392G>C	p.R131T	FDSLWDYDVKNYKGMPLTCNKNLTH[p.R131T]TKDQQHNKSSIHFSLKQSVSIRDSAH	HTKDQQHNK,CNKNLTHTK	CESC
ZNF680	c.1501C>T	p.R501W	TLANHKRIHAREKPYKCEECGKAFN[p.R501W]WSSHLTRHKKIHTGEKLYKPEKCDNN	FNWSSHLTR,WSSHLTRHKK,AFNWSSHLTR,FNWSSHLTRH	TGCT
ZNF687	c.2573T>G	p.F858C	DTVFTHKPLLSSHFDQHLLPQRVSV[p.F858C]CKCPSCPLLFAQKRTMLEHLKNTHQS	LLPQRVSVC,CKCPSCPLLF	KIRC
ZNF699	c.122G>T	p.R41I	QDSVVFEDVAVDFTQEEWALLDLAQ[p.R41I]INLYRDVMLENFQNLASLGYPLHTPH	LLDLAQINL,DLAQINLYR,LDLAQINLY,AQINLYRDV,QINLYRDVM,WALLDLAQI,LLDLAQINLY,ALLDLAQINL,AQINLYRDVM	CRC
ZNF7	c.1010G>T	p.R337I	TGEKPYRCEECGKAFGQSSSLIHHQ[p.R337I]IIHTGERPYGCRECGKAFSQQSQLVR	SSSLIHHQI,SSLIHHQII,SLIHHQIIHT,QSSSLIHHQI	CRC
ZNF70	c.731G>T	p.R244I	TGKRPYECRECGKDFSRSSSLRKHE[p.R244I]IIHTGERPYQCKECGKSFNQSSGLSQ	SLRKHEIIH,RSSSLRKHEI,EIIHTGERPY	CRC
ZNF700	c.1946C>G	p.S649C	NLRKHGRTHTGEKPYECKQCGKAFR[p.S649C]CASNLQMHERTHTGEKPYECKECEKA	KAFRCASNL,FRCASNLQM,CASNLQMHER,AFRCASNLQM,GKAFRCASNL	CLL
ZNF700	c.1954A>C	p.N652H	KHGRTHTGEKPYECKQCGKAFRSAS[p.N652H]HLQMHERTHTGEKPYECKECEKAFCK	ASHLQMHER,AFRSASHLQ,RSASHLQMH,FRSASHLQM,SASHLQMHER,AFRSASHLQM	CLL
ZNF700	c.1961A>G	p.Q654R	GRTHTGEKPYECKQCGKAFRSASNL[p.Q654R]RMHERTHTGEKPYECKECEKAFCKFS	ASNLRMHER,AFRSASNLR,FRSASNLRM,KAFRSASNLR,SASNLRMHER,AFRSASNLRM	CLL
ZNF705A	c.892G>A	p.D298N	GNKIIHTGEKPHACLLCGKAFSLSS[p.D298N]NLR*	AFSLSSNLR,KAFSLSSNLR	CLL

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ZNF706	c.23T>A	p.I8N	MARGQQK[p.I8N]NQSQQKNAKKQAGQKKKQGHDQKAAA	QQKNQSQQK,KNQSQQKNAK	BLCA
ZNF709	c.1403G>T	p.R468I	TGEKPYECKQCGKAFSCSSSFRMHE[p.R468I]IIHTGEKPYECKQCGKAFSFSSSFRM	RMHEIIHTG,SFRMHEIIH,SSFRMHEII,SFRMHEIIHT,CSSSFRMHEI,SSFRMHEIIH	UCEC
ZNF711	c.1231G>T	p.V411L	ICKKHFTGRSSLIVHQIVHTGEKPY[p.V411L]LCGECGKAFSQSAYLIEHQRIHTGEK	YLCGECGKA,LCGECGKAF,YLCGECGKAF,GEKPYLCGEC	LUAD
ZNF711	c.2211delA	p.L737fs	SVHTKDQPLKCKRCKRGFRQQNELK[p.L737fs]N!*	RQQNELKNI	STAD
ZNF716	c.788A>T	p.H263L	EKPYRCEECGKAFSWSASLTKHKRI[p.H263L]LTGEKPYTCEERGKVFSRSTLTNYKR	LTKHKRILT,SLTKHKRIL,KHKRILTGEK	LUAD
ZNF717	c.1781A>T	p.N594I	GKSFHCKSFLTIHQRTHAGKKPYEC[p.N594I]IECEKTFINKLNLGIHKRTHTGERPY	YECIECEKTF	MM
ZNF717	c.2530T>A	p.C844S	CRKTFSQKSKLFVHHRTHTGEKPFR[p.C844S]SNECRKTFSQKSGLSIHQRTHTGEKP	RSNECRKTF,KPFRSNECRK,RSNECRKTFS,FRSNECRKTF	MM
ZNF717	c.945G>C	p.W315C	KPSISKSDLMLQCKMPTEEKPYACN[p.W315C]CCEKLFSYKSSLIIHQRIHTGEKPYG	KPYACNCCEK,YACNCCEKLF	MM
ZNF750	c.287_288delCT	p.S96fs	LDPKQTNQPDATAKPASSKSVANGL[p.S96fs]CLRLEASAQLCQGRHQGKPGAASPGNPQVPGTEASPPQGITLQEPSSGSRPRCPACSGRRSSAFCICSSRRAQTQGARQRRGARDTGFTQPHCQGRVFPHQVGLPHSWLPLESRLTFPSTRVST*	RVFPHQVGL,GLPHSWLPL,RLTFPSTRV,SVANGLCLR,SAFCICSSR,HSWLPLESR,SWLPLESRL,GSRPRCPAC,SGRRSSAFC,GARQRRGAR,AFCICSSRR,QTQGARQRR,FTQPHCQGR,RPRCPACSG,QPHCQGRVF,FPHQVGLPH,LPLESRLTF,CSGRRSSAF,KSVANGLCL,LRLEASAQL,HQGKPGAAS,RRGARDTGF,HQVGLPHSW,TEASPPQGI,LESRLTFPS,SVANGLCLRL,GLCLRLEASA,CLRLEASAQL,FTQPHCQGRV,KSVANGLCLR,SSAFCICSSR,SAFCICSSRR,WLPLESRLTF,SSGSRPRCPA,GSRPRCPACS,RPRCPACSGR,SGRRSSAFCI,SSRRAQTQGA,RAQTQGARQR,RVFPHQVGLP,EASAQLCQGR,TLQEPSSGSR,ESRLTFPSTR,EASPPQGITL,SKSVANGLCL,HQGKPGAASP,ACSGRRSSAF,RQRRGARDTG,QRRGARDTGF,TQPHCQGRVF,GRVFPHQVGL,HQVGLPHSWL,VGLPHSWLPL,HSWLPLESRL,LESRLTFPST	HNSC
ZNF765	c.761C>T	p.S254L	LLRKHQLIHLGEKQYKCDICGKVFN[p.S254L]LKRYVARHRRCHTGEKPYKCNECGKT	KVFNLKRYV,FNLKRYVAR,GKVFNLKRY,KVFNLKRYVA,CGKVFNLKRY,DICGKVFNLK,VFNLKRYVAR,NLKRYVARHR	UCEC
ZNF774	c.1268G>A	p.R423Q	TGERPYKCGECGKSFNQSSHFITHQ[p.R423Q]QIHLGDRPYRCPECGKTFNQRSHFLT	FITHQQIHL,QIHLGDRPY,SHFITHQQI,SSHFITHQQI,QQIHLGDRPY,QIHLGDRPYR,SHFITHQQIH	CRC
ZNF780A	c.1397G>A	p.R466Q	SNEKPFVCRECEMAFRYHCQLIEHS[p.R466Q]QIHTGDKPFECQDCGKAFNRGSSLVQ	HSQIHTGDK,QIHTGDKPF,CQLIEHSQI,QLIEHSQIH,QLIEHSQIHT,SQIHTGDKPF,CQLIEHSQIH	UCEC
ZNF782	c.1450G>T	p.G484W	FNYKSILIVHQRTHTGEKPFECNEC[p.G484W]WKSFSHMSGLRNHRRTHTGERPYKCD	NECWKSFSH,KPFECNECW,CWKSFSHMSG,FECNECWKSF,NECWKSFSHM,WKSFSHMSGL	LUAD
ZNF782	c.434G>T	p.C145F	KPHNRDINIFRARMMPCKCDIAGSA[p.C145F]FQGLSLMAPHCQYSKEKAHERNVCDK	SAFQGLSLM,KCDIAGSAF,IAGSAFQGL,GSAFQGLSL,FQGLSLMAP,DIAGSAFQGL,CKCDIAGSAF,AGSAFQGLSL,GSAFQGLSLM,SAFQGLSLMA,FQGLSLMAPH	TGCT
ZNF782	c.740A>C	p.K247T	KAFLEKAALVTSNSTHPKGKSYNFN[p.K247T]TFGENKYDKSTFIIPQNMNPEKSHYE	KGKSYNFNT,KSYNFNTFG,GKSYNFNTF,FNTFGENKY,NTFGENKYDK,KGKSYNFNTF	CRC
ZNF799	c.121T>G	p.W41G	IRVDAGHKPHEYQEYGEKRNTRKQF[p.W41G]GKTFSYCHSFQTHKISHTGHKPYDCK	KQFGKTFSY,RNTRKQFGK,TRKQFGKTF,KRNTRKQFGK,RKQFGKTFSY,KQFGKTFSYC,GKTFSYCHSF	BLCA
ZNF799	c.127A>G	p.T43A	VDAGHKPHEYQEYGEKRNTRKQFWK[p.T43A]AFSYCHSFQTHKISHTGHKPYDCKEC	KQFWKAFSY,KAFSYCHSF,NTRKQFWKA,TRKQFWKAF,KAFSYCHSFQ,RKQFWKAFSY,NTRKQFWKAF,WKAFSYCHSF,KQFWKAFSYC	BLCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZNF799	c.1357T>C	p.C453R	KAYRISSSLRRHETTHTGEKPYKCK[p.C453R]RGKAFIDFYSFQNHKTTHAGEKPYEC	KPYKCKRGK,KCKRGKAFI,RGKAFIDFY,YKCKRGKAF,KRGKAFIDF,RGKAFIDFYS,KRGKAFIDFY,KPYKCKRGKA,CKRGKAFIDF	TGCT
ZNF804B	c.1930_1931CC>AG	p.P644S	NDIDEDLSFPSYISRFKKHKLIPCS[p.P644S]SHLEFEDERQFNCKSSPCTVGGHSDHG	KLIPCSSHL,IPCSSHLEF,HKLIPCSSH,LIPCSSHLEF,HKLIPCSSHL	TGCT
ZNF814	c.959_960GG>AA	p.G320E	KHECGECGKSFSKYVSFSNHQRVHT[p.G320E]EKRPYECGECGKSFSKYASFSNHQRVH	HQRVHTEKR,RVHTEKRPY,RVHTEKRPYE,QRVHTEKRPY	KIRP
ZNF814	c.968C>A	p.P323H	CGECGKSFSKYVSFSNHQRVHTGKR[p.P323H]HYECGECGKSFSKYASFSNHQRVHTE	RVHTGKRHY,RVHTGKRHYE,HQRVHTGKRH,QRVHTGKRHY	KIRP
ZNF814	c.970T>C	p.Y324H	GECGKSFSKYVSFSNHQRVHTGKRP[p.Y324H]HECGECGKSFSKYASFSNHQRVHTEK	RVHTGKRPH,RVHTGKRPHE	TGCT
ZNF823	c.1640G>T	p.R547I	SGEKPYECKECGKAFSWLTCLLRHE[p.R547I]IIHTGEKPYECLQCGKAFTRSRFLRG	WLTCLLRHEI	UCEC
ZNF831	c.146_147insC	p.A49fs	PGGQASPHLTLGPVLLPPEQGLAPP[p.A49fs]HCVPEGPAHPTVPHGASRGPPAPRPASDGQPRWGQRALHTQPCAAA*	ALHTQPCAA,HGASRGPPA,ASRGPPAPR,RALHTQPCA,DGQPRWGQR,QPRWGQRAL,ALHTQPCAAA,RALHTQPCAA,VPEGPAHPTV,GQPRWGQRAL,GQRALHTQPC,RPASDGQPRW	STAD
ZNF831	c.1849C>A	p.Q617K	AREAMAGKGRAGGRKCGQRRLKMFS[p.Q617K]KEKWQVYGDETFKRIYQKMKASPHGG	RLKMFSKEK,MFSKEKWQV,QRRLKMFSK,FSKEKWQVY,LKMFSKEKW,KMFSKEKWQV,GQRRLKMFSK,RRLKMFSKEK,MFSKEKWQVY,RLKMFSKEKW	LUAD
ZNF831	c.2847G>T	p.E949D	QAPRVLSALADNAFSPKYLLRLPQA[p.E949D]DTPLPLPIPWGPRHSQDSLCSSGWPE	RLPQADTPL,PQADTPLPL,LPQADTPLPL,LRLPQADTPL	CRC
ZNF831	c.4178G>A	p.R1393Q	EGDCRQTLGTLSLGTSSRIVREMDK[p.R1393Q]QTVKDISPSAGEHGDCTTHSTAATSG	REMDKQTVK,QTVKDISPSA	SKCM
ZNF836	c.1712T>A	p.I571N	RIHTGEQPYKCNVCGKVFNYSGNLS[p.I571N]NHKRIHTGEKPFQCNECGTVFRNYSC	YSGNLSNHK,FNYSGNLSNH	CLL
ZNF836	c.1822A>C	p.K608Q	QCNECGTVFRNYSCLARHLRIHTGQ[p.K608Q]QPYKCNVCGKVFNDSGNLSNHKRIHT	RIHTGQQPY,GQQPYKCNV,RIHTGQQPYK,LRIHTGQQPY	CLL
ZNF836	c.1889G>T	p.R630I	TGQKPYKCNVCGKVFNDSGNLSNHK[p.R630I]IIHTGEKPFQCNECGKVFSYYSCLAR	KIIHTGEKPF	UCEC
ZNF836	c.2561G>T	p.R854I	TGDKPYKCNECGKAFIERSKLVYHQ[p.R854I]INHTGEKPYKCIECGKAFGRFSCLNK	KLVYHQINH,HQINHTGEK,RSKLVYHQI,INHTGEKPY,KLVYHQINHT,RSKLVYHQIN,INHTGEKPYK,QINHTGEKPY	UCEC
ZNF841	c.2270G>T	p.R757I	TGEMPYKCIECGKVFNSTTTLARHR[p.R757I]IIHTGEKPYKCNECGKVFRYRSGLAR	TTTLARHRI	UCEC
ZNF845	c.1269G>A	p.M423I	LTRHRRLHTGEKPYKCNDCGKTFSQ[p.M423I]ISSLVYHRRLHTGEKPYKCEECDEAF	FSQISSLVY,KTFSQISSL,QISSLVYHR,ISSLVYHRR,TFSQISSLV,SQISSLVYH,KTFSQISSLV,SQISSLVYHR,QISSLVYHRR,TFSQISSLVY,GKTFSQISSL	CLL
ZNF845	c.2774G>A	p.R925H	AHLACHHRIHTGEKPYKCNECGKTF[p.R925H]HHNSVLVIHKTIHTGEKPYKCNECGK	KTFHHNSVL,GKTFHHNSV,FHHNSVLVI,KTFHHNSVLV,TFHHNSVLVI,CGKTFHHNSV,HHNSVLVIHK,GKTFHHNSVL,FHHNSVLVIH	PRAD
ZNF880	c.1217A>G	p.Q406R	ECKECGKVFRHKFCLTNHHRMHTGE[p.Q406R]RPYKCNECGKAFRDCSGLTAHLIHT	HHRMHTGER,HRMHTGERPY	KIRC
ZP3	c.1085_1086insG	p.V362fs	VMSQWSRSASRNRRHVTEEADVTVG[p.V362fs]ATDLPGQEG*	EEADVTVGA,EEADVTVGAT,TEEADVTVGA	KIRC
ZPBP	c.460C>T	p.R154C	NFEESMSGIYTCFLEYKPTVEEIVK[p.R154C]CLQLKYAIYAYREPHYYYQFTARYHA	IVKCLQLKY,CLQLKYAIY,EEIVKCLQL,CLQLKYAIYA,IVKCLQLKYA,KCLQLKYAIY,VEEIVKCLQL	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZSCAN18	c.674_675insC	p.P225fs	SSILSDGVYERHMDPLLLPGELASP[p.P225fs]QPGPWSWGDPGTF*	WSWGDPGTF,LASPQPGPW,SPQPGPWSW,GELASPQPG	STAD
ZSWIM2	c.641C>A	p.S214Y	TSMLKCPLCRKEFAPLKLILEEFKN[p.5214Y]YSKLVAAAEKERLDKHLGIPCNNCKQ	KNYSKLVAA,LILEEFKNY,FKNYSKLVA,EEFKNYSKL,ILEEFKNYSK,YSKLVAAAEK,KNYSKLVAAA,KLILEEFKNY,FKNYSKLVAA,LEEFKNYSKL,EEFKNYSKLV	LUAD
ZSWIM4	c.1219G>A	p.E407K	GPSLQPTMAPAPELLQKGSTCITNT[p.E407K]KGWVGHPLDPIGCLCRALLEACRLEE	GSTCITNTK,TKGWVGHPL,KGSTCITNTK,NTKGWVGHPL	CESC
ZSWIM6	c.1829delA	p.Q610fs	LAIAIVNTLRRQQQKQLEMFRTQKK[p.Q610fs]SYPIKT*	RTQKKSYPI,TQKKSYPIK,MFRTQKKSY,RTQKKSYPIK,EMFRTQKKSY,FRTQKKSYPI	KICH
ZZEF1	c.89T>C	p.V30A	PSHSSEDEAAAAGGEGWGPHQDWAA[p.V30A]ASGTTPGPGVAAPALPPAAALLEPAR	GPHQDWAAA,WAAASGTTPG	ACC
ZZZ3	c.14G>A	p.R5Q	MAAS[p.R5Q]QSTRVTRSTVGLNGLDESFCGRTLRN	MAASQSTRV,ASQSTRVTR,SQSTRVTRST	HNSC
ZZZ3	c.485G>A	p.R162Q	IKSDKESVEQRSTVVDNDADFQGTK[p.R162Q]QACRCLILDDCEKREIKKVNVSEEGP	KQACRCLIL,GTKQACRCLI,DFQGTKQACR,TKQACRCLIL	LUSC

Example 5

[00418] Recurrent Mutations for Cancer Subtype Specific Immunogenic compositions. The Cancer Genome Atlas (TCGA) contains comprehensive large-scale genome sequencing data from tumor samples to catalogue genetic mutations responsible for cancer. Tumor-specific neoantigenic peptides for use in an immunogenic composition can be selected based on a number of criteria. The first criteria is based on gene expression. The fraction of patients (per tumor type) who express the gene at >10 transcripts per million was determined. Estimates assume a random assortment of HLA type vs. mutation status of each gene vs. gene expression (per tumor type). National yearly incidence was used to quantify the population that could be treated with each peptide. Peptides were ranked by expected population. The results of the analysis is shown in Table 9.

Table 9

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
RBM14 p.AAAAAAA286del (uc009yrj.2)	VTAASTSYY	19282	Pancreatic Cancer	HLA.A01.01 HLA.A03.01 HLA.A11.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.01 HLA.B15.03 HLA.B15.17 HLA.B58.01
HRAS p.G12D (uc001lpv.2) KRAS p.G12D (uc001rgp.1) NRAS p.G12D (uc009wgu.2)	KLVVVGADGV	16466	Colorectal Cancer Pancreatic Cancer Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	KLVVVGAVGV	13995	Colorectal Cancer Lung Adenocarcinoma Pancreatic Cancer Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	VVGAVGVGK	11278	Colorectal Cancer Lung Adenocarcinoma Pancreatic Cancer Uterine Corpus Endometrial Carcinoma	HLA.A03.01 HLA.A11.01
KRAS p.G12C (uc001rgp.1) NRAS p.G12C (uc009wgu.2) HRAS p.G12C (uc001lpv.2)	KLVVVGACGV	7538	Colorectal Cancer Lung Adenocarcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
KRAS p.G12C (uc001rgp.1) NRAS p.G12C (uc009wgu.2) HRAS p.G12C (uc001lpv.2)	VVGACGVGK	5751	Colorectal Cancer Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	VVVGAVGVGK	5535	Colorectal Cancer Lung Adenocarcinoma Pancreatic Cancer	HLA.A11.01 HLA.A68.01
TP53 p.R248W (uc002gim.2)	GMNWRPILTI	5006	Breast Cancer Colorectal Cancer Pancreatic Cancer	HLA.A02.01 HLA.A02.03
PIK3CA p.E542K (uc003fjk.2)	AISTRDPLSK	4852	Bladder Cancer Breast Cancer	HLA.A03.01 HLA.A11.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
FRG1B p.I10T (uc010ztl.1)	KLSDSRTAL	4782	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.B07.02 HLA.B15.03
GATA3 p.H435fs (uc001ijz.2)	KIMFATLQR	4535	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
HRAS p.G12D (uc001lpv.2) KRAS p.G12D (uc001rgp.1) NRAS p.G12D (uc009wgu.2)	VVGADGVGK	4530	Colorectal Cancer Pancreatic Cancer	HLA.A11.01
NRAS p.Q61R (uc009wgu.2) KRAS p.Q61R (uc001rgp.1) HRAS p.Q61R (uc001lpv.2)	ILDTAGREEY	4433	Melanoma Thyroid Cancer	HLA.A01.01
NRAS p.Q61K (uc009wgu.2) HRAS p.Q61K (uc001lpv.2) KRAS p.Q61K (uc001rgp.1)	ILDTAGKEEY	4203	Colorectal Cancer Melanoma	HLA.A01.01
GATA3 p.H435fs (uc001ijz.2)	MLTGPPARV	4113	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
RBM47 p.495_502AAAAAAAA>A (uc003gvc.2)	AAAAVIPTV	4035	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01 HLA.B15.17
RBM47 p.495_502AAAAAAAA>A (uc003gvc.2)	AAAAAVIPTV	3864	Pancreatic Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06 HLA.A68.02
GATA3 p.H435fs (uc001ijz.2)	YMFLKAESK	3832	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	SMLTGPPARV	3718	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	YMFLKAESKI	3718	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	TLQRSSLWCL	3621	Breast Cancer	HLA.A02.01 HLA.A02.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
AP3S1 p.K41fs (uc003krl.2)	LVSEMKMFV	3603	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
PIK3CA p.H1047R (uc003fjk.2)	FMKQMNDAR	3582	Breast Cancer	HLA.A31.01 HLA.A33.01 HLA.A68.01
KRAS p.Q61L (uc001rgp.1) NRAS p.Q61L (uc009wgu.2) HRAS p.Q61L (uc001ipv.2)	LLDILDTAGL	3563	Colorectal Cancer Lung Adenocarcinoma Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	FATLQRSSL	3551	Breast Cancer	HLA.B07.02 HLA.B08.01 HLA.B39.01
AP3S1 p.K41fs (uc003krl.2)	HLVSEMKMFV	3524	Pancreatic Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06 HLA.A68.02
FRG1B p.L52S (uc010ztl.1)	ALSASNSCFI	3502	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.L52S (uc010ztl.1)	FQNGKMALSA	3502	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
RBM14 p.AAAAAAA286del (uc009yrj.2)	AVTAASTSY	3477	Pancreatic Cancer	HLA.A26.02 HLA.A29.02 HLA.B15.01 HLA.B15.03 HLA.B15.17
KRAS p.G12R (uc001rgp.1) NRAS p.G12R (uc009wgu.2)	VVGARGVGK	3176	Pancreatic Cancer	HLA.A03.01 HLA.A11.01
PIK3CA p.E545K (uc003fjk.2)	SEITKQEKDF	3090	Breast Cancer	HLA.B44.02
FRG1B p.A53T (uc010ztl.1)	LLTSNSCFI	3016	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
FRG1B p.A53T (uc010ztl.1)	ALLTSNSCFI	2959	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.I10T (uc010ztl.1)	RTALKSGYGK	2787	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
FRG1B p.A50P (uc010ztl.1)	FQNGKMPLL	2781	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B15.03 HLA.B39.01
PIK3CA p.H1047L (uc003fjk.2)	FMKQMNDAL	2610	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B08.01 HLA.B15.01 HLA.B15.03
KRAS p.Q61L (uc001rgp.1) NRAS p.Q61L (uc009wgu.2) HRAS p.Q61L (uc001ipv.2)	ILDTAGLEEY	2555	Colorectal Cancer Lung Adenocarcinoma Melanoma	HLA.A01.01
FRG1B p.A11T (uc010ztl.1)	ITLKSGYGK	2523	Prostate Cancer Melanoma	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
ANAPC1 p.T537A (uc002thi.2)	VSAPKPLSK	2521	Pancreatic Cancer Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01
GATA3 p.H435fs (uc001ijz.2)	FLKAESKIM	2496	Breast Cancer	HLA.A02.03 HLA.B08.01 HLA.B15.01 HLA.B15.03
FRG1B p.A50P (uc010ztl.1)	FQNGKMPLLA	2486	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
PIK3CA p.H1047R (uc003fjk.2)	YFMKQMNDAR	2478	Breast Cancer	HLA.A33.01 HLA.A68.01
GATA3 p.S408fs (uc001ijz.2)	AIQPVLWTT	2371	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.06
RBM14 p.AAAAAAA286del (uc009yrj.2)	AVTAASTSYY	2363	Pancreatic Cancer	HLA.A11.01
FRG1B p.I10T (uc010ztl.1)	KLSDSRTALK	2356	Prostate Cancer	HLA.A03.01 HLA.A11.01
FRG1B p.A11T (uc010ztl.1)	KLSDSRITL	2328	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B15.03
ANAPC1 p.T537A (uc002thi.2)	GVSAPKPLSK	2260	Pancreatic Cancer Prostate Cancer	HLA.A03.01 HLA.A11.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TP53 p.Y220C (uc002gim.2)	VVVPCEPPEV	2200	Breast Cancer	HLA.A02.01 HLA.A02.06
TP53 p.R248W (uc002gim.2)	SSCMGGMNWR	2135	Colorectal Cancer	HLA.A11.01 HLA.A68.01
KRAS p.G12R (uc001rgp.1) NRAS p.G12R (uc009wgu.2)	GARGVGKSAL	2075	Pancreatic Cancer	HLA.B07.02
RAC1 p.P29S (uc003spx.2)	TTNAFSGEY	2042	Melanoma	HLA.A01.01 HLA.A11.01 HLA.A25.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.01 HLA.B15.03 HLA.B15.17
GATA3 p.H435fs (uc001ijz.2)	GPPARVPAV	2039	Breast Cancer	HLA.B07.02
GATA3 p.H435fs (uc001ijz.2)	KPKRDGYMF	2039	Breast Cancer	HLA.B07.02
GATA3 p.H435fs (uc001ijz.2)	KPKRDGYMFL	2039	Breast Cancer	HLA.B07.02
KRAS p.G12A (uc001rgp.1) HRAS p.G12A (uc001lpv.2) NRAS p.G12A (uc009wgu.2)	KLVVVGAAGV	2034	Colorectal Cancer Lung Adenocarcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
SPOP p.F133L (uc002ipg.2)	FVQGKDWGL	2002	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
GATA3 p.H435fs (uc001ijz.2)	CSMLTGPPAR	1995	Breast Cancer	HLA.A11.01 HLA.A33.01 HLA.A68.01
WASH3P p.G175S (uc002cdi.2) WASH2P p.G175S (uc002tkh.2)	SIRQAGGISK	1978	Prostate Cancer Melanoma	HLA.A03.01 HLA.A11.01
ARFGAP3 p.N299fs (uc003bdd.2)	EIAEVLFHI	1959	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A26.02 HLA.A26.03 HLA.A68.02 HLA.A69.01
GATA3 p.S408fs (uc001ijz.2)	ALQPLQPHA	1906	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
ARFGAP3 p.N299fs (uc003bdd.2)	SAWDLEIAEV	1892	Prostate Cancer	HLA.A02.01 HLA.A02.06 HLA.A68.02
FRG1B p.I59V (uc010ztl.1) FRG1 p.I157V (uc003izs.2)	LLASNSCFV	1824	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
ARFGAP3 p.N299fs (uc003bdd.2)	KMLTQTDSA	1818	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
PTH2 p.L22del (uc002pnn.1) CTSA p.L37del (uc002xqh.2) AGPAT2 p.17_18insL (uc004cii.1)	LLLLLLLLV	1807	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
TP53 p.R248Q (uc002gim.2)	SSCMGGMNQR	1795	Bladder Cancer	HLA.A11.01 HLA.A68.01
KRAS p.G12C (uc001rgp.1) NRAS p.G12C (uc009wgu.2) HRAS p.G12C (uc001lpv.2)	VVVGACGVGK	1785	Colorectal Cancer Lung Adenocarcinoma	HLA.A11.01
PIK3CA p.N345K (uc003fjk.2)	KILCATYVK	1776	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01
FRG1B p.A11T (uc010ztl.1)	KLSDSRITLK	1749	Prostate Cancer	HLA.A03.01 HLA.A11.01
FRG1B p.A11T (uc010ztl.1)	RITLKSGYGK	1749	Prostate Cancer	HLA.A03.01 HLA.A11.01
GATA3 p.H435fs (uc001ijz.2)	AVPFDLHFCR	1749	Breast Cancer	HLA.A11.01 HLA.A68.01
PIK3CA p.E542K (uc003fjk.2)	ISTRDPLSK	1746	Breast Cancer	HLA.A11.01
TP53 p.G245S (uc002gim.2)	SSCMGSMNR	1732	Colorectal Cancer	HLA.A11.01 HLA.A31.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	AESKIMFATL	1731	Breast Cancer	HLA.B40.01 HLA.B44.02
AKT1 p.E17K (uc001ypk.2) AKT2 p.E17K (uc002onf.2)	WLHKRGKYIK	1717	Breast Cancer	HLA.A03.01
PIK3CA p.N345K (uc003fjk.2)	ILCATYVKV	1715	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
FRG1B p.I59V (uc010ztl.1) FRG1 p.I157V (uc003izs.2)	ALLASNSCFV	1698	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
FRG1B p.L52S (uc010ztl.1)	SASNSCFIR	1685	Prostate Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
PIK3CA p.N345K (uc003fjk.2)	KILCATYVKV	1679	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
AP3S1 p.K41fs (uc003krl.2)	ETFHLVSEM	1635	Pancreatic Cancer	HLA.A25.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A68.01 HLA.A68.02 HLA.A69.01 HLA.B15.17
PIK3CA p.N345K (uc003fjk.2)	KVNIRDIDK	1620	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01
KRAS p.G12A (uc001rgp.1) HRAS p.G12A (uc001ipv.2) NRAS p.G12A (uc009wgu.2)	VVGAAGVGK	1613	Colorectal Cancer Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01
CDC27 p.D555E (uc002ile.3)	TLWHLQKEV	1577	Colorectal Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	ESKIMFATL	1573	Breast Cancer	HLA.A68.02 HLA.B08.01
TP53 p.P75fs (uc002gim.2)	KPTRAATVSV	1536	Colorectal Cancer	HLA.B07.02
CTNNB1 p.T41A (uc010hia.1)	ATAPSLSGK	1536	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
CDC27 p.D555E (uc002ile.3)	HLQKEVALSV	1530	Colorectal Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
PIK3CA p.H1047L (uc003fjk.2)	ALHGGWTTK	1513	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01
UBC p.R73L (uc002gyy.3)	RLRGGMQIFV	1474	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
PEX1 p.I370fs (uc003uly.2)	KMRRPVCYK	1456	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TP53 p.C238Y (uc002gim.2)	TTIHYNYMY	1454	Colorectal Cancer	HLA.A01.01 HLA.A11.01 HLA.A25.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.17
ANAPC1 p.T537A (uc002thi.2)	APKPLSKLL	1449	Pancreatic Cancer	HLA.B07.02
FRG1B p.A53T (uc010ztl.1)	LTSNSCFIR	1447	Prostate Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
RNF43 p.G659fs (uc002iwf.2)	TQLARFFPI	1442	Colorectal Cancer Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A23.01 HLA.A30.01 HLA.A31.01 HLA.A69.01 HLA.B08.01 HLA.B08.03 HLA.B15.03 HLA.B38.01 HLA.B39.01 HLA.B40.01 HLA.B40.02
AP3S1 p.K41fs (uc003krl.2)	ETFHLVSEMK	1440	Pancreatic Cancer	HLA.A11.01 HLA.A68.01
PIK3CA p.H1047R (uc003fjk.2)	ARHGGWTTK	1426	Breast Cancer	HLA.B27.05
PIK3CA p.H1047R (uc003fjk.2)	ARHGGWTTKM	1426	Breast Cancer	HLA.B27.05
GATA3 p.S408fs (uc001ijz.2)	QPVLWTTPPL	1421	Breast Cancer	HLA.B07.02
FRG1B p.A50P (uc010ztl.1)	MPLLASNSCF	1374	Prostate Cancer	HLA.B07.02
WASH3P p.G175S (uc002cdi.2) WASH2P p.G175S (uc002tkh.2)	ISKAKLRSM	1337	Prostate Cancer Melanoma	HLA.A30.01 HLA.B08.01 HLA.B15.17
HRAS p.G13R (uc001lpv.2) NRAS p.G13R (uc009wgu.2)	VVGAGRVGK	1324	Colorectal Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
ACADS p.R330H (uc001tza.3)	RLLTWHAAM	1321	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B08.01 HLA.B15.01 HLA.B15.03 HLA.B15.17
HRAS p.G12D (uc001lpv.2) KRAS p.G12D (uc001rgp.1) NRAS p.G12D (uc009wgu.2)	LVVVGADGV	1284	Pancreatic Cancer	HLA.A02.06 HLA.A68.02 HLA.A69.01
KRAS p.G12S (uc001rgp.1) HRAS p.G12S (uc001lpv.2) NRAS p.G12S (uc009wgu.2)	KLVVVGASGV	1278	Colorectal Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
TP53 p.A159V (uc002gim.2)	RVRVMAIYK	1271	Bladder Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01
HLA-A p.Q78R (uc003nol.2)	IEREGPEYW	1271	Prostate Cancer	HLA.B44.02 HLA.B44.03
GATA3 p.H435fs (uc001ijz.2)	LQRSSLWCL	1248	Breast Cancer	HLA.A02.06 HLA.B15.01 HLA.B15.03
ZMIZ2 p.VAAAAATATATATAT153del (uc003tlr.2)	ALQEKQSQEL	1226	Pancreatic Cancer	HLA.A02.01 HLA.A02.03
GIGYF2 p.Q1005del (uc002vtj.3)	KLSGWGNVSK	1204	Pancreatic Cancer	HLA.A03.01 HLA.A11.01
FRG1B p.L52S (uc010ztl.1)	LSASNSCFIR	1190	Prostate Cancer	HLA.A11.01 HLA.A68.01
AKT1 p.E17K (uc001ypk.2) AKT2 p.E17K (uc002onf.2)	WLHKRGKYI	1172	Breast Cancer	HLA.A02.03 HLA.B08.01
PEX1 p.I370fs (uc003uly.2)	KLGQIIMKK	1165	Prostate Cancer	HLA.A03.01 HLA.A11.01
RAC1 p.P29S (uc003spx.2)	FSGEYIPTV	1152	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
GATA3 p.H435fs (uc001ijz.2)	IMKPKRDGY	1151	Breast Cancer	HLA.B15.01 HLA.B15.03
AEBP1 p.K1133del (uc003tkb.2)	EEEIATGQAF	1143	Pancreatic Cancer	HLA.B44.02
FBXW7 p.R465H (uc003ims.2)	TVHCMHLHEK	1142	Colorectal Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TSPAN4 p.L92V (uc001isd.1)	LTFFLLLLV	1140	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01 HLA.B15.17
TP53 p.R158L (uc002gim.2)	RVLAMAIYK	1136	Lung Squamous Cell Carcinoma	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	LVVVGAVGV	1130	Pancreatic Cancer	HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
GATA3 p.S408fs (uc001ijz.2)	HMSSLSHISA	1127	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
CTNNB1 p.S37F (uc010hia.1)	YLDSGIHFG	1121	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.02 HLA.A02.06
CTNNB1 p.S37F (uc010hia.1)	YLDSGIHFGA	1120	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
CTNNB1 p.S37C (uc010hia.1)	YLDSGIHCGA	1111	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
SF3B1 p.K700E (uc002uue.2)	GLVDEQQEV	1099	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
KRAS p.G12R (uc001rgp.1) NRAS p.G12R (uc009wgu.2)	VVVGARGVGK	1082	Pancreatic Cancer	HLA.A11.01
EGFR p.L858R (uc003tqk.2)	KITDFGRAK	1054	Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01 HLA.A30.01
TP53 p.E271K (uc002gim.2)	NLLGRNSFK	1046	Bladder Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01
TSPAN4 p.L92V (uc001isd.1)	FLLLLVVFL	1044	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	LLVVFLLEA	1044	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TSPAN4 p.L92V (uc001isd.1)	LLLLVVFLL	1030	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	FLLLLVVFLL	1027	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	LLLVVFLLEA	1027	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	LLTFFLLLLV	1027	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
ARFGAP3 p.N299fs (uc003bdd.2)	LEIAEVLFHI	1024	Prostate Cancer	HLA.B40.01 HLA.B44.02
FRG1B p.I10T (uc010ztl.1)	TALKSGYGK	1020	Prostate Cancer	HLA.A11.01 HLA.A68.01
RBM14 p.AAAAAAA286del (uc009yrj.2)	ATAAAVTAA	1020	Pancreatic Cancer	HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
KRAS p.G12S (uc001rgp.1) HRAS p.G12S (uc001ipv.2) NRAS p.G12S (uc009wgu.2)	VVGASGVGK	1019	Colorectal Cancer	HLA.A03.01 HLA.A11.01
UBC p.L149R (uc002gyy.3)	STLHLVLRR	1014	Prostate Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
PIK3CA p.N345K (uc003fjk.2)	ATYVKVNIR	1007	Breast Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
ERBB3 p.V104M (uc001sjh.2)	RMVRGTQVY	990	Colorectal Cancer	HLA.A03.01 HLA.A29.02 HLA.A80.01 HLA.B15.01 HLA.B15.03 HLA.B15.17
GATA3 p.H435fs (uc001ijz.2)	AESKIMFAT	984	Breast Cancer	HLA.B40.01 HLA.B40.02 HLA.B45.01
FRG1B p.L52S (uc010ztl.1)	ALSASNSCF	982	Prostate Cancer	HLA.B15.01 HLA.B15.03
TP53 p.E271K (uc002gim.2)	LLGRNSFKV	978	Bladder Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TP53 p.E271K (uc002gim.2)	NLLGRNSFKV	969	Bladder Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.A11T (uc010ztl.1)	TLKSGYGKY	969	Prostate Cancer	HLA.A26.02 HLA.A29.02 HLA.B15.01 HLA.B15.03
NFE2L2 p.E79Q (uc002ulh.3)	QLDEQTGEFL	966	Lung Squamous Cell Carcinoma	HLA.A02.01 HLA.A02.06
TP53 p.K132N (uc002gim.2)	ALNNMFCQL	955	Bladder Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B15.01 HLA.B15.03
MAP2K1 p.P124S (uc010bhq.2)	NSSYIVGFY	943	Melanoma	HLA.A01.01 HLA.A26.01 HLA.A26.02 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.03 HLA.B15.17
TSPAN9 p.S50L (uc001qlp.2)	ATFSPSFPL	937	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.02 HLA.A69.01 HLA.B15.03 HLA.B15.17 HLA.B58.01
SF3B1 p.K700E (uc002uue.2)	QEVRTISAL	936	Breast Cancer	HLA.B15.03 HLA.B39.01 HLA.B40.01 HLA.B40.02 HLA.B44.02 HLA.B44.03
ZNF91 p.R333H (uc002nre.2)	FSHSSTLAK	907	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A68.01
FNBP4 p.TT58del (uc009ylv.2)	APSAATTTA	905	Prostate Cancer	HLA.B07.02
FNBP4 p.TT58del (uc009ylv.2)	APSAATTTAV	905	Prostate Cancer	HLA.B07.02

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
RAC1 p.P29S (uc003spx.2)	YTTNAFSGEY	901	Melanoma	HLA.A01.01 HLA.A68.01
ACADS p.R330H (uc001tza.3)	LTWHAAMLK	896	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
TP53 p.C242F (uc002gim.2)	SSFMGGMNR	889	Lung Squamous Cell Carcinoma	HLA.A03.01 HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLPAPEL	878	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.06
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLLLLLPA	876	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLLLLPA	876	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLLPAPEL	876	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
ZMIZ2 p.VAAAAATATATATAT153del (uc003tlr.2)	AAAAAVAAL	855	Pancreatic Cancer	HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.B07.02 HLA.B15.03 HLA.B15.17
PODXL p.28_30PSP>P (uc003vqw.3)	SPSPSQNAT	852	Prostate Cancer	HLA.B07.02
PODXL p.28_30PSP>P (uc003vqw.3)	SPSQNATQTT	852	Prostate Cancer	HLA.B07.02
AP3S1 p.K41fs (uc003krl.2)	HLVSEMKMF	849	Pancreatic Cancer	HLA.A26.02 HLA.B15.01 HLA.B15.03
STK19 p.D89N (uc003nyv.2)	NPIFRFSSL	849	Melanoma	HLA.A26.02 HLA.B07.02 HLA.B08.01 HLA.B39.01
NUF2 p.S340L (uc001gcq.1)	NLFKRLMIV	845	Colorectal Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B08.01
FRG1B p.A53T (uc010ztl.1)	ALLTSNSCF	833	Prostate Cancer	HLA.B15.01 HLA.B15.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
UBC p.L149R (uc002gyy.3)	LVLRRRGGM	829	Prostate Cancer	HLA.B08.01
TP53 p.A159P (uc002gim.2)	RVRPMAIYK	820	Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
FRG1B p.K13N (uc010ztl.1)	IALNSGYGK	791	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	VPFDLHFCR	791	Breast Cancer	HLA.A33.01 HLA.A68.01
UBC p.L149R (uc002gyy.3)	STLHLVLRRR	789	Prostate Cancer	HLA.A11.01 HLA.A33.01 HLA.A68.01
ACADS p.R330H (uc001tza.3)	LLTWHAAML	789	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	ATLQRSSLW	782	Breast Cancer	HLA.B15.17 HLA.B57.01 HLA.B58.01
MAP2K1 p.P124S (uc010bhq.2)	VLHECNSSYI	779	Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
ACADS p.R330H (uc001tza.3)	RLLTWHAAML	773	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
RXRA p.S427F (uc004cfb.2) RXRG p.S428F (uc001gda.2)	RLPALRFIGL	771	Bladder Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
ERBB3 p.V104M (uc001sjh.2)	LPLPNLRMV	765	Colorectal Cancer	HLA.B07.02
TSPAN9 p.S50L (uc001qlp.2)	LLSAANLVI	759	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.B15.01 HLA.B15.03 HLA.B15.17
CTNNB1 p.S33F (uc010hia.1)	YLDFGIHSGA	755	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
CTNNB1 p.S33F (uc010hia.1)	YLDFGIHSG	754	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.02 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
PTEN p.R130G (uc001kfb.2)	GTGVMICAY	751	Uterine Corpus Endometrial Carcinoma	HLA.A29.02 HLA.B15.01 HLA.B15.17
RXRA p.S427F (uc004cfb.2) RXRG p.S428F (uc001gda.2)	LPALRFIGL	748	Bladder Cancer	HLA.B07.02 HLA.B08.01
NOTCH2 p.P6fs (uc001eik.2)	MPALRRSAV	747	Bladder Cancer	HLA.B07.02 HLA.B08.01
JMY p.PPPPPPPPPPP811del (uc003kfx.3)	LPPTPPPLPV	733	Pancreatic Cancer	HLA.B07.02
JMY p.PPPPPPPPPPP811del (uc003kfx.3)	SPLPPTPPPL	733	Pancreatic Cancer	HLA.B07.02
ACADS p.R330H (uc001tza.3)	LLTWHAAMLK	729	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	RSSIMKPKR	703	Breast Cancer	HLA.A30.01 HLA.A31.01
OGFOD1 p.G477fs (uc002ejb.2)	FLLLTLPKV	702	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
HERC2P3 p.A803V (uc001ytg.2)	RVRDMKCLM	699	Pancreatic Cancer	HLA.A30.01 HLA.B07.02 HLA.B15.17
C1QB p.GPKGPMGPKGGPGAPGAP90del (uc001bgd.2)	ESGDYKATQK	697	Pancreatic Cancer	HLA.A68.01
SLC38A10 p.1071_1072ll>l (uc002jzz.1)	GLNPLPDVQV	689	Pancreatic Cancer	HLA.A02.01 HLA.A02.03
UBB p.I188fs (uc002gpx.2) UBC p.I191T (uc002gyy.3)	IPPTSRGSSL	686	Prostate Cancer	HLA.B07.02
UBB p.I188fs (uc002gpx.2) UBC p.I191T (uc002gyy.3)	PPTSRGSSL	686	Prostate Cancer	HLA.B07.02
CTNNB1 p.D32N (uc010hia.1)	YLNSGIHSGA	672	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.K13N (uc010ztl.1)	ALNSGYGKYL	670	Prostate Cancer	HLA.A02.01 HLA.A02.03
NBPF14 p.R25C (uc001eqf.2)	KLCPQLAENK	667	Pancreatic Cancer	HLA.A03.01 HLA.A11.01
IARS2 p.R832C (uc001hmc.2)	VIVCSFAPI	662	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01 HLA.B15.03
PIK3CA p.H1047R (uc003fjk.2)	KQMNDARHG	661	Breast Cancer	HLA.B15.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
CTNNB1 p.D32N (uc010hia.1)	YLNSGIHSG	658	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.02 HLA.A02.03
SIK3 p.950_951QQ>Q (uc001ppy.2)	QEYQELFRHM	653	Pancreatic Cancer	HLA.B40.01 HLA.B44.02
IARS2 p.R832C (uc001hmc.2)	ILDVIVCSFA	651	Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
AP3S1 p.K41fs (uc003krl.2)	RETFHLVSEM	650	Pancreatic Cancer	HLA.B40.01
PPP2R1A p.P179R (uc002pyp.2)	RMVRRAAASK	649	Uterine Corpus Endometrial Carcinoma	HLA.A03.01 HLA.A11.01
ZMIZ2 p.VAAAAATATATATAT153del (uc003tlr.2)	AAAAAAVAAL	641	Pancreatic Cancer	HLA.B07.02
HSD17B7P2 p.N175S (uc010qex.1)	SARKSNFSL	637	Prostate Cancer	HLA.A30.01 HLA.B07.02 HLA.B08.01 HLA.B15.17
ARL16 p.G6R (uc002kbf.2)	RVAGRRALSR	632	Melanoma	HLA.A03.01 HLA.A11.01 HLA.A33.01 HLA.A68.01
GATA3 p.S408fs (uc001ijz.2)	TTPPLQHGHR	623	Breast Cancer	HLA.A33.01 HLA.A68.01
AP3S1 p.K41fs (uc003krl.2)	FHLVSEMKM	619	Pancreatic Cancer	HLA.B38.01 HLA.B39.01
PLEKHA6 p.V328fs (uc001hau.2)	SIMMSWMPPL	613	Colorectal Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.B07.02
LZTS1 p.RTQDLEGALRTKGLEL432del (uc003wzr.2)	KLEGLELEV	609	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
HSD17B7P2 p.N175S (uc010qex.1)	WTSSRSARK	607	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A68.01
RBM14 p.AAAAAAA286del (uc009yrj.2)	GAAATAAAV	606	Pancreatic Cancer	HLA.A02.03 HLA.A68.02
TP53 p.R249M (uc002gim.2)	MPILTIITL	606	Lung Adenocarcinoma	HLA.A69.01 HLA.B07.02 HLA.B08.01 HLA.B15.03 HLA.B39.01 HLA.B53.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
IRF2BPL p.114_115QQ>Q (uc001xsy.2)	QLNHVDGSSK	605	Prostate Cancer	HLA.A03.01 HLA.A11.01
POLI p.D17del (uc002lfj.3)	EEDAEAWAM	599	Prostate Cancer	HLA.B40.01 HLA.B44.02 HLA.B44.03
ZNF780A p.Q600H (uc010xvh.1)	HMHLIRHQK	594	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
FRG1B p.I10T (uc010ztl.1)	LSDSRTALK	589	Prostate Cancer	HLA.A11.01
PARG p.A584T (uc001jih.2)	EETEAQHLY	585	Prostate Cancer	HLA.B44.02 HLA.B44.03
GATA3 p.S408fs (uc001ijz.2)	SSLSHISAL	573	Breast Cancer	HLA.A02.06 HLA.B08.01 HLA.B15.03 HLA.B15.17 HLA.B39.01
EGFR p.L858R (uc003tqk.2)	FGRAKLLGA	564	Lung Adenocarcinoma	HLA.B08.01
TP53 p.R249M (uc002gim.2)	RMPILTIITL	563	Lung Adenocarcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
PARG p.A584T (uc001jih.2)	TEAQHLYQSI	557	Prostate Cancer	HLA.B40.01 HLA.B44.02
CDC27 p.D555E (uc002ile.3)	EVALSVLSK	557	Colorectal Cancer	HLA.A11.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	MFLKAESKI	554	Breast Cancer	HLA.A23.01
FRG1B p.K13N (uc010ztl.1)	RIALNSGYGK	546	Prostate Cancer	HLA.A03.01 HLA.A11.01
CTNNB1 p.G34R (uc010hia.1)	YLDSRIHSGA	530	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.L52S (uc010ztl.1)	LSASNSCFI	528	Prostate Cancer	HLA.A68.02 HLA.B15.17 HLA.B58.01
AXIN2 p.W663fs (uc002jfi.2)	TPAPPPVPT	520	Colorectal Cancer	HLA.B07.02
AXIN2 p.W663fs (uc002jfi.2)	VPTCSPRTL	520	Colorectal Cancer	HLA.B07.02
FCGBP p.A2493V (uc002omp.3)	RPGLHRFVV	504	Pancreatic Cancer	HLA.B07.02 HLA.B08.01

Example 6

[00419] Therapeutic targeting of recurrent mutations expressed in genes containing extracellular domains. Tumor-specific mutations present in greater than 1% of a population of cancer patients may be targeted with a drug or therapy that recognizes the tumor-specific neoepitope resulting from the mutation. The mutation is preferably within an extracellular domain. The drug or therapy is an antibody, antibody fragment, antibody drug conjugate, aptamer, CAR, or T cell receptor. The antibody or fragment thereof may be humanized, fully humanized, or chimeric. The antibody fragment may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment.

[00420] A recurrent mutation that may be targeted is FGFR3:p.S249C. Fibroblast growth factor receptor 3 (FGFR3) is a protein that in humans is encoded by the FGFR3 gene. FGFR3 has also been designated as CD333 (cluster of differentiation 333). The full-length protein includes an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The mutation occurs in the extracellular domain of the protein. The mutation is present in 6.92% of bladder cancer (BLCA) patients analyzed and 1.12% of lung squamous cell carcinoma (LUSC) patients analyzed.

[00421] Another recurrent mutation that may be targeted is ERBB3:p.V104M. Receptor tyrosine-protein kinase erbB-3, also known as HER3 (human epidermal growth factor receptor 3), is a membrane bound protein that in humans is encoded by the ERBB3 gene. ErbB3 is a member of the epidermal growth factor receptor (EGFR/ERBB) family of receptor tyrosine kinases. The mutation is present in 1.72% of colorectal cancer (CRC), 2.86% of colon adenocarcinoma (COAD), 2.42% of stomach adenocarcinoma (STAD), and 2.06% of cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC) patients analyzed.

[00422] Another recurrent mutation that may be targeted is EGFR:p.L858R. The epidermal growth factor receptor (EGFR; ErbB-1; HER1 in humans) is the cell-surface receptor for members of the epidermal growth factor family (EGF-family) of extracellular protein ligands. The mutation is present in 3.24% of lung adenocarcinoma (LUAD) patients analyzed.

[00423] Another recurrent mutation that may be targeted is MUC4:p.H4205Q. Mucin 4 (MUC 4) is a mucin protein that in humans is encoded by the MUC4 gene. This gene encodes an integral membrane glycoprotein found on the cell surface, although secreted isoforms may exist.

The mutation is present in 2.3% of prostate adenocarcinoma (PRAD), 2.31% of bladder urothelial carcinoma (BLCA), and 7.14% of uterine carcinosarcoma (UCS) patients analyzed.

[00424] Another recurrent mutation that may be targeted is PDGFRA:p.R483fs. Platelet-derived growth factor receptor, alpha polypeptide is a protein that in humans is encoded by the PDGFRA gene. This gene encodes a cell surface tyrosine kinase receptor for members of the platelet-derived growth factor family. The mutation is present in 1.92% of prostate adenocarcinoma (PRAD) patients analyzed.

[00425] Another recurrent mutation that may be targeted is TMEM52 23_26LLPL>L. Transmembrane protein 52 is encoded by the TMEM52 gene. The mutation is present in 1.53% of prostate adenocarcinoma (PRAD) patients analyzed.

[00426] Another recurrent mutation that may be targeted is PODXL 28_30PSP>P. Podocalyxin-like protein 1 is a protein that in humans is encoded by the PODXL gene. The mutation is present in 1.53% of prostate adenocarcinoma (PRAD), 15.56% of adrenocortical carcinoma (ACC), and 3.57% of uterine carcinosarcoma (UCS) patients analyzed.

* * *

[00427] Having thus described in detail preferred embodiments of the present invention, it is to be understood that the invention defined by the above paragraphs is not to be limited to particular details set forth in the above description as many apparent variations thereof are possible without departing from the spirit or scope of the present invention.

FURTHER ASPECTS

Further aspects and embodiments of the invention are now set out in the following numbered Paragraphs; it is to be understood that the invention encompasses these aspects:

Paragraph 1. A pharmaceutical composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein: (a) the composition comprises at least one neoantigenic peptide comprising a tumor-specific mutation present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer; (b) the composition comprises at least one neoantigenic peptide comprising a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer; and (c) the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

Paragraph 2. The pharmaceutical composition according to Paragraph 1, wherein the population of subjects is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS).

Paragraph 3. The pharmaceutical composition according to Paragraph 1 or 2, wherein the population suffering from cancer was treated with, is being treated with, or is selected to

be treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitor or antiestrogen therapy.

Paragraph 4. The pharmaceutical composition according to any of Paragraphs 1 to 3, wherein the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations.

Paragraph 5. The pharmaceutical composition according to any of Paragraphs 1 to 4, wherein the at least one neoantigenic peptide comprises at least one neoantigenic peptide derived from a long peptide region flanking and including the tumor specific mutation, and wherein all contiguous segments within the long peptide are included.

Paragraph 6. The pharmaceutical composition according to any of Paragraphs 1 to 5, wherein the tumor-specific mutations are present in one or more genes listed in any of the Tables.

Paragraph 7. The pharmaceutical composition according to any of Paragraphs 1 to 6, wherein the composition comprises at least one neoantigenic peptide as defined in any of the Tables.

Paragraph 8. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein the tumor-specific mutations are present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1.

Paragraph 9. The pharmaceutical composition according to Paragraph 8, wherein at least one tumor-specific mutation is derived from alternative splicing of PD-L1 or AR.

Paragraph 10. The pharmaceutical composition according to Paragraph 9, wherein at least one tumor-specific mutation is derived from splice variant sPD-L1, AR-V1 or AR-V7.

Paragraph 11. The pharmaceutical composition according to any of Paragraph 1 to 8, wherein the tumor-specific mutations comprise drug resistance mutations.

Paragraph 12. The pharmaceutical composition according to Paragraph 11, wherein at least one tumor-specific mutation is a drug resistance mutation selected from the group

consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L.

Paragraph 13. The pharmaceutical composition according to any of Paragraphs 1 to 12, wherein the at least one tumor-specific mutation has an incidence of at least 500 patients a year in the population of subjects suffering from cancer, and wherein the at least one mutation comprises a mutation listed for the population in Table 9.

Paragraph 14. The pharmaceutical composition according to Paragraph 13, wherein the at least one neoantigenic peptide comprises at least one peptide listed in Table 9.

Paragraph 15. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from CLL; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of SF3B1:p.K700E, MYD88:p.L273P, NOTCH1:p.P2514fs, ABCA11P:p.E901D, AHNAK:p.D3823E, ZNF814:p.E348D, AHNAK:p.V1220I, AHNAK:p.H1203N, ANKRD30A:p.A232V, APOOL:p.I138L, EGR2:p.H397N, MKI67:p.H2213D, NRAS:p.Q61R, PLIN4:p.M691V, XPO1:p.E571K, ZCRB1:p.L76F, ZNF700:p.N652H, ZNF700:p.Q654R, ZNF844:p.D458H, AHNAK:p.A4046V, ANKRD36:p.P337R, C1orf170:p.T203I, CAST:p.D639E, EGR2:p.E369K, GPR123:p.L630P, IKZF3:p.L162R, MUC4:p.P4224R, OR9Q1:p.M34L, PKD2:p.Y486F, PRAMEF11:p.R104Q, SYNJ1:p.I681F, TP53:p.R248Q, TP53:p.R248W, TRPV2:p.L627del, ZNF254:p.S498A, ZNF732:p.A459T, ZNF749:p.E530Q, ZNF845:p.M423I, ABCA11P:p.G900E, ACRC:p.E243D, ACRC:p.A244V, ACSL3:p.T188S, ADAMTS2:p.D948N, AGAP6:p.S127I, AHNAK:p.A2114G, ANKRD36:p.D1014Y, ARID3A:p.G550fs, ARID4A:p.D1154E, ATP2B4:p.R183H, ATRNL1:p.L1244F, BNC1:p.Y937N, BRAF:p.K601N, BTLA:p.Q86K, C14orf177:p.G90V, C2orf44:p.N456K, C3orf15:p.R552Q, CACNA2D1:p.Y376N, CALD1:p.E340K, CCDC15:p.P488H, CCDC79:p.N440T, CCNB3:p.A932T, CD109:p.L470Q, CD209:p.Q189L, CKAP2:p.*684K, CMA1:p.I81K, CMIP:p.A230T,

CNTNAP4:p.I12F, CRYM:p.*315K, DICER1:p.E1705K, DPCR1:p.L716P, EIF3A:p.M1093L, EIF4G3:p.R8H, ETFDH:p.I281F, EWSR1:p.Y656C, F5:p.L1332P, F5:p.L1253F, FAM50A:p.H317R, FBXL13:p.S102R, FBXW7:p.R465H, FHL1:p.D184E, FILIP1:p.I522K, FRG1B:p.Q39K, GNB1:p.I80T, GPR110:p.R443G, GPR98:p.Y6152F, HDGFL1:p.188_189insA, IGF2BP2:p.T186S, IL1R2:p.L364fs, KIAA1109:p.L4680P, KRAS:p.G13D, KRTAP19-1:p.G61S, MAF:p.G53fs, MAGEC1:p.L609H, MAP2K1:p.K57N, MED12:p.L36R, MED12:p.G44S, METAP2:p.Y137N, METTL9:p.Y57F, MGP:p.V15L, MKI67:p.R2222K, MUC16:p.T11005I, MUC4:p.S3941N, MUC4:p.S3941G, MUC4:p.V3091L, MUC4:p.S2951Y, MUC4:p.A2841S, MUC4:p.S2760A, MUC4:p.T2335M, MUC4:p.T1627K, MUC4:p.T1547S, MUC4:p.H1133Q, MYD88:p.M240T, NEDD4L:p.P194del, NEFH:p.S704T, NRG4:p.G21fs, OR2A25:p.S105C, OR4C16:p.Y63F, OR4N4:p.L150fs, PABPC1:p.K254fs, PIWIL1:p.P372fs, PLCD3:p.E499fs, PLEKHB1:p.S146P, PPIL4:p.S382R, PRDM4:p.*802K, PRG4:p.N675H, PRKAB1:p.P104H, R3HDM2:p.S592G, R3HDM2:p.S588N, R3HDM2:p.R206W, RPS2:p.R200G, RPTN:p.G364S, SF3B1:p.K666E, SF3B1:p.N626Y, SF3B1:p.Y623C, SIX3:p.I27L, SLC39A7:p.L456fs, SLC6A9:p.R94K, TFG:p.A382V, TGOLN2:p.K83R, TGOLN2:p.T80S, TLR2:p.D327V, TNKS2:p.T619fs, TP53:p.R273H, TP53:p.C242F, TP53:p.R175H, TWISTNB:p.H306Q, UBXN7:p.A276V, WDR78:p.N110K, XIRP2:p.V3008E, ZNF382:p.H186Q, ZNF578:p.R306H, ZNF578:p.G311S, ZNF578:p.H334R, ZNF700:p.S649C, ZNF705A:p.D298N, ZNF836:p.K608Q, and ZNF836:p.I571N.

Paragraph 16. The pharmaceutical composition according to Paragraph 15, wherein at least 17.49% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 17. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from BLCA; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, FGFR3:p.S249C, TP53:p.R248Q, PIK3CA:p.E542K, RXRA:p.S427F, ZNF814:p.D404E, FBXW7:p.R505G, NOTCH2:p.P6fs, TP53:p.E285K, ANKRD30A:p.A353P, C3orf70:p.S6L, EFCAB6:p.R379K, ERCC2:p.N238S, FAM47C:p.Q225E, FOXQ1:p.S135L, HLA-A:p.Q78R, MUC4:p.H4205Q, OTUD4:p.T909I, SLAMF1:p.S277fs, SPRED3:p.S128del, TMCO2:p.S15fs, TP53:p.R280T, TP53:p.E271K, TP53:p.A159V, ZNF706:p.I8N, ZNF706:p.R3P, ACACB:p.E2318Q, ACPP:p.E321K, ACRC:p.A264V, ADAMTS2:p.23_24insL, AFF3:p.E919K, AHNAK:p.S4150F,

AHNAK:p.D2889H, AHNAK:p.V1940A, ALX4:p.R126Q, ANKRD12:p.E627K, ANKRD32:p.T999N, ARID1A:p.S614L, ASXL2:p.117_118SS>S, ATP12A:p.R858C, ATP9A:p.R519Q, BCAS3:p.T214M, BPI:p.M255I, CACNG8:p.V146G, CAMSAP1:p.T466fs, CDC27:p.I91fs, CDKN1A:p.E44fs, CEP192:p.S2058L, CGB8:p.T18A, CHRNA3:p.L23del, CHST4:p.D352N, CLIP1:p.S1018fs, COX6A1:p.S8L, CREBBP:p.D1435H, CRIPAK:p.M48fs, CSPG5:p.D119N, CUL1:p.E485K, DLC1:p.S741T, DLL3:p.D318H, DOPEY2:p.E1196K, ECM1:p.E266K, EEF1A2:p.Y418S, EEF2K:p.E673K, EMILIN1:p.R27G, ERBB2:p.S310F, ERBB3:p.M91I, ERBB3:p.V104L, ERBB3:p.D297Y, ERCC2:p.Y14C, FAM155A:p.Q86del, FAM43B:p.E272del, FASTKD3:p.Q625E, FBXW7:p.S546L, FGFR3:p.R248C, FGFR3:p.G380R, FGFRL1:p.H479fs, GBE1:p.M587I, GIMAP1-GIMAP5:p.S311C, GNA13:p.R200G, H1FOO:p.A214fs, HEATR7B2:p.E1109K, HIST1H1D:p.I81M, HRAS:p.G12D, HRCT1:p.H92P, ILF3:p.E484K, KCNK2:p.S6W, KIAA0907:p.Q446P, KIF23:p.E350K, KLF5:p.S118L, KLHL15:p.D185G, LAMA4:p.E639K, LILRA1:p.H410Y, LILRB1:p.L479del, LLGL2:p.P955fs, LPIN1:p.S974L, LRRC16A:p.D227N, LRTM2:p.S139L, LURAP1L:p.55_56insGGG, MAGEC1:p.P553del, MCL1:p.E171del, MN1:p.S472L, MUC7:p.A191V, MVP:p.E412K, NBPF10:p.E3455K, NFE2L2:p.E79K, NFE2L2:p.R34G, NOS1AP:p.Q306del, OR2T35:p.V319fs, OR4N2:p.L150fs, PABPC3:p.K333fs, PAX3:p.S197L, PBX2:p.E70K, PBXIP1:p.H729del, PCDP1:p.E537K, PEX1:p.I370fs, PHLDA3:p.E82K, PLEKHM2:p.S459L, PLVAP:p.A321V, POLR3B:p.L372F, POTEC:p.R477Q, PPL:p.H326Y, PPP1R15A:p.E196K, PRDM16:p.E271Q, PRIC285:p.E1289Q, PRMT8:p.S31P, PUF60:p.S396L, RAB11FIP4:p.S596L, RAD51C:p.D167N, RAD51C:p.Y224H, RALGPS1:p.R381Q, RARS2:p.R6C, RBM26:p.P644A, RERE:p.K176N, RXRA:p.S427Y, SERPINA12:p.R211G, SF3B1:p.E902K, SLC6A9:p.R243W, SLC9A5:p.L447F, SPESP1:p.F121L, SRPRB:p.G14S, SYN2:p.A34del, SYTL2:p.I440M, TAB3:p.R211T, TAF1B:p.R292C, TAOK2:p.L981del, TAS1R3:p.E525K, TAS2R9:p.E163Q, TBC1D1:p.S71F, TBC1D2B:p.R920Q, TFPI2:p.R222C, TM6SF1:p.S15W, TMEM131:p.K640fs, TMEM19:p.G331fs, TP53:p.R273C, TP53:p.R248W, TP53:p.R175H, TP53:p.K132N, TRAM1:p.E41Q, TSKS:p.E513K, TTN:p.C20935G, UBOX5:p.S417L, UGP2:p.D262H, VGF:p.E433K, XAB2:p.E782K, XYLB:p.S87F, ZC3H4:p.E798K, ZNF208:p.K852E, ZNF208:p.I647S, ZNF626:p.G198E, ZNF749:p.Q457E, ZNF761:p.H373R, ZNF799:p.T43A, ZNF799:p.W41G, ZNF799:p.E589G, ZNF844:p.P503R,

ZNF845:p.M423T, ZNF845:p.T479M, ZNF860:p.H464R, ZNF878:p.S181R, ZNF91:p.R333H, and ZNF91:p.H305R.

Paragraph 18. The pharmaceutical composition according to Paragraph 17, wherein at least 26.92% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 19. The pharmaceutical composition according to any of Paragraphs 1 to 14, wherein: (a) the population of subjects is suffering from a neoplasia; and (b) the at least one tumor-specific mutation comprises a frameshift mutation resulting from an insertion of at least one nucleotide in the coding sequence of GATA3.

Paragraph 20. The pharmaceutical composition according to Paragraph 19, wherein: (a) the population of subjects is suffering from BRCA; and (b) the at least one tumor-specific mutation comprises any combination of frameshift mutations selected from the group consisting of GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, and GATA3:p.S408fs.

Paragraph 21. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from BRCA; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.H1047R, PIK3CA:p.E545K, PIK3CA:p.E542K, AKT1:p.E17K, TP53:p.R175H, PIK3CA:p.N345K, PIK3CA:p.H1047L, SF3B1:p.K700E, GATA3:p.S408fs, PIK3CA:p.E726K, TP53:p.Y220C, TP53:p.H193R, PIK3CA:p.Q546R, TP53:p.R273C, TP53:p.R248W, TP53:p.R273H, TP53:p.I195T, TP53:p.H179R, FGFR2:p.N549K, NUP93:p.E14K, PIK3CA:p.C420R, PIK3CA:p.E453K, PIK3CA:p.Q546K, TP53:p.V216M, TP53:p.C176F, CDH1:p.E243K, ERBB2:p.L755S, KRAS:p.G12V, PIK3CA:p.E545A, TBL1XR1:p.I141fs, TP53:p.G266E, TP53:p.R248Q, TP53:p.Y163C, TP53:p.C141Y, TP53:p.G108fs, ACPP:p.R43W, AKT2:p.I289M, ARHGAP9:p.R137C, C9orf174:p.R136W, CDC42BPA:p.P675T, COL12A1:p.S395L, CRISPLD1:p.R222W, CT47B1:p.234_243EKLTEEATEE>E, CYP1A2:p.V483M, DAB2IP:p.E161K, DGKB:p.S13L, DMD:p.K1772N, DPEP1:p.V11L, ERBB2:p.S310F, ERBB2:p.D769Y, ERBB3:p.E928G, ESYT1:p.R816W, FAM179A:p.A831T, FAM58BP:p.A70T, FMN2:p.S751F, GALNTL6:p.K567del, GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs,

GATA3:p.H434fs, GATA3:p.H435fs, GDAP1:p.T307A, GRB14:p.A300T, GUCY2C:p.G549C, IL17B:p.R34W, KCNB2:p.R231H, KIF1B:p.R1320W, KIF26B:p.V1113M, KLF4:p.K434Q, LY9:p.I69L, MAP2K4:p.S184L, MAP2K4:p.S251I, MAP2K4:p.T261fs, MAP3K1:p.L318fs, MAP3K1:p.I761fs, MAP3K1:p.V1346del, MAP3K1:p.L1384fs, MAPK13:p.E315K, MAPK4:p.V100M, MARCH5:p.R170C, MBP:p.E120K, MEFV:p.R377H, METTL15:p.Q53E, MS4A4A:p.V99M, MUC17:p.R4415H, MYH6:p.T847M, MYO5B:p.A405V, NARS2:p.P240R, NLGN4X:p.D382N, NLRC4:p.R288W, OR13G1:p.R258H, OR2AK2:p.V45I, OTOF:p.T388M, PACSIN2:p.Q331H, PALM2-AKAP2:p.A299T, PCDH19:p.R286C, PCDHGC5:p.D664N, PIK3CA:p.R88Q, PIK3CA:p.E110del, PIK3CA:p.K111del, PIK3CA:p.PVPHGLEDL447del, PIK3CA:p.L455fs, PIK3CA:p.M1004I, PIK3CA:p.M1043I, PIK3CA:p.N1044Y, PIK3R1:p.KPDL567del, PREX2:p.R363Q, PRRX1:p.A196V, PTEN:p.V317fs, RGSL1:p.V222I, RUNX1:p.R142fs, RUNX1:p.D96fs, SCN2A:p.R36K, SLC25A32:p.Q83E, SLC25A45:p.G106C, STRA6:p.Q68R, STX6:p.H153D, TBX3:p.H187Y, TFPT:p.S252C, TINAG:p.R332W, TMEM71:p.R63Q, TP53:p.E286K, TP53:p.R282W, TP53:p.V272M, TP53:p.S241fs, TP53:p.C238fs, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.Y220S, TP53:p.R209fs, TP53:p.G199V, TP53:p.L194R, TP53:p.H193L, TP53:p.H193Y, TP53:p.V173L, TP53:p.V173M, TP53:p.K132N, TP53:p.R110fs, TUBD1:p.A200V, VLDLR:p.R231H, VWA3A:p.V955I, VWF:p.K1720N, XPO1:p.E571K, and ZNF268:p.F901del.

Paragraph 22. The pharmaceutical composition according to Paragraph 21, wherein at least 36.04% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 23. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from COAD; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofKRAS:p.G12D, BRAF:p.V600E, KRAS:p.G12V, ACVR2A:p.K435fs, GRB14:p.KKK295del, SEC63:p.L532fs, TGFBR2:p.E125fs, ATR:p.K771fs, ICA1:p.N204fs, KRAS:p.G12C, TP53:p.R175H, ABCA8:p.R842Q, ACTL7B:p.R354H, ACVR2A:p.K435fs, AIM2:p.K340fs, ALG2:p.S302Y, ANKIB1:p.K144fs, ARSG:p.V131I, ATP10D:p.R311H, AXIN2:p.W663fs, C5orf30:p.D4N, CACNG3:p.V134I, CASP5:p.K78fs, CC2D2A:p.R1284C, CDH10:p.E349K, DNMT1:p.E432K, DOCK2:p.G170R, DOCK5:p.E177K, EGR2:p.R390H, ERBB3:p.V104M, FAM135B:p.R884H,

FBXW7:p.R505C, FBXW7:p.R465H, FHDC1:p.R254W, FOXL1:p.N89K, HCN4:p.R525H, HLA-DMA:p.E84K, HTR3B:p.R236C, ITGA4:p.T673M, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KRAS:p.A146T, KRAS:p.G13D, LPHN3:p.R1183Q, MAP2K4:p.R287H, MAPK8IP1:p.L217fs, MFSD5:p.R280Q, MUC16:p.R8606H, MYO6:p.D1180N, NAA25:p.S807Y, NBPF14:p.V44L, NRAS:p.Q61K, NRAS:p.G13R, PAX3:p.T424M, PGAM1:p.R240H, PHF3:p.R1410I, PIK3CA:p.R88Q, PIK3CA:p.E545K, PIK3CA:p.H1047R, PLXNA3:p.V14fs, POSTN:p.R508C, PTPRU:p.D1434N, PYGO2:p.Q150fs, RBBP7:p.E274K, SFPQ:p.R611Q, SGSM1:p.F1117L, SLC25A40:p.R96Q, SLC8A1:p.R431H, SLITRK3:p.S298L, SPATA22:p.S150L, SUN3:p.E128K, TGFBR1:p.S241L, TP53:p.R273H, TP53:p.R273C, TP53:p.R248W, TRPV5:p.R492H, USP40:p.S851L, VPS13C:p.D1359Y, ZBTB24:p.L607I, ZNF434:p.R306C, ZNF443:p.R301I, ZNF484:p.R138C, and ZNF770:p.S441P.

Paragraph 24. The pharmaceutical composition according to Paragraph 23, wherein at least 27.14% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 25. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from GBM; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, IDH1:p.R132H, EGFR:p.A289V, EGFR:p.G598V, WASH3P:p.G175S, ZNF814:p.D404E, RPSA:p.Q111E, NBPF10:p.E3455K, TP53:p.R248Q, BRAF:p.V600E, EGFR:p.A289T, PRB2:p.N230del, RGPD5:p.P1760A, TP53:p.R175H, CHEK2:p.K373E, EGFR:p.R108K, EGFR:p.R222C, PIK3CA:p.E545K, PIK3R1:p.G376R, POTEC:p.K507E, SDHAP2:p.V195E, SLC6A10P:p.K88N, TP53:p.R282W, TP53:p.R273H, CD3EAP:p.K219del, DST:p.R146C, EGFR:p.A289D, EGFR:p.H304Y, FRG1B:p.S71N, GOLGA8DP:p.A116E, KRTAP4-11:p.R121K, KRTAP4-11:p.S48R, MAP3K1:p.P324L, OGDH:p.I78fs, PODXL:p.S162fs, PSPH:p.V145I, SPINT1:p.A316V, TP53:p.R248W, TP53:p.G245S, TP53:p.Y220C, TP53:p.R158H, TSHZ2:p.A222T, UBC:p.L149R, ZDHHC4:p.R300H, ZNF844:p.R447P, AASS:p.T878fs, ABCC10:p.R570W, ADAM29:p.V205I, ADAMTS8:p.V524M, AGAP3:p.R766W, AICDA:p.Y144F, AK7:p.A159V, AK8:p.D243A, ANO2:p.R334C, AOX1:p.A507V, ARHGAP5:p.M691L, CALN1:p.V231I, CARM1:p.A202V, CD163L1:p.V721M, CD1D:p.L25fs, CD209:p.A283T, CDH18:p.A195T, CILP2:p.V553M, CIZ1:p.L89P, CLOCK:p.L123fs, COL6A5:p.T2224M, CSF2RB:p.G298S, CSMD3:p.E171K, CYP2D6:p.H352R, DCAF12L1:p.R335H,

DCAF12L2:p.R246H, DPP10:p.V183I, DPY19L2P1:p.R378Q, DQX1:p.R505H, DRD5:p.S275R, DVL2:p.V66G, EFCAB6:p.R379K, EGFR:p.L62R, EGFR:p.R252C, EGFR:p.P596S, EGFR:p.P596L, EGFR:p.G598A, EGFR:p.E709K, EPHA1:p.A184T, ERC2:p.R20H, ESPNP:p.R627Q, FAM126B:p.R382H, FBN3:p.V886I, FGF14:p.T229M, FLG2:p.H1901fs, FLG:p.R2886H, FLNA:p.V1240M, FOXG1:p.H57del, FPR2:p.R54Q, FRG1B:p.K13N, FRG1B:p.A53T, GABRA6:p.V314I, GJB3:p.R160H, GLT8D2:p.A178V, GRM3:p.R183C, HERC1:p.R2330H, HNF1B:p.T417M, HTRA3:p.Q403R, IDH1:p.R132G, IFNA10:p.L80F, IFNA10:p.V79A, JHDM1D:p.R313H, JPH1:p.A395T, KEL:p.V411M, KIAA0907:p.R516fs, KIAA1704:p.D88del, KLK6:p.R120H, KRAS:p.G12D, KRTAP4-7:p.L121V, KRTAP4-7:p.L148V, KRTAP5-4:p.S131C, LAT2:p.L18W, LIMK2:p.R203H, LUM:p.R330C, MCOLN3:p.V141I, MGAT4B:p.T444P, MUC17:p.V77M, MUC17:p.3204_3205insP, MYO1D:p.T109M, MYO6:p.Q914fs, NAP1L5:p.140_141EE>E, NF1:p.F1658fs, NHP2L1:p.R84C, NLRP5:p.R737W, NPTX1:p.A263T, NUFIP2:p.Q29del, ODF4:p.R61C, OR11H12:p.H154P, OR2A7:p.V18I, OR2H1:p.V287I, OR2T12:p.R184H, OR5D13:p.R236C, OR5P2:p.A100V, OR6N2:p.R293C, PASD1:p.A236del, PCDH11X:p.T486M, PCDHB13:p.P221L, PDGFRA:p.E229K, PDGFRB:p.S650L, PHC3:p.T35del, PIK3C2B:p.R287fs, PIK3CA:p.M1V, PIK3CA:p.R88Q, PIK3CA:p.M1043V, PIK3CA:p.H1047R, PIK3R1:p.K379N, PODNL1:p.A150V, POTEE:p.V166M, POTEG:p.R136H, PRKCD:p.G432fs, PROKR2:p.V297I, PTEN:p.C136Y, PTEN:p.S170N, PTEN:p.R173H, PTEN:p.T277I, PTEN:p.V317fs, PTPN14:p.E716del, R3HDM2:p.412_413QQ>Q, RAB11FIP5:p.R170H, RASAL3:p.R82H, RB1:p.N316fs, RDH8:p.A198V, REN:p.15_16LL>L, RIMBP2:p.R830H, SCAF11:p.E926fs, SCN7A:p.R1358H, SCNN1G:p.R564H, SDHAP2:p.R31C, SDHAP3:p.A66T, SEMG2:p.R292C, SH3RF2:p.R318C, SHB:p.A460T, SIGLEC10:p.T250M, SLC13A5:p.Q273P, SLC17A9:p.V324I, SLC22A9:p.R407Q, SLC26A3:p.V88I, SLC5A3:p.A302fs, SLC9A4:p.R631H, SPAM1:p.R346Q, SPEN:p.E803fs, SPTA1:p.A2011V, SUSD5:p.T513M, SYNE1:p.R8468H, TARSL2:p.G366D, TAS2R41:p.A255T, TAT:p.R367H, TFPI2:p.R206C, THSD7B:p.R90C, TMEM147:p.A92V, TMEM156:p.R81C, TMPRSS6:p.V302I, TNFSF9:p.A232T, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.V216M, TP53:p.H179R, TP53:p.T155N, TRAPPC10:p.K133fs, TTN:p.R21402W, TTN:p.V16403M, TUBBP5:p.V102M, TYRP1:p.T352fs, UBC:p.R73L, UGT2B28:p.P289H, USH2A:p.R3719H, WASH6P:p.L211V, ZFP42:p.V227I,

ZFP42:p.T264M, ZNF181:p.V305G, ZNF280B:p.E400K, ZNF534:p.N583K, ZNF563:p.W208fs, ZNF844:p.F487L, and ZPBP:p.R154C.

Paragraph 26. The pharmaceutical composition according to Paragraph 25, wherein at least 34.36% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 27. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from HNSC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofPIK3CA:p.E545K, PIK3CA:p.E542K, TP53:p.R175H, PIK3CA:p.H1047R, TP53:p.R282W, TP53:p.R248Q, TP53:p.R273H, TP53:p.R248W, TP53:p.G245S, RHOA:p.E40Q, EP300:p.D1399N, HRAS:p.G13V, MB21D2:p.Q311E, NFE2L2:p.E79Q, TP53:p.H179Y, FBXW7:p.R505G, HIST1H2BF:p.E77K, HRAS:p.G12D, MAPK1:p.E322K, NFE2L2:p.D29H, TP53:p.P278S, TP53:p.C242F, TP53:p.Y220C, TP53:p.H193L, TP53:p.H179R, TP53:p.V157F, TP53:p.R110L, AKNAD1:p.K620R, ANXA6:p.R231Q, AP1G2:p.D243N, ATAD5:p.D441N, ATP6AP2:p.E119Q, B2M:p.M1I, BCL11A:p.E579K, C1orf172:p.Y30fs, C7orf57:p.E30K, CCDC135:p.E313K, CDH12:p.P706T, CDH7:p.Q225K, CDK11B:p.E79del, CDKN2A:p.H83Y, CHCHD4:p.T79M, CIRH1A:p.S250I, CLSTN2:p.P759L, CRB1:p.L628fs, DENND5B:p.G1023E, DNAH5:p.Q1797E, DSP:p.R160G, EDA:p.L58F, EFCAB6:p.E1002K, ELF4:p.S415L, EP300:p.C1164Y, EPHA3:p.T802R, EPHA6:p.D952H, ERBB2:p.M916I, ESRRA:p.D219N, FAM101A:p.I89del, FBXO24:p.M553V, FCAR:p.V233M, GPANK1:p.Y351fs, GPR20:p.V300I, GPRASP1:p.S706L, GPRIN3:p.R633fs, GRID2:p.T649fs, GRM3:p.F682L, GUCY2F:p.S404L, HCRTR2:p.D100Y, HIST1H3C:p.K37M, HIST1H4C:p.R68P, HLX:p.S12T, HOXD10:p.Y151C, HPS3:p.K812N, HRAS:p.G12A, HRAS:p.G12S, IFT140:p.E664K, INPPL1:p.T493M, ITGA10:p.R669Q, ITGB1:p.D158N, KIAA1429:p.D1526N, KIAA1429:p.S138F, KPRP:p.E553fs, KSR2:p.T555M, LINGO2:p.P410T, LPCAT1:p.V187del, MAGEB3:p.V75A, MAP3K7:p.E524Q, MAP4K3:p.P657fs, MAP9:p.K485N, MARS2:p.R481Q, MBOAT7:p.R424W, MUC16:p.R12774H, MUC5B:p.T4388M, MYH11:p.E993K, MYOCD:p.T493M, MYOM1:p.R63Q, NANOS3:p.S183L, NCOR1:p.R1561Q, NCOR1:p.Q169E, NCR1:p.D213N, NFE2L2:p.E79K, ODZ1:p.R366M, OPN1MW:p.A285T, OR2M2:p.A95fs, OR2M3:p.M273I, OR2T33:p.R120S, OR6V1:p.I248fs, PABPC5:p.P58L, PACSIN1:p.E359K, PIK3CA:p.M1043V, PIK3CA:p.H1047L, PIWIL1:p.V699M,

PLIN5:p.430_431insNG, PLXNA3:p.P58S, PRB1:p.R274fs, PRSS1:p.D107N, RAC1:p.A159V, RGS7:p.L21fs, RPA1:p.R31H, RPL18:p.R178fs, SFI1:p.R821Q, SLC35D3:p.*417S, SLC5A7:p.G336C, SMARCA4:p.P913L, STAT3:p.D661V, SYCP2:p.K474N, SYT6:p.R249H, TBX21:p.E494K, THSD7A:p.R1046C, THSD7A:p.C728F, TMC3:p.R934S, TMTC2:p.T409R, TP53:p.E285K, TP53:p.C275F, TP53:p.R273C, TP53:p.G266E, TP53:p.G262V, TP53:p.R249S, TP53:p.G245V, TP53:p.C238F, TP53:p.M237I, TP53:p.Y236C, TP53:p.Y236D, TP53:p.R196P, TP53:p.PHHERC177del, TP53:p.V173L, TP53:p.V173M, TP53:p.Y163C, TP53:p.P151T, TP53:p.V143M, TP53:p.P58fs, URI1:p.S13fs, ZNF177:p.K384N, ZNF750:p.S96fs, and ZZZ3:p.R5Q.

Paragraph 28. The pharmaceutical composition according to Paragraph 27, wherein at least 21.61% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 29. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from KIRC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of WASH3P:p.G175S, VHL:p.L89H, VHL:p.S111N, WDR52:p.V1227G, KRT1:p.552_559YGSGGSSY>Y, KRTAP1-1:p.S34C, PALM2-AKAP2:p.1075_1076insEA, ZNF814:p.D404E, DOPEY2:p.Y2048S, KAT2B:p.W111fs, PABPC1:p.E156fs, PCDHGC5:p.G599V, PIK3CA:p.E545K, RRAD:p.A278E, SIRPA:p.D131del, UQCRFS1:p.I83V, VHL:p.P45L, VHL:p.V74D, VHL:p.R82P, VHL:p.L116fs, VHL:p.L158V, VHL:p.L169P, WDR73:p.DGTRSQ315del, ABCA3:p.E95D, ABCC5:p.L1090fs, ACADS:p.R330H, ACAN:p.G952E, ACSM2A:p.L402fs, ADAM23:p.K380M, ADH1A:p.D154V, AFF3:p.SA620del, AGAP6:p.D69fs, AGAP7:p.E71fs, AHNAK:p.5_6insE, AIDA:p.K247M, ALAS1:p.G302R, ANAPC16:p.R95fs, ANK2:p.N453S, ANKRD36:p.K378R, ARHGEF5:p.E487G, ARSD:p.AGV234del, ARSD:p.A234G, ATP2A1:p.G704C, ATP7A:p.Q990fs, AVIL:p.G299fs, AXDND1:p.EQ991del, BAP1:p.N78S, BAP1:p.M1I, BLM:p.H660Q, BMPER:p.RIAL444del, BRK1:p.K70Q, BTRC:p.I416M, C16orf55:p.D118A, C19orf33:p.K102E, C20orf132:p.E382D, C2orf71:p.1225_1226insS, C6orf132:p.173_182PPPLLLEPPP>P, CASP5:p.R23fs, CATSPER4:p.T425M, CCDC120:p.I8V, CCR5:p.S185I, CCZ1:p.E214D, CD7:p.P174fs, CDAN1:p.L646fs, CDH23:p.F1132Y, CDK5RAP2:p.H1592Q, CENPB:p.E410V, CERCAM:p.A85fs,

CHEK2:p.K373E, CHIT1:p.P284fs, CLCN2:p.645_645R>RR, CLUL1:p.G463R, CNTNAP4:p.Y436S, CUL9:p.D1726E, CWC25:p.K364E, CXorf51B:p.V43I, DDX39B:p.F149fs, DIRAS1:p.G79C, DISP2:p.F1021S, DNMBP:p.T78P, DOCK8:p.A177fs, DPCR1:p.H383N, DPCR1:p.L768del, EGFR:p.L838M, ENPEP:p.F289C, ESPNP:p.W122fs, FAM105A:p.H126N, FAM186A:p.IPPQAQELEIPL1556del, FAM194B:p.EEEEYL135del, FAM22F:p.S691del, FAM22F:p.P690fs, FAM47A:p.LRPEPPETGVSH235del, FAM47C:p.P388S, FAM78A:p.W192L, FBXO34:p.Q294fs, FGFR3:p.R571fs, FGFR3:p.P716H, FMN2:p.AIPPPPPLPGA956del, FOXD4L4:p.C405fs, FUT6:p.S140fs, GJA1:p.A311fs, GOLGA5:p.L492I, GPM6A:p.A50V, GPRIN1:p.231_239RKEDPGSLR>R, GRAMD1B:p.P356H, GREB1:p.S344Y, GRM6:p.A718fs, GUSB:p.L501V, GUSB:p.C500R, HBB:p.F86C, HDAC6:p.G977D, HEXDC:p.T482P, HNF1B:p.N302K, HNRPLL:p.M327V, HRC:p.P439fs, HSFX2:p.D92E, IL1RAP:p.F50C, IVL:p.EQQEGQLKHP167del, KANK4:p.S253P, KCNJ18:p.E378K, KIAA1751:p.K97N, KRT1:p.SSYGSGG557del, KRT2:p.L299W, KRT4:p.F154fs, KRTAP10-6:p.49_49P>PSCCAP, KRTAP5-7:p.C120Y, KRTAP9-2:p.CCQP140del, LARS:p.P185fs, LCP1:p.P445fs, LOC338651:p.PHRSHSPPWS102del, LRCH2:p.D717G, LTA4H:p.F107L, LYST:p.Q710H, MAFA:p.207_208HH>H, MAGEC1:p.P239del, MAP2K5:p.Q445R, MAPKAPK2:p.T214fs, MARCKS:p.K152fs, MED12L:p.P2071S, MEGF6:p.A582fs, MGST3:p.G143fs, MLXIPL:p.S790R, MOCOS:p.S849P, MST1R:p.M464V, MTOR:p.C1483F, MTOR:p.L1460P, MUC16:p.P11260A, MUC17:p.R1227fs, MUC17:p.H1228fs, MUC2:p.1480_1481insI, MUC6:p.P1569fs, MYO3A:p.N525S, NBPF3:p.D491V, NCOR1P1:p.L52P, NDUFA4L2:p.G3fs, NEFH:p.651_651K>KAKSPEK, NES:p.V611L, NFAT5:p.Q906E, NOXO1:p.G3fs, NR2C1:p.S270I, NSMCE2:p.Q31fs, NUDT21:p.W13fs, ODZ2:p.W628fs, ONECUT1:p.L424M, OR10A3:p.F73V, OR4F4:p.E15G, OR4N2:p.L150fs, OR51B5:p.A66fs, OR7C1:p.F104fs, PABPC1:p.Y408F, PABPC1:p.K333fs, PABPC1:p.A181T, PABPC3:p.P191T, PALLD:p.A996T, PALM2-AKAP2:p.G1118fs, PARD6A:p.G84fs, PASK:p.T62I, PCDH15:p.C1713F, PCNT:p.G136S, PGM5:p.G426fs, PGPEP1L:p.R164fs, PIK3C2B:p.F1473L, PIK3CA:p.N1044K, PIK3R5:p.L371R, PITRM1:p.P816T, PLIN4:p.T347I, PODXL:p.28_30PSP>P, POLR1C:p.K332Q, POTED:p.I214V, PPM1E:p.R311W, PRKCE:p.Q157fs, PROX1:p.V225D, PRRC2C:p.P1883T, PRX:p.P549L, PSD3:p.T563P, PTCH1:p.P689H, RANBP3:p.L386W, RASGEF1C:p.A188T, RGPD6:p.F946L, RHEB:p.Y35N, RIMBP3:p.A396del, RIN3:p.L449V, RLIM:p.S501L, RNF17:p.S351C, RUNX2:p.P466H, SCAF1:p.P208fs,

SDK1:p.K508fs, SECISBP2:p.D608E, SERPINB3:p.S209C, SESTD1:p.I306M, SFRP4:p.P325fs, SH3KBP1:p.P563fs, SIPA1L3:p.G777A, SLC13A2:p.L493fs, SLC16A9:p.CVLLGG470del, SLC25A5:p.A118T, SLC44A5:p.V70F, SLC4A8:p.N229K, SLC52A1:p.G370del, SLC52A2:p.G399fs, SLC6A10P:p.K88N, SLC6A14:p.A85fs, SLC9B1:p.V446fs, SON:p.VLESSAVT1359del, SP8:p.G165del, SPAG1:p.353_354insD, SPATA9:p.C189F, SPEG:p.A992fs, SPTB:p.T1864I, SRA1:p.V110L, STAT6:p.P354fs, STK11IP:p.A155E, STXBP3:p.E279G, SVIL:p.M93T, SYNE1:p.R8468S, SYNJ2:p.K832T, SYNPO:p.G619fs, TAOK2:p.Q899fs, TAS2R38:p.I311T, TBC1D12:p.F608Y, TBC1D1:p.H277R, TBC1D3:p.A556fs, TBC1D3C:p.A495fs, TBC1D3F:p.A556fs, TCF7:p.H140P, TDRD10:p.W276C, THRAP3:p.K551R, TMEM102:p.A110P, TMEM161B:p.L142P, TMEM230:p.D140G, TMEM47:p.G87S, TRDN:p.*730Y, TTBK1:p.T1065S, UBE2O:p.R1118fs, UBR5:p.T1306fs, UPK3A:p.G272fs, VHL:p.G39S, VHL:p.S65L, VHL:p.N78D, VHL:p.R79P, VHL:p.W88L, VHL:p.L89P, VHL:p.R107P, VHL:p.S111R, VHL:p.H115N, VHL:p.D121Y, VHL:p.G123fs, VHL:p.D126fs, VHL:p.L128H, VHL:p.L135F, VHL:p.I151T, VHL:p.L153P, VHL:p.L158P, VHL:p.Q164fs, VHL:p.L184P, VHL:p.L188P, WASH6P:p.315_316insAPP, WASH6P:p.T201M, WWP2:p.G458A, ZCCHC6:p.K937N, ZFAND2B:p.I149T, ZFR2:p.Y107N, ZNF273:p.N319K, ZNF462:p.S650T, ZNF516:p.A256D, ZNF519:p.H431Y, ZNF687:p.F858C, ZNF732:p.E227Q, ZNF880:p.Q406R, ZP3:p.V362fs, and ZRANB1:p.*735fs.

Paragraph 30. The pharmaceutical composition according to Paragraph 29, wherein at least 6% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 31. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from LAML; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NPM1:p.W288fs, DNMT3A:p.R882H, NPM1:p.L287fs, IDH2:p.R140Q, IDH1:p.R132C, FLT3:p.D835Y, DNMT3A:p.R882C, FLT3:p.600_601insFREYEYD, IDH1:p.R132H, NRAS:p.G13D, U2AF1:p.S34F, KIT:p.D816V, FLT3:p.D835E, IDH2:p.R172K, NRAS:p.G12D, WT1:p.S381fs, ABTB1:p.L249fs, DNMT3A:p.R736H, FLT3:p.D835H, KRAS:p.G12D, NPM1:p.L287fs, NRAS:p.Q61H, NRAS:p.Q61K, PHACTR1:p.V251fs, RBBP4:p.E330K, RUNX1:p.R135G, and U2AF1:p.S34Y.

Paragraph 32. The pharmaceutical composition according to Paragraph 31, wherein at least 47.45% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 33. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from LUAD; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12C, KRAS:p.G12V, EGFR:p.L858R, U2AF1:p.S34F, KRAS:p.G12A, TP53:p.R158L, KRAS:p.G12D, PIK3CA:p.E545K, TP53:p.R273L, EGFR:p.ELREA746del, KRAS:p.G13D, A2ML1:p.S654fs, BRAF:p.G469V, CTNNB1:p.S37F, EGFR:p.G719A, KRAS:p.G13C, MYOF:p.G165fs, EGFR:p.S768I, FAM47C:p.G948W, KRAS:p.Q61L, MYH10:p.L1091fs, NRAS:p.Q61L, OR4C3:p.H130fs, PI15:p.V22F, RAD50:p.D69Y, RIT1:p.M90I, TP53:p.C275F, TP53:p.R249M, TP53:p.R249G, TP53:p.R248P, TP53:p.R175H, TP53:p.Y163C, TP53:p.A159P, TP53:p.V157F, TP53:p.G154V, ABCB1:p.R467L, ACBD3:p.R224L, ACTA1:p.G275C, ACTN2:p.D893Y, ADAM30:p.Q741H, ADAMTS14:p.G238C, ADAMTS20:p.R1251S, ADAMTS20:p.R541L, ADAMTS5:p.L549M, ADAMTS9:p.G659W, ADCY2:p.P1016T, ADCY5:p.G623C, AFP:p.A182G, AHDC1:p.P155Q, AKAP1:p.LDRNEEG317del, ALKBH1:p.K137E, ANK2:p.Q3076L, ANKRD44:p.G339C, ANO3:p.A41S, AP1G1:p.R723L, APBB2:p.T243fs, APOB:p.L973M, APOBR:p.R840L, AQP10:p.Q261L, ARAP3:p.R1226L, ARFIP2:p.R86L, ARHGAP36:p.P16H, ARL13B:p.R358L, ASCC2:p.R365L, ASPM:p.S240F, ASXL3:p.P1470Q, ATRN:p.P197Q, AVIL:p.G64W, AXDND1:p.W101R, B3GAT1:p.R125L, BARX2:p.R68P, BCL9L:p.G980C, BCOR:p.N1459S, BEND2:p.P536Q, BMS1:p.G455V, BRAF:p.V600E, BRAF:p.G466V, BRD9:p.G330W, BRF1:p.V469L, BRWD3:p.H160N, BTRC:p.G260W, C11orf68:p.V135L, C15orf2:p.V753F, C15orf2:p.G906W, C18orf8:p.M61I, C1GALT1:p.G299V, C1orf173:p.G1454S, C1orf173:p.S688Y, C1orf87:p.R541L, C2orf53:p.P272H, C3orf20:p.R740L, C7:p.R687S, C7orf58:p.G140W, C7orf58:p.R238L, CACNA1A:p.S772Y, CACNA1D:p.R1073L, CACNA1E:p.R2089Q, CACNA2D1:p.A352E, CACNG3:p.R232W, CADPS:p.R959S, CALB2:p.R258C, CAMK2B:p.G131V, CARD11:p.I1065M, CCDC111:p.R417L, CCDC141:p.E1204V, CCDC19:p.R279L, CCDC19:p.R207L, CCKAR:p.L271M, CD1B:p.W41L, CDH10:p.S577R, CDH10:p.R472C, CDH10:p.R128S, CDH18:p.A721S, CDH20:p.P433H, CDH6:p.Q237K, CDK13:p.R880S, CDK4:p.R24L, CELF4:p.A309P, CFDP1:p.P129fs, CHN1:p.K264N, CHRNA4:p.S396R, CHRNA9:p.P361Q, CLCNKA:p.P124Q, CLEC12B:p.W217L, CLK4:p.R68L,

CNTFR:p.D252Y, CNTN6:p.R807M, CNTNAP2:p.F395L, COL19A1:p.P538Q, COL5A2:p.G612W, COL5A2:p.G516W, COL9A1:p.P211Q, CPE:p.P290Q, CPNE8:p.Q127H, CPSF4:p.P219Q, CRIPAK:p.S180fs, CROT:p.Q580H, CRTC3:p.S363L, CSMD2:p.P1855Q, CSMD3:p.T2810N, CSMD3:p.P2727T, CSMD3:p.Q174H, CUBN:p.G596C, CUL4B:p.R91S, CUL7:p.L371F, CXCL9:p.K122N, CXCR4:p.E345Q, CXorf59:p.R198M, CYP11B1:p.R498G, CYP27A1:p.P112Q, CYP2B6:p.A444E, DACH2:p.R539L, DCC:p.R446H, DDX56:p.R329L, DEFA1:p.W90C, DENND2A:p.R688Q, DENND2A:p.R499L, DMBT1:p.R1521L, DNAH5:p.R3822L, DNAH9:p.S2993R, DNAI2:p.V231L, DPP6:p.L757F, DSG4:p.R128L, DST:p.A4410S, DZIP3:p.M322L, EBF3:p.R231S, EFCAB4B:p.E265Q, EHHADH:p.Q704H, ELAVL2:p.L263F, EMR1:p.R493H, ENAH:p.R514L, ENPP1:p.G738E, EPB41L3:p.A896S, EPG5:p.R2289L, EPHA1:p.G111V, EPHB6:p.R337H, EPRS:p.V1151L, ERBB2:p.S310Y, ERBB2:p.774_775insAYVM, ERBB2:p.776_776G>VC, ERN2:p.T295K, FAM120B:p.P467H, FAM127C:p.F52L, FAM135B:p.W240C, FAM210B:p.L112F, FAM47A:p.R690L, FAM47B:p.W163C, FAM47B:p.L567F, FAM5C:p.R457G, FAM70B:p.P277T, FAM71B:p.L583M, FAM75A6:p.R304S, FAM75A6:p.P54L, FAM75D1:p.R1265S, FARP1:p.R299L, FAT1:p.R4359L, FAT3:p.R1266H, FAT3:p.G1899V, FAT3:p.H3574N, FBXO18:p.M144I, FBXO31:p.G443fs, FCGBP:p.A1022S, FCRL2:p.V505L, FERD3L:p.P92H, FGB:p.E339Q, FGFR2:p.E116K, FGFRL1:p.R243L, FGFRL1:p.V274L, FKBPL:p.R320L, FLG2:p.G1545V, FLG2:p.L572F, FLG:p.P3254H, FLG:p.P2466Q, FMN2:p.P992T, FOLH1:p.A643S, FOXRED1:p.R136L, FRAS1:p.C382F, FRG2B:p.D142Y, FRMPD1:p.E1093Q, FSHB:p.T43N, GABRA5:p.Q224K, GADL1:p.L352I, GAL3ST3:p.A271S, GALNT14:p.D234E, GAS8:p.R313S, GATA3:p.M443I, GCDH:p.R82C, GEM:p.R268L, GFRAL:p.Q308K, GIT2:p.R123L, GJB4:p.R22S, GLB1L2:p.I407M, GLOD4:p.Q223fs, GNAO1:p.P283Q, GPNMB:p.I174M, GPR137B:p.G240C, GPR158:p.P762T, GPR98:p.G4307W, GRB7:p.R239L, GRHL1:p.G608W, GRID1:p.R683L, GRIK1:p.R368Q, GRM5:p.P895fs, GTF2E1:p.R192L, H3F3C:p.R131L, HAO2:p.H12N, HCN1:p.P231Q, HECW1:p.A183S, HGF:p.M686T, HIP1:p.R940L, HIST1H1E:p.R25P, HLA-DMA:p.A236fs, HOXA5:p.G11C, HS3ST3A1:p.G399W, HSD17B6:p.F209L, HSPA13:p.V85L, HSPBAP1:p.R282L, HTR5A:p.W298C, IGHMBP2:p.R615S, IL2:p.R103M, IL2RA:p.G61W, IL32:p.P215T, ING1:p.A220S, INMT:p.G56V, ITGA8:p.G616C, ITGAD:p.L528fs, ITGAX:p.R283H, ITIH1:p.G254W, ITIH2:p.L842V, ITK:p.R29L, ITPR2:p.P358Q, JMJD1C:p.R1198S,

KCNA1:p.G376C, KCNH8:p.M455I, KCNJ3:p.L430F, KCNK18:p.G23V, KCNK2:p.R166L, KEAP1:p.G603W, KEAP1:p.R260L, KEAP1:p.S144F, KHDRBS2:p.S203L, KIAA1211:p.P1203Q, KIAA1549:p.L1272F, KIAA1755:p.Q108H, KIF15:p.E252Q, KIF9:p.G480R, KIRREL:p.G604C, KLF5:p.E419Q, KRAS:p.Q61H, KRTAP10-12:p.R64P, KRTAP27-1:p.M124I, KRTAP4-5:p.C91F, KRTAP5-1:p.S193Y, L1CAM:p.R632S, L3MBTL4:p.W162L, LAMA1:p.D1030Y, LAMB1:p.T1610fs, LAMB4:p.G1239W, LAMB4:p.G588W, LEF1:p.I53V, LEKR1:p.Q450K, LIM2:p.S150T, LIPJ:p.P236Q, LPHN3:p.E740D, LPPR4:p.R527S, LRFN5:p.N132K, LRP1B:p.G3563C, LRP2:p.M4039I, LRRC4C:p.Q10L, LRRIQ1:p.W792L, LRRTM4:p.S243Y, MAGEA10:p.R7H, MAGEC2:p.W109C, MAGI1:p.G1156V, MAGI2:p.P1044T, MAK:p.P373Q, MAP2K1:p.K57N, MARCH11:p.R193L, MEPE:p.G142C, MKI67:p.R1081S, MKRN3:p.P448H, MLL3:p.N393K, MLL3:p.Q356K, MMRN1:p.A1013S, MOGAT2:p.Q66fs, MXRA5:p.D324Y, MYH4:p.T790M, MYH8:p.R1117C, MYH8:p.H1006N, MYO5B:p.R708L, MYO7B:p.P2040H, MYO9B:p.R94L, MYT1L:p.P351Q, NAA11:p.T184K, NAB1:p.L72F, NAV1:p.R938L, NBPF15:p.G665E, NCAM2:p.G698C, NCAPD2:p.R220L, NDST3:p.V427I, NEK2:p.R239S, NFIA:p.L294F, NLRP3:p.R157C, NOTCH2:p.R2105L, NR4A2:p.R314L, NRG1:p.V481L, NRXN1:p.R813S, NRXN1:p.A660S, NRXN3:p.P23H, NRXN3:p.R103C, NTM:p.G333C, NUAK1:p.G173C, NYAP2:p.P437L, ODZ3:p.P218Q, OIT3:p.R508S, OOEP:p.R101C, OPN1LW:p.P283H, OR10H4:p.M199I, OR10J1:p.L157Q, OR10X1:p.L298I, OR10Z1:p.L205F, OR14A16:p.G160C, OR2A25:p.M80I, OR2AG2:p.G249W, OR2AK2:p.W37C, OR2H2:p.L205F, OR2J2:p.G234W, OR2L13:p.M106I, OR2L13:p.T242A, OR2L3:p.M1I, OR2L3:p.L67I, OR2L8:p.R121C, OR2L8:p.R171S, OR2M2:p.F177L, OR2M2:p.F323L, OR2M5:p.V205L, OR2T12:p.M258L, OR2T27:p.D11Y, OR2T33:p.P165Q, OR2T34:p.C246F, OR2T6:p.V213L, OR4C12:p.D309Y, OR4C12:p.M279I, OR4C16:p.L162M, OR4M2:p.A119S, OR4M2:p.A161S, OR51V1:p.P298T, OR5AS1:p.M39I, OR5B12:p.S289C, OR5B17:p.M266I, OR5D14:p.H246N, OR5D16:p.P264T, OR5D18:p.R123H, OR5F1:p.G44V, OR5J2:p.A36S, OR5L1:p.T275N, OR6C65:p.I154fs, OR6C75:p.G94W, OR6K2:p.P79Q, OR8D2:p.R306M, OR9A2:p.R289W, OR9G9:p.R169L, P2RX7:p.P142Q, P2RY10:p.T10K, P2RY10:p.V196L, PABPC5:p.R99S, PAPPA2:p.P917T, PAPPA2:p.P1706H, PBLD:p.P55Q, PCDH10:p.R587S, PCDH10:p.V986L, PCDH11X:p.R1010I, PCDHAC2:p.A742V, PCDHB5:p.P649S, PCDHGC5:p.K12N, PCDHGC5:p.P684H, PCLO:p.P3946T, PCMTD1:p.R271M,

PDPR:p.G793W, PDYN:p.G191W, PDZD2:p.R565S, PDZD8:p.S980G, PFKM:p.R118S, PIGM:p.R225L, PIK3CA:p.E542K, PIK3CG:p.V165I, PILRA:p.S291fs, PLCE1:p.G564C, PLCL1:p.M564I, PLEKHA6:p.R110L, PNKP:p.G174W, POGZ:p.G75W, POLE:p.R573L, POM121L12:p.P231T, POM121L12:p.P242H, POTEE:p.V288M, POTEM:p.S78R, POU3F3:p.D321Y, PPT2:p.R265L, PRDM16:p.P1036L, PRELP:p.D201Y, PRPF40B:p.R160S, PRPF6:p.R763L, PTEN:p.R234L, PTPN11:p.G503V, PTPN13:p.E2067K, PTPRJ:p.G334W, PTPRT:p.R928L, PTPRU:p.P559S, PXDNL:p.P1456T, QSOX1:p.R401L, QSOX2:p.R683L, RAB13:p.R167L, RAB8A:p.G20W, RAPGEFL1:p.R356L, RBM19:p.G390W, RCL1:p.P112Q, REG1B:p.W57L, REG3A:p.S150L, REG4:p.G110V, RIMS2:p.R55L, RIT2:p.R85L, RLN2:p.S138C, RNF20:p.P529Q, RORB:p.G94W, RPL10L:p.K187T, RPRD2:p.R97S, RTN1:p.S103W, RUNX2:p.R337M, RYR2:p.K2413N, RYR2:p.M4334I, RYR3:p.P1670T, S100PBP:p.R5L, S1PR1:p.L104F, SAGE1:p.H298Q, SALL1:p.E965K, SALL1:p.R898W, SALL4:p.R187L, SBSPON:p.G133W, SCAF8:p.G740C, SCG2:p.P252Q, SCML4:p.L261F, SCN2A:p.T155K, SEC24D:p.A50fs, SEC61A2:p.G126V, SERPINA12:p.D253Y, SERPINA9:p.M414I, SERPINC1:p.R45L, SGIP1:p.R502L, SH3GL3:p.R174L, SH3PXD2A:p.S759L, SI:p.V1217F, SKOR1:p.Y883C, SLC1A2:p.F348fs, SLC24A5:p.R35S, SLC25A48:p.R101S, SLC35E2:p.R201L, SLC39A12:p.C628S, SLC39A6:p.R53L, SLC4A5:p.I533V, SLC5A1:p.G53W, SLC5A7:p.G442V, SLC6A11:p.W299L, SLC6A2:p.S354C, SLC8A1:p.G433C, SLIT1:p.R1460L, SLITRK5:p.R68L, SLITRK5:p.R468M, SLITRK6:p.N741K, SORL1:p.R205L, SOS1:p.N233Y, SOX9:p.E75K, SPAG16:p.V439L, SPIN4:p.Y171C, SPRR2D:p.P30fs, SPTA1:p.G2367C, SPTA1:p.D2243Y, SSX3:p.P127T, ST18:p.H778Q, STAC3:p.G117W, STOML3:p.D86Y, STX2:p.R107L, SUMF2:p.G110E, SUN3:p.P339Q, SV2C:p.P60Q, SYNDIG1:p.D135Y, SYNE1:p.K8632E, TARS2:p.E199K, TAS2R16:p.Q177H, TCOF1:p.K264R, TCTE1:p.S127I, TDO2:p.Q197H, THSD7A:p.G810W, THSD7A:p.R801L, TIFAB:p.D43E, TIGD4:p.S312F, TLL1:p.P53Q, TMPRSS11E:p.G259C, TMTC1:p.A864D, TMTC1:p.G212V, TMX3:p.R151C, TNNI1:p.R67L, TNR:p.L692I, TOP2A:p.R736L, TP53:p.R337L, TP53:p.E285K, TP53:p.R283P, TP53:p.D281N, TP53:p.C277F, TP53:p.V274F, TP53:p.R273H, TP53:p.I255F, TP53:p.R249S, TP53:p.M237I, TP53:p.S215I, TP53:p.C176F, TP53:p.R110L, TP53:p.G105C, TP53:p.P72fs, TPO:p.E558K, TRAF6:p.R502S, TRIM42:p.Q127K, TRIM48:p.A93D, TRIM4:p.R398L, TRIM51:p.W131C, TRIM9:p.R337S, TRIML1:p.H399Q, TRPM3:p.G298W, TSC1:p.G378C, TSG101:p.R276S, TSHZ1:p.K501N,

TSHZ3:p.G677V, TTF2:p.R761S, TUBA3C:p.Q176fs, UBAC1:p.K330N, UBE2J2:p.G193W, UBR1:p.G1647W, UGT2B7:p.M214I, VMP1:p.E369Q, VPS13B:p.G2575W, VSTM2A:p.G75V, VWA3B:p.R557L, WBP11:p.P227fs, WDR52:p.G612C, WDR59:p.R837S, WDR75:p.P287Q, WDR88:p.G100W, ZCCHC5:p.G335W, ZFHX4:p.L811F, ZFHX4:p.T1663N, ZFHX4:p.H2511Q, ZFP14:p.Q17L, ZIC1:p.A112E, ZNF154:p.T408N, ZNF223:p.G23W, ZNF295:p.S732C, ZNF322:p.K106N, ZNF385D:p.T226S, ZNF454:p.S190I, ZNF492:p.P392H, ZNF521:p.G640C, ZNF521:p.P270H, ZNF536:p.G186C, ZNF536:p.G663W, ZNF644:p.G21W, ZNF716:p.H263L, ZNF71:p.V411L, ZNF782:p.G484W, ZNF831:p.Q617K, ZNF98:p.C492F, and ZSWIM2:p.S214Y.

Paragraph 34. The pharmaceutical composition according to Paragraph 33, wherein at least 33.42% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 35. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from LUSC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, TP53:p.R158L, KRTAP5-5:p.GCG47del, NFE2L2:p.E79Q, CDKN2A:p.D108Y, DHX9:p.V40G, MAFA:p.207_208HH>H, NFE2L2:p.R34Q, PBX2:p.Y262F, PIK3CA:p.E542K, TP53:p.R273L, TP53:p.C242F, TP53:p.R175G, TP53:p.Y163C, TP53:p.V157F, AICDA:p.R131G, ALPK2:p.D53N, ANKFN1:p.M280I, ARPC1A:p.F212L, ASXL2:p.S1081L, C1orf74:p.D254N, C3orf30:p.D227E, CCDC121:p.W397L, CHN2:p.I43M, CLEC4C:p.R179L, CLN3:p.G206S, CNTN5:p.T178N, COL12A1:p.G2753C, CPS1:p.T855K, CSMD3:p.T1094K, CSMD3:p.Q691K, DDX11:p.R167T, EGFR:p.L861Q, EME1:p.D570H, EP300:p.D1399N, ESYT3:p.S574F, FAM135B:p.L648M, FAM135B:p.Q285H, FAM47A:p.G372W, FBXW7:p.R505G, FGFR3:p.S249C, GALNT13:p.G358C, GNL3L:p.K20N, GPC5:p.R347L, HCN1:p.A714S, HCN1:p.R659L, HCN1:p.G499V, HCN1:p.P326T, HERC2P3:p.A803V, HEXDC:p.T482P, HIST1H3B:p.E74K, HIST2H2BE:p.G54D, IFNA10:p.V79A, IL7R:p.S54L, INADL:p.P1340A, ISX:p.C2F, ITGAX:p.R685H, ITPR1:p.E1883Q, KCNN3:p.80_81insQQ, KEAP1:p.G480W, KEAP1:p.R470C, KEAP1:p.V155F, KIAA1751:p.L63F, KIAA2022:p.C345F, KIR3DL2:p.K229E, KLF5:p.E419Q, LAMA4:p.M1293I, LMLN:p.G199C, LRP2:p.A516V, LRRC66:p.F458L, LSG1:p.R517L, LUM:p.R310L, MB21D2:p.Q311E, MCHR1:p.S306F, MKRN3:p.G270V, MUC16:p.N11594K,

NFE2L2:p.G81S, NFE2L2:p.G31A, NFE2L2:p.L30F, NFE2L2:p.D29H, OR2B11:p.G10V, OR2T2:p.F13V, OR4K2:p.C254F, OR51F2:p.R67P, OR51S1:p.R159Q, OR5D18:p.T271K, OR8H2:p.L166F, OR8J3:p.S160L, OR8K3:p.K235N, PCDHB1:p.N568K, PHIP:p.I1681M, PIK3CA:p.E726K, PIK3CA:p.H1047R, PLCE1:p.G439C, PRSS57:p.E39Q, PYHIN1:p.G148A, RANBP6:p.I984L, RBMXL1:p.G305C, REG1B:p.M67I, RGS6:p.W366L, RNF5:p.T136I, RP1:p.S1771L, RRP15:p.L214F, RYR2:p.E711K, SAMD3:p.Q206H, SLITRK3:p.R214L, SON:p.S908L, SP4:p.E11del, STK11:p.G279fs, TARBP1:p.L782V, TBCD:p.R476C, TMPRSS11F:p.R274Q, TP53:p.R337L, TP53:p.E271K, TP53:p.R267P, TP53:p.G245V, TP53:p.Y234C, TP53:p.Y220C, TP53:p.H214R, TP53:p.H193L, TP53:p.H179L, TPTE:p.M541I, TRIM7:p.L332I, TTN:p.T32425M, ZFP36L2:p.D240N, ZNF208:p.H883Q, ZNF48:p.R235H, ZNF626:p.K473R, ZNF676:p.P43T, ZZZ3:p.R162Q.

Paragraph 36. The pharmaceutical composition according to Paragraph 35, wherein at least 7.87% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 37. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from OV; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R273H, TP53:p.Y220C, TP53:p.R248Q, TP53:p.R175H, TP53:p.R273C, TP53:p.I195T, TP53:p.R248W, TP53:p.R282W, TP53:p.C176Y, TP53:p.V157F, TP53:p.S241F, TP53:p.H179R, TP53:p.G245S, TP53:p.H193R, ADCY2:p.V888I, B2M:p.M1V, BAP1:p.R227C, CYP4A11:p.V185F, DNAH5:p.R3197Q, GART:p.K807fs, GRIN2B:p.R519Q, HRNR:p.M1fs, KLHL29:p.L716fs, KRAS:p.G12V, MGA:p.R2435Q, MYO3A:p.N525S, NPAS2:p.Q201R, NRAS:p.Q61R, PDAP1:p.K55fs, PGAP1:p.F565C, TP53:p.S315fs, TP53:p.C275Y, TP53:p.R273L, TP53:p.V272M, TP53:p.G266V, TP53:p.G266R, TP53:p.D259Y, TP53:p.P250L, TP53:p.G245D, TP53:p.G245V, TP53:p.G244C, TP53:p.C238fs, TP53:p.Y236C, TP53:p.Y234C, TP53:p.V216M, TP53:p.S215R, TP53:p.Y205C, TP53:p.L194R, TP53:p.P191del, TP53:p.Y163C, TP53:p.A159V, TP53:p.K132N, TRPC7:p.D210V, UXS1:p.V100L, WNT11:p.C344Y, and ZNF295:p.E885A.

Paragraph 38. The pharmaceutical composition according to Paragraph 37, wherein at least 22.78% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 39. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from READ; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12V, TP53:p.R273H, KRAS:p.A146T, KRAS:p.G12D, TP53:p.R175H, AKAP9:p.L3482I, APBA1:p.E624K, BAG5:p.D439N, C17orf97:p.E230D, CDH23:p.F177L, CERS3:p.E95D, DNAH5:p.R982H, ERBB2:p.V842I, GABRB3:p.D500N, KRAS:p.G13D, KRAS:p.G12C, KRAS:p.G12S, LRP6:p.R675Q, MACF1:p.F722L, MBOAT2:p.R43Q, MYO1D:p.E246K, NLRC4:p.E409K, NRAP:p.E327K, NRAS:p.Q61K, PCDH15:p.R1552I, PIK3CA:p.N345K, PIK3CA:p.E545K, POLE:p.S459F, PPP2R2B:p.P326L, SMAD4:p.R361H, TP53:p.R248W, ZFP2:p.R150I, and ZNF563:p.K26N.

Paragraph 40. The pharmaceutical composition according to Paragraph 39, wherein at least 20.51% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 41. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from SKCM; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, NRAS:p.Q61K, HSD17B7P2:p.N175S, BRAF:p.V600K, DISP1:p.G732L, IDH1:p.R132C, NRAS:p.Q61L, MUC16:p.P5119S, RAC1:p.P29S, WASH3P:p.G175S, AGAP9:p.M248V, C15orf23:p.S24F, DNAH5:p.D3236N, SPTLC3:p.R97K, TMC5:p.R276C, CFB:p.R314M, FRG1B:p.A50P, INMT:p.S212F, LOC649330:p.G93E, MAP2K1:p.P124S, RGS7:p.R44C, STK19:p.D89N, ADAM30:p.G97L, ARL16:p.G6R, ARMC4:p.E22K, BRAF:p.K601E, CAPN13:p.P405S, CD1C:p.R89C, CLCC1:p.P406Q, CNTN5:p.S379F, DNAH5:p.R742Q, EEF1B2:p.S43G, FRG1B:p.I59V, GABRG1:p.E205K, IARS2:p.R832C, IL32:p.D218fs, ISX:p.R86C, KLHDC7A:p.E635K, NAP1L4:p.P285Q, NBPF10:p.Q908E, OR2A5:p.S71L, OR4E2:p.R226Q, OR4M1:p.G41E, OR4M2:p.S268F, OR4N2:p.G41E, OR51B2:p.S163L, PCDHGC5:p.R293C, PCLO:p.R4133C, PHGDH:p.G173L, POTEG:p.D51N, PPP6C:p.R301C, PRAMEF11:p.C84S, PSG9:p.E404K, PTPRB:p.D1560N, RNF152:p.P95S, SPAG16:p.P488S, SPATA8:p.E18K, TAF1A:p.R172M, TCEB3C:p.E308K, THSD7B:p.E126K, TTN:p.E12129K, XIRP2:p.D2439N, and ZNF831:p.R1393Q.

Paragraph 42. The pharmaceutical composition according to Paragraph 41, wherein at least 90.91% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 43. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from UCEC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RPL22:p.K15fs, PTEN:p.R130G, PTEN:p.R130Q, KRAS:p.G12D, KRAS:p.G12V, PIK3CA:p.H1047R, PIK3CA:p.R88Q, PIK3CA:p.E545K, PTEN:p.V317fs, FGFR2:p.S252W, PIK3CA:p.E542K, CTNNB1:p.S37F, POLE:p.P286R, PPP2R1A:p.P179R, CTNNB1:p.S37C, KRAS:p.G13D, CTNNB1:p.D32N, CTNNB1:p.S33F, CTNNB1:p.G34R, KIAA2026:p.R574C, LIMCH1:p.R806fs, PIK3CA:p.H1047L, ALPK2:p.K523fs, CTNNB1:p.S33C, FBXW7:p.R505C, HPD:p.R284fs, KRAS:p.G12A, PIK3CA:p.R93Q, POLE:p.V411L, TP53:p.R248W, ABCA11P:p.R385I, ABI1:p.K445N, ACSM2B:p.K195N, APOB:p.F3102L, ASCC3:p.R136Q, C12orf4:p.R335Q, CCDC132:p.R838C, CHD4:p.R975H, CSDE1:p.R220C, CTNNB1:p.D32Y, CTNNB1:p.S33Y, CTNNB1:p.T41I, EXOC1:p.R588C, FBXW7:p.R465H, FGFR2:p.N549K, FUBP1:p.R430C, GEN1:p.S509L, IK:p.E90fs, KIF20B:p.E54K, MAX:p.H28R, MBOAT2:p.R43Q, METTL14:p.R298P, MFGE8:p.D170N, MS4A8B:p.S3L, NSMCE1:p.D244N, OXR1:p.E122K, PCDH19:p.E530K, PIK3CA:p.R108H, PIK3CA:p.N345K, PIK3CA:p.C420R, PIK3CA:p.Q546P, PIK3CA:p.Q546R, PTEN:p.R130L, RBL2:p.E127K, RXFP1:p.S223Y, SF3B1:p.R957Q, SLC20A1:p.P328fs, SOX17:p.S403I, TNS1:p.Q659del, TP53:p.R273H, TP53:p.R273C, TP53:p.R248Q, TTN:p.D16823N, TXNL1:p.R234C, ZFHX3:p.R1893fs, ZNF180:p.R625I, ZNF257:p.R392I, ZNF354B:p.D609N, ZNF43:p.R280C, ZNF709:p.R468I, ZNF765:p.S254L, ABCA5:p.R1476Q, ACVR1:p.R206H, ADAD1:p.S11L, ADAM9:p.R256Q, ADD3:p.E570K, ADGB:p.S1124L, AGXT2:p.R502C, AMBN:p.S225Y, ANKDD1A:p.R24H, ARHGEF33:p.R46I, ATP10B:p.L1304I, ATP2C1:p.E724K, ATP9A:p.R290Q, ATR:p.R1814fs, AVL9:p.F34L, BMPER:p.R241Q, BTN3A2:p.E153K, C14orf118:p.R279I, C14orf166B:p.F230L, C3orf23:p.R217C, C3orf62:p.R185Q, CACNA1C:p.S710L, CAGE1:p.E539K, CARD10:p.KE272del, CCDC144A:p.S1264L, CCDC168:p.D5020Y, CCDC36:p.R209I, CD55:p.E156K, CEP44:p.S253L, CIITA:p.E728K, CREBBP:p.P2094L, CTNNB1:p.S37A, CTTNBP2:p.S420L, DCT:p.R532Q, DIAPH2:p.E121K, DLG2:p.S624L, DNAH10:p.R1888Q, DNAH14:p.R1367C, DNAH7:p.R2961Q, DNAH8:p.R1347H, DNAJC13:p.E1248K, DNMT1:p.E51K, DST:p.S1767Y, DYNC2H1:p.E883D, EMR1:p.R631Q, EPHX4:p.R282Q, ERCC6L2:p.L445I, F10:p.E117K, FAM155B:p.E158K, FAM83B:p.R206Q, FARP1:p.S383L, FAT3:p.A4159T, FBXW7:p.R689W, FBXW7:p.R465C, FBXW7:p.G423V,

FN1:p.R290C, FZD6:p.R416Q, GABRA3:p.R73H, GABRA4:p.R460Q, GALNTL2:p.E395K, GFAP:p.A233T, GGA2:p.A63V, GIGYF2:p.R227H, GNPTAB:p.R1189Q, GPR112:p.S1283Y, GPR98:p.R4142W, GRIA3:p.S646Y, GRM6:p.E363D, HMCN1:p.S133Y, HSPA4L:p.R483C, HTR2A:p.S219L, INTS7:p.R940C, INTS7:p.R106I, ITM2C:p.E167K, JAKMIP2:p.R283I, KCND3:p.S438L, KCNS2:p.D211N, KDM1B:p.F361L, KIAA0556:p.L330I, KIAA1147:p.A149V, KIF23:p.R150Q, KIF27:p.K925N, KIF9:p.R594Q, KLHL13:p.E213K, KLHL28:p.E33K, LIN9:p.R183W, LRBA:p.E2103K, LRP2:p.R2432I, MAGI2:p.L450M, MC5R:p.A109T, MEGF10:p.S1053L, MKI67:p.T1664fs, MKLN1:p.F485L, MMRN1:p.F917L, MSH4:p.E730K, MTOR:p.S2215Y, MUC7:p.S336L, MYBPC2:p.R646H, N4BP2L2:p.R506C, NAPSA:p.R121Q, NCOA7:p.E369D, NCR1:p.R258W, NEK11:p.R374Q, NHEJ1:p.R109Q, NNMT:p.E233K, NOTCH4:p.15_16LL>L, NPY1R:p.A371T, NRAS:p.Q61R, OGDHL:p.R57C, OMA1:p.R445Q, OPRM1:p.R462C, OR4C12:p.F248L, OR5AK2:p.K89N, OSBPL6:p.R577Q, PCDHAC2:p.K138N, PCDHB12:p.R289C, PCDHGC5:p.A70T, PIK3CA:p.R38H, PIK3CA:p.E39K, PIK3CA:p.E110del, PIK3CA:p.K111E, PIK3CA:p.Q546K, PIK3CA:p.M1043V, PIK3CA:p.M1043I, PLA2G3:p.R201Q, PLXNA1:p.E1295K, PON1:p.R306Q, POTEE:p.R303I, POTEF:p.K674N, PPP2R1A:p.S256F, PPP2R3B:p.F310L, PRAM1:p.A268T, PREX1:p.E1246K, PRKCQ:p.A324V, PTEN:p.R130P, PVRL4:p.A358T, RAI2:p.S385Y, RBM39:p.T353I, RELN:p.F2722L, RFPL1:p.R148Q, ROBO2:p.D1018N, ROS1:p.R245I, RPS6KA6:p.S394Y, RSBN1:p.E572K, RYR1:p.A2576T, SACS:p.R2906Q, SCAPER:p.R366Q, SELP:p.R429W, SENP7:p.S673Y, SEPHS1:p.E13K, SFRP4:p.R232Q, SGK1:p.K367del, SIX1:p.E191K, SLC10A7:p.S261L, SLC12A2:p.R828Q, SLC16A14:p.R495Q, SLC7A2:p.R322W, SMCR8:p.E175K, SOS1:p.N233Y, SPOP:p.E50K, STRN3:p.K218N, STXBP6:p.D92N, SULT1E1:p.R77Q, SUN3:p.L124I, SUSD1:p.R343C, SYNM:p.R516Q, TAF1:p.R843W, TDRD3:p.R322Q, THADA:p.S1941L, TLN2:p.S208L, TMEM161B:p.R315Q, TMPRSS3:p.R16Q, TP53:p.Y220C, TPTE:p.S423L, TRANK1:p.E846K, TRPC5:p.S490L, TRPM3:p.R429W, TSSK1B:p.E301K, TTLL7:p.R751H, TTN:p.S20317L, TTN:p.E6404K, TTN:p.R4434Q, TTN:p.R2506Q, UGT8:p.E102K, USF1:p.R52Q, USP16:p.R455Q, USP25:p.R873H, USP33:p.R36Q, VPRBP:p.R802Q, VPS13B:p.R692Q, WDR65:p.F110C, YTHDC2:p.E185K, ZFYVE1:p.R266Q, ZKSCAN1:p.R541fs, ZNF117:p.R157I, ZNF180:p.R569I, ZNF195:p.R59Q, ZNF254:p.K179N, ZNF263:p.R510I, ZNF333:p.R554Q, ZNF354B:p.R402I, ZNF442:p.R309Q, ZNF454:p.R376I, ZNF485:p.R374I,

ZNF488:p.R206Q, ZNF559:p.E284K, ZNF594:p.R287I, ZNF611:p.R390I, ZNF645:p.R154C, ZNF649:p.R338Q, ZNF649:p.R198I, ZNF674:p.R405I, ZNF675:p.R220I, ZNF678:p.R564I, ZNF732:p.R354I, ZNF780A:p.R466Q, ZNF823:p.R547I, ZNF836:p.R854I, ZNF836:p.R630I, ZNF841:p.R757I, and ZNF98:p.R370I.

Paragraph 44. The pharmaceutical composition according to Paragraph 43, wherein at least 67.74% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 45. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from ACC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ZFPM1:p.EPL444del, GARS:p.P42A, ZNF517:p.V349A, LRIG1:p.L24V, CCDC102A:p.R96W, OPRD1:p.C27F, SOWAHA:p.R124P, LACTB:p.M5L, TOR3A:p.F13L, ZFPM1:p.E444fs, ZNF787:p.D367del, LRIG1:p.L26V, IRX3:p.L422P, TRIOBP:p.H1300R, TUBA1C:p.L146F, ZFPM1:p.P445fs, ZFPM1:p.446_447LA>P, TPO:p.S398T, USP42:p.R779P, ERCC2:p.D312N, GLTPD2:p.D209E, OTOP1:p.LLW104del, RINL:p.P402L, AMDHD1:p.S3G, ASPDH:p.Q266R, KCNK17:p.S21G, TMEM247:p.Q128E, MUC5B:p.D682G, OBSCN:p.R4516W, FAM184B:p.R784W, SEMA5B:p.V840D, ZNF598:p.E25G, ADAD2:p.G44E, C1orf106:p.R538C, ZAR1:p.Q42H, PANK2:p.G126A, PODXL:p.28_30PSP>P, SALL3:p.L593V, THEM4:p.L17R, C2orf81:p.T315P, CLDN23:p.V210M, FAM109A:p.GGG156del, FPGS:p.I22V, HHIPL1:p.V692A, MUC5B:p.M2869T, PLEC:p.R1386Q, SYT8:p.R373W, TAF5:p.S130A, TMEM189-UBE2V1:p.N6D, UQCRFS1:p.S6A, B3GNT6:p.L316fs, CCDC105:p.P499T, CLIC6:p.Q298E, IDUA:p.T374P, NOTCH2:p.C19W, RGS9BP:p.A96S, RREB1:p.G783V, SP8:p.G165del, WDR34:p.W60G, C19orf10:p.G12R, CELSR2:p.16_17insP, FAM75C1:p.71_71H>HLVSQRH, GPRIN2:p.R446H, KBTBD13:p.A81V, OGFR:p.S557T, PODXL:p.30_30P>PSP, BHLHE22:p.L62Q, C4orf32:p.G32E, C5orf65:p.Q245R, KNDC1:p.V806D, KRTAP10-6:p.49_49P>PSCCAP, LRP11:p.P92R, MAP1S:p.S411C, NOL9:p.S58A, RASIP1:p.R601C, RGMB:p.S63R, SARM1:p.R23P, TSC22D2:p.A419T, ZNF628:p.T230A, ZNF814:p.A337V, AATK:p.A541T, BTBD11:p.G265A, CRIPAK:p.C143R, KCTD3:p.F9V, KRT8:p.S59A, MUC5B:p.S681G, NCOR2:p.1846_1847insSSG, OGFR:p.E556K, APOE:p.C130R, C10orf95:p.A85S, C13orf33:p.R59G, CRIPAK:p.C174R, FAM18B2:p.C51Y, GLI3:p.P998L, GLTSCR2:p.Q389R, HECTD2:p.P19A, IRF2BPL:p.123_125QQQ>Q,

MEX3C:p.179_182AAAA>A, NEFH:p.EE658del, RNF149:p.S9G, RNF222:p.A133T, SEZ6L2:p.R74P, TNIP2:p.R73G, ARRDC4:p.T79A, B3GNT6:p.P330fs, BAG1:p.G45R, C22orf26:p.P28L, CHDH:p.E40A, COQ2:p.V66L, CTGF:p.H83D, DLEU7:p.A83V, EPPK1:p.D2378H, FAM86C1:p.R30P, FZD1:p.93_94insP, GPRIN2:p.V241M, GPX1:p.11_13AAA>A, HES3:p.P96T, JMJD4:p.A11V, KANK3:p.R359H, LPPR2:p.A186S, NEFH:p.665_666insEE, NOM1:p.R24G, RNF39:p.G263C, SCRT1:p.S133A, SNED1:p.L1228P, TTLL11:p.122_123insKA, ZCCHC3:p.A159del, ZNF219:p.QP233del, ASB16:p.T249A, ASB2:p.H515P, ATP9B:p.S39G, AVL9:p.G7fs, C17orf96:p.L63V, C19orf29:p.A499V, CRB2:p.T1110M, CRIPAK:p.P173R, CRIPAK:p.I190L, CSGALNACT2:p.L362F, CTBS:p.LAL31del, CTNNB1:p.S45P, DMRT1:p.S45T, DOK7:p.G461D, FBRSL1:p.A836V, FEZ2:p.P50L, FRG1:p.S169N, HSD17B1:p.G313S, IBA57:p.S130R, KIF1A:p.E917D, KRTAP9-1:p.160_160Q>QPSCGSSCCQ, LURAP1L:p.55_56insGGG, NMU:p.A19E, NMU:p.A18E, NOXA1:p.D6E, NPTX1:p.G100D, PLIN5:p.R306W, TBP:p.95_96insQ, TMEM200C:p.S498G, TNXB:p.V706fs, VARS:p.P51S, ZC3H12D:p.P405S, and ZZEF1:p.V30A.

Paragraph 46. The pharmaceutical composition according to Paragraph 45, wherein at least 20% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 47. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from CESC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, PIK3CA:p.E542K, MAPK1:p.E322K, EP300:p.D1399N, ERBB2:p.S310F, ERBB3:p.V104M, KRAS:p.G12D, ANKRD12:p.E721Q, ANKRD36:p.M1144T, MICA:p.G318fs, PIK3CA:p.E726K, PTEN:p.R130Q, ABCD1:p.S606P, ACTL7B:p.E211K, ADAM21:p.F129C, ADAMTS12:p.P1053A, AKT1:p.E17K, ANKLE1:p.V643L, ANO3:p.M956I, AOAH:p.R326T, APOD:p.S115L, ASCC1:p.H207Y, ATM:p.S800F, AURKA:p.S387L, BAG5:p.M286I, C12orf43:p.E28Q, C16orf3:p.G65S, C3orf70:p.S6L, C4orf21:p.E800Q, CALB2:p.K60N, CALCB:p.R81T, CCDC152:p.E153Q, CCDC53:p.R58C, CDC27:p.P242S, CFHR5:p.R441H, CLOCK:p.L123fs, CMYA5:p.E2733K, CNTRL:p.P185S, CSHL1:p.R117Q, CSMD3:p.H952Y, CTNNB1:p.D32G, CTSH:p.E254Q, DHPS:p.F49L, DMPK:p.R44H, DNAH14:p.F622fs, DNAH3:p.E3367Q, DNAH8:p.E587D, DNASE1L1:p.D212N, ECE2:p.D254N, FAM71B:p.H445D, FAM73A:p.G23V, FAS:p.E261K, FBXW7:p.R505G,

FBXW7:p.R465C, FEZF2:p.E82K, FKBPL:p.E161Q, FMNL1:p.E927Q, GPATCH3:p.E275Q, GPR142:p.R304T, GPRIN2:p.T100P, GRAMD2:p.I123M, HERC2:p.S329F, HGF:p.G229A, HIF3A:p.A72T, HIST1H1B:p.K188N, HIST1H2AL:p.R30P, HIST2H2AC:p.R30P, HLA-C:p.N104K, HLA-DPB1:p.G114fs, HRNR:p.G2539S, INVS:p.R799K, JPH3:p.Q433H, JUP:p.S627L, KIAA1211:p.R308fs, KIAA1211:p.E309fs, KLK2:p.E161K, KRAS:p.G13D, KRAS:p.G12V, LIN9:p.E231K, LOC151174:p.P90S, LRRC37A3:p.A406D, LRTM2:p.L176V, MEPE:p.S30T, MUC12:p.R2634C, MUC4:p.S2936L, MYOM2:p.D988N, NFE2L2:p.D29H, NOTCH2:p.R2298W, NPIPL1:p.P250L, NR5A2:p.E80K, NYAP2:p.R197Q, OBSL1:p.E1642K, OR13C2:p.L9V, OSBP:p.Q721H, PAOX:p.H107Y, PDILT:p.E500K, PIAS3:p.D460N, PLEKHO2:p.E351Q, PNRC1:p.R73C, PPP4R1:p.L597F, PREP:p.F469L, PRKDC:p.Q3568E, PSME3:p.R231W, RANBP6:p.R915W, RCAN2:p.D440N, RNPC3:p.E116fs, SDHAP1:p.H66Y, SDHAP2:p.S37fs, SERPINA3:p.K158N, SERPINA4:p.R98C, SF1:p.R255W, SGSM1:p.E818K, SIM1:p.V213M, SLC10A4:p.F281L, SLC25A5:p.I79F, SLC35G2:p.K62fs, SLC4A9:p.R617C, SLCO2A1:p.M479I, SND1:p.Q38E, SPATA17:p.R72K, SRSF12:p.S150C, TADA2B:p.E67K, TCTEX1D2:p.S74L, TEDDM1:p.M166I, TEX15:p.E1652Q, TMC2:p.E92D, TMEM131:p.E1319Q, TNKS2:p.T619fs, TNS1:p.Q659del, TP53:p.E285K, TRAF3:p.S9F, TRIM61:p.K98N, TRPM1:p.M996I, TUFT1:p.L101F, U2AF1:p.S34F, UNC93B1:p.V498M, USP4:p.L259V, VCAN:p.S1308C, WDR17:p.P278S, ZBED4:p.S385L, ZEB2:p.E1094K, ZFYVE9:p.M1147I, ZNF16:p.R452W, ZNF677:p.R131T, and ZSWIM4:p.E407K.

Paragraph 48. The pharmaceutical composition according to Paragraph 47, wherein at least 23.71% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 49. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from CRC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12D, KRAS:p.G12V, BRAF:p.V600E, KRAS:p.G13D, TP53:p.R175H, PIK3CA:p.E545K, FBXW7:p.R465H, KRAS:p.A146T, PIK3CA:p.H1047R, TP53:p.R248W, CDC27:p.D555E, SMAD4:p.R361H, TP53:p.R273H, KRAS:p.G12C, NRAS:p.Q61K, ERBB2:p.V842I, ERBB3:p.V104M, FBXW7:p.R465C, PIK3CA:p.R88Q, PIK3CA:p.E542K, TP53:p.R273C, TP53:p.G245S, AXIN2:p.G665fs, C16orf45:p.T106N, C20orf26:p.R1088Q, DNMT1:p.E432K, FBXW7:p.R505C, HLCS:p.E362K, HPSE2:p.K58N, KIF14:p.R598Q,

KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KLK2:p.P57T, KRAS:p.G12A, KRAS:p.G12S, LPHN3:p.R1183Q, LRP6:p.R675Q, MYH8:p.R1048Q, NRAP:p.E327K, NRAS:p.G12C, PIK3CA:p.N345K, POSTN:p.R508C, PPP2R1A:p.R183W, PTEN:p.R130Q, RAF1:p.S257L, SDK1:p.T1181M, SGSM1:p.F1117L, TCF7L2:p.R482fs, TP53:p.R282W, TRIM23:p.R289Q, UGT8:p.E102K, ZNF491:p.R343Q, A2M:p.R732Q, AADACL4:p.A266T, ABCA8:p.E1158K, ABCA8:p.R842Q, ABCA8:p.A696T, ABCB8:p.R345H, ACACA:p.R1731C, ACADM:p.F48C, ACOT9:p.R50Q, ACPP:p.R105Q, ACTL7B:p.R354H, ACTL9:p.R331H, ACVR1:p.S290L, ADAM30:p.S314Y, ADAM32:p.R559Q, ADAMTS16:p.D817N, ADAMTS4:p.R156W, ADCY5:p.R661H, AGMAT:p.V313M, AGPAT4:p.A212T, AKAP12:p.E1282K, AKAP9:p.L3482I, ALB:p.S294L, ALDH1L1:p.A870T, ALG2:p.S302Y, AMOTL1:p.R676Q, AMPD1:p.K502N, AMPH:p.R292W, ANKRD6:p.R479C, APBA1:p.K730N, APBA1:p.E624K, APC:p.E847fs, APC:p.F1354fs, APC:p.M1413fs, APOB:p.R3136C, APOB:p.A43V, APPL1:p.R668W, AQPEP:p.A309T, ARF4:p.R149H, ARFGEF1:p.D1632N, ARHGAP32:p.E1253K, ARHGAP36:p.R128C, ARHGAP36:p.A147V, ARHGAP5:p.D890fs, ARNTL:p.T395M, ARPP21:p.R338H, ARSG:p.V131I, ASCC3:p.R1197Q, ATP10D:p.R311H, ATP6V0A4:p.R191Q, ATP9B:p.R265Q, AXDND1:p.E930D, AXIN2:p.W663fs, B2M:p.L13fs, B3GALNT1:p.R145Q, BACH1:p.R538Q, BAG5:p.D439N, BBOX1:p.F176V, BCL2L11:p.R91Q, BCL7A:p.T52M, BCLAF1:p.R37fs, BEND5:p.R198C, BICD2:p.R162H, BLVRA:p.S44L, BMP3:p.R344W, BNC2:p.R512W, BRPF1:p.R66C, BRWD3:p.R787C, BTBD7:p.S436L, BUB1B:p.F996L, BZRAP1:p.V1627I, C11orf30:p.R1111C, C14orf101:p.E295K, C14orf102:p.D115N, C14orf105:p.R100I, C15orf2:p.V488I, C15orf33:p.D340N, C16orf87:p.R151I, C1RL:p.L351fs, C22orf40:p.P32fs, C3orf39:p.R333W, C5orf30:p.D4N, C5orf4:p.R114Q, C6orf170:p.K724T, C7orf63:p.A10T, CACHD1:p.S720Y, CACNA1A:p.T665M, CACNA2D3:p.A332T, CACNB2:p.R608H, CACNG3:p.V134I, CACNG3:p.A138V, CACNG5:p.G121R, CADM1:p.S190L, CADPS:p.A1073T, CAPRIN2:p.E13K, CARD11:p.R423Q, CASC1:p.R54Q, CASP14:p.R5W, CBFB:p.E152K, CC2D2A:p.R1284C, CCDC18:p.K615N, CCDC60:p.R230H, CCDC81:p.R259I, CCDC88C:p.P1851fs, CCKBR:p.V236M, CD101:p.D283Y, CD101:p.R594Q, CD180:p.N228T, CDC14B:p.R375C, CDCA7L:p.P405fs, CDH10:p.E349K, CDH12:p.D674N, CDH20:p.A134V, CDH23:p.F177L, CDH2:p.D547Y, CDH9:p.F523L, CDK16:p.R108C, CEACAM5:p.L640I, CEP152:p.E21K, CERS3:p.E95D, CHD4:p.R975H, CHD5:p.A801T, CIZ1:p.V668A, CLEC18A:p.R423H,

CLTCL1:p.R481W, CMAS:p.R110Q, CNRIP1:p.R102W, COBLL1:p.K732N, COL14A1:p.R1082I, COL17A1:p.P1004L, COL4A6:p.L550I, COL6A3:p.D2792N, COPB1:p.R425C, CORO2A:p.*526R, COX15:p.L86I, CSMD1:p.S781Y, CTCFL:p.E423K, CTDNEP1:p.E126K, CTTNBP2:p.R164C, CYP4B1:p.E434D, DACH2:p.R539C, DBC1:p.V216I, DBF4B:p.S254Y, DCHS2:p.F2149L, DCLK2:p.S549Y, DDI1:p.R275Q, DENND4A:p.P357H, DENND4C:p.R1081Q, DHTKD1:p.R410Q, DISP1:p.R763C, DKK2:p.R230H, DKK4:p.R203Q, DLC1:p.A350V, DLC1:p.E222D, DMD:p.R3195H, DNAH5:p.R982H, DNAH5:p.R224Q, DNAH9:p.D1547N, DNAJC24:p.E61K, DNM1:p.A251T, DNMT1:p.E1531Q, DNMT3B:p.R92W, DOCK10:p.A1830V, DOCK1:p.E864K, DOCK2:p.G170R, DOCK3:p.R1183C, DOCK5:p.E177K, DOK5:p.R274W, DPP8:p.G165R, DPY19L1:p.F378L, DUOX2:p.F880L, DVL2:p.A601fs, EBAG9:p.E187K, EBF3:p.G255fs, EDNRB:p.L450R, EGR2:p.R390H, EHD3:p.E44K, EIF2C1:p.R139Q, ELF3:p.F305fs, ELMOD2:p.T141M, EMR2:p.S75L, ENAM:p.R373H, ENOX2:p.R356W, ENTPD7:p.E327K, EPG5:p.D369N, EPHB2:p.R392H, ERCC6:p.V780I, ERCC6L:p.R505Q, ERRFI1:p.A421T, ESCO1:p.R300Q, ETV6:p.R369W, F8:p.S2269Y, FAM123B:p.F173fs, FAM135B:p.R884H, FAM169B:p.K165N, FAM170A:p.E56K, FAM171B:p.D459N, FAM181A:p.R109H, FAM5B:p.R402C, FBXO11:p.A432V, FBXW7:p.R689W, FBXW7:p.S582L, FBXW7:p.R14Q, FGF14:p.A236V, FHDC1:p.R254W, FHOD3:p.A225T, FHOD3:p.E813K, FMO3:p.F510L, FNDC1:p.R652H, FOXK1:p.R354W, FOXN3:p.P96fs, FPGT-TNNI3K:p.R455H, FZD3:p.D367N, GABRA4:p.R460Q, GABRA5:p.S126N, GABRB3:p.D500N, GALNTL5:p.R262I, GJA1:p.R362Q, GLRA3:p.L454I, GLRA3:p.F132L, GOLGA4:p.Q1536H, GP2:p.S41L, GPC6:p.A214T, GPLD1:p.R717Q, GPR125:p.R113Q, GPR156:p.F754L, GPR158:p.D566N, GPR21:p.R216H, GPR61:p.A62T, GPR98:p.R4142W, GPRC5A:p.V30I, GRAP2:p.E69D, GRIA1:p.R218C, GRIA2:p.R845Q, GRM7:p.R679Q, GTF3A:p.K306N, HAO1:p.R172C, HARS2:p.R168H, HBB:p.F42L, HCN4:p.R525H, HDAC5:p.A1044T, HGF:p.S467Y, HIPK4:p.R280H, HLA-DMA:p.E84K, HMG20A:p.E248D, HPS3:p.S468L, HRSP12:p.R120Q, HS3ST1:p.E287K, HTR3B:p.R236C, HTR5A:p.R152C, HTT:p.D1548N, HYDIN:p.R1187C, HYDIN:p.R939Q, HYDIN:p.R451Q, HYOU1:p.R158C, IFT172:p.A944V, IGJ:p.R77Q, IL17RA:p.Q803fs, IL1RAPL2:p.T647M, IL3:p.A90T, IL5RA:p.L47I, INPP5D:p.R523Q, INPP5K:p.R263C, IRAK3:p.R267Q, IREB2:p.R419Q, ITGA4:p.T673M, ITGA4:p.F900L, ITIH5:p.A912T, ITK:p.E196K, JAG1:p.A462T, JAK1:p.V310I, KAL1:p.V303I, KBTBD8:p.V549I, KCNA3:p.A415V, KCND3:p.S438L,

KCNMB4:p.F209L, KCTD20:p.L314fs, KDELC1:p.L447I, KIAA0528:p.R181Q, KIAA0556:p.R1082W, KIAA1109:p.S4937Y, KIAA1804:p.V474M, KIAA1804:p.R477W, KIF16B:p.R145Q, KIF26B:p.A1114V, KPNA4:p.R29Q, KRAS:p.K117N, KRAS:p.Q61L, KRAS:p.Q61K, KRT6B:p.L197P, L1CAM:p.T186M, LALBA:p.A41T, LAMA4:p.A558V, LBX1:p.R176W, LPAR4:p.R145Q, LRP1B:p.K2623N, LRP2:p.R3043C, LRP2:p.S737L, LRRC18:p.R218W, LRRC31:p.K23T, LRRC7:p.R1389H, LZTS2:p.P100fs, MACF1:p.S292L, MACF1:p.F722L, MAEL:p.R345C, MAGEE1:p.V380M, MAGI1:p.R1198C, MAP1B:p.E2046D, MAP2:p.K530N, MAP2K4:p.R287H, MAP3K4:p.R275Q, MAP7D2:p.R487C, MAPK8IP1:p.L217fs, MBOAT2:p.R43Q, MCF2L2:p.R926Q, MECOM:p.R969C, METTL16:p.R200Q, METTL21A:p.R174Q, METTL6:p.F56L, MFF:p.R162C, MFSD5:p.R280Q, MIA3:p.Q356H, MMAA:p.R326C, MORC1:p.D113Y, MORC2:p.R740H, MPDZ:p.L804I, MR1:p.S46L, MRPL47:p.L234I, MS4A8B:p.S3L, MSH4:p.K464N, MSH6:p.T1085fs, MSH6:p.R1095H, MUC16:p.R8606H, MYH13:p.D311N, MYH7:p.R1689C, MYO1D:p.E246K, MYO3A:p.N525H, MYO6:p.D1180N, MYO9A:p.R2179Q, MYO9A:p.R167Q, MYOZ2:p.E251K, MYT1:p.E226K, NAA25:p.S807Y, NCAM1:p.R474W, NCOA4:p.R562Q, NEB:p.D5434N, NEB:p.L1591I, NEB:p.E1214K, NEDD9:p.A798T, NEDD9:p.A316T, NEK1:p.R608C, NFASC:p.V256I, NINL:p.R1366C, NLRC4:p.D593N, NLRC4:p.E409K, NLRP4:p.V229I, NLRP5:p.R392H, NME9:p.E75K, NOLC1:p.T428M, NPC1:p.E451K, NPSR1:p.R235Q, NRAS:p.Q61L, NRAS:p.G13R, NRAS:p.G12D, NRG2:p.T246M, NTN4:p.E59K, NUB1:p.R373Q, NUDT15:p.S83Y, NUF2:p.S340L, NUP88:p.A302V, ODZ1:p.R2556W, OGDHL:p.A427T, OGFRL1:p.E427K, OLFM4:p.K132N, OPRM1:p.R353H, OR10A3:p.S93Y, OR2M3:p.R235H, OR52W1:p.R133C, OR5AU1:p.R312H, OR5B17:p.R163H, OR8S1:p.A99V, OSTN:p.R115Q, OTOL1:p.V431I, OTUD3:p.R277I, PAN3:p.S580N, PANK3:p.R260I, PAX3:p.T424M, PCBP1:p.L102Q, PCDH10:p.V477M, PCDH15:p.R1552I, PCDHAC2:p.A519T, PCDHAC2:p.E190K, PCDHAC2:p.A266T, PCDHAC2:p.A156V, PCDHAC2:p.E271K, PCDHAC2:p.A736V, PCDHB5:p.D51Y, PCDHB8:p.D235N, PCDHGC5:p.S289L, PCDHGC5:p.V662M, PCNXL2:p.R135Q, PCOLCE2:p.A348V, PCOLCE2:p.R87H, PDE4B:p.S417L, PGAM1:p.R240H, PHF3:p.R1410I, PIAS2:p.S519L, PIGR:p.A580T, PIK3CA:p.D350G, PIK3CA:p.E545A, PIK3CA:p.E545G, PIK3CA:p.Q546K, PIP4K2C:p.R204H, PKHD1L1:p.F1856L, PLA2G4A:p.E443K, PLCG2:p.E544K, PLCG2:p.D973N, PLEKHA6:p.V328fs, PLEKHG4B:p.E384K, PLK1:p.D233G, PLOD3:p.R297fs, PLSCR3:p.E77K,

PLXNC1:p.S462L, PLXNC1:p.R819C, POLA1:p.E603D, POLE:p.S459F, POLE:p.V411L, POLQ:p.R860Q, PPP2R2B:p.P326L, PPP2R5C:p.S259Y, PRAMEF4:p.R248H, PREX1:p.V731I, PRKAA2:p.R407Q, PRKAR2B:p.S309L, PRKCI:p.R480C, PRKRA:p.K122N, PSG8:p.R397C, PSG8:p.R320C, PSMD12:p.R201Q, PTPDC1:p.R430W, PTPN12:p.R765Q, PTPN13:p.S887L, PTPRD:p.L1053I, PTPRU:p.D1434N, PXDN:p.P856fs, PXDNL:p.T1312M, QRSL1:p.S226L, RAB7L1:p.R79W, RALGAPA1:p.R398C, RANBP2:p.R1231C, RBBP7:p.E313K, RBBP7:p.E274K, RBFOX2:p.A340T, RBMXL1:p.R331Q, RHOBTB1:p.T464M, RIMS2:p.R599Q, RIN3:p.S708L, RLBP1:p.D281N, RLBP1:p.A72V, RNASET2:p.A127V, RNF113B:p.A172V, RNF150:p.R236Q, RNF150:p.S208L, RNF43:p.S216L, ROR2:p.D672N, RPL6:p.F193C, RPS6KA5:p.E166K, RSPO2:p.R28C, RUVBL1:p.E431K, RUVBL1:p.R117C, RWDD2B:p.R254H, RXFP3:p.R113C, RYR3:p.R2705Q, SAGE1:p.R229C, SCFD2:p.R545W, SCML4:p.R194Q, SCN10A:p.T1570M, SCN11A:p.A1688T, SCN11A:p.V1289I, SCN11A:p.V566I, SCUBE2:p.V342M, SEMA3A:p.D81N, SEMA4D:p.R252Q, SEPHS1:p.R371Q, SEZ6L:p.S207L, SFPQ:p.R611Q, SFSWAP:p.S617Y, SGCG:p.A220V, SGCZ:p.I41M, SH3TC2:p.R89C, SIGLEC11:p.S363F, SIPA1L1:p.R1063Q, SIPA1L1:p.S1227Y, SLC12A1:p.S292L, SLC22A15:p.S201L, SLC24A2:p.A134V, SLC25A40:p.R96Q, SLC2A7:p.A65T, SLC30A9:p.R194H, SLC33A1:p.S542L, SLC35F3:p.A280T, SLC39A7:p.R382C, SLC43A1:p.P133L, SLC43A3:p.R216H, SLC44A5:p.R185H, SLC6A2:p.A562T, SLC8A1:p.R431H, SLFN12L:p.F232fs, SLITRK1:p.R52H, SLITRK3:p.S298L, SMAD2:p.R321Q, SMARCA4:p.R381Q, SOCS5:p.S464L, SORBS1:p.V1156M, SORBS1:p.F570L, SORCS2:p.R320W, SOX6:p.R719W, SPATA22:p.S150L, SPEG:p.A944V, SPTB:p.R86C, SPTBN4:p.A1993V, STIM2:p.R572Q, STT3B:p.D583Y, SULT1C4:p.R85Q, SUN3:p.E128K, SUPT6H:p.A957T, SYNE1:p.I1249L, SYNE1:p.R170W, SYNE2:p.K3103N, SYNGR4:p.R169Q, SYT7:p.T349M, TANK:p.S380L, TAS1R2:p.R270C, TAS2R1:p.F183L, TCF7L2:p.R488C, TDRD10:p.S322L, TECTB:p.L29I, TEKT5:p.R401H, TGFBR1:p.S241L, THAP5:p.S287Y, THSD7B:p.R90H, TLL1:p.T153M, TLL2:p.S872L, TM9SF2:p.R91H, TMCC3:p.R110H, TMEM132A:p.R481C, TMEM132D:p.R578W, TMEM55A:p.R189Q, TMEM74:p.R125Q, TMPRSS11A:p.S288L, TNIP2:p.A139T, TOP2B:p.R656H, TOX:p.S354L, TP53:p.G244D, TP53:p.R175C, TPO:p.A826T, TPR:p.S2155L, TPTE2:p.R258Q, TPTE:p.S423L, TRAK1:p.D627N, TRAPPC11:p.R568Q, TRIM23:p.R396Q, TRIM44:p.D331N, TRIO:p.R661W,

TRPA1:p.K54N, TRPC5:p.S490L, TRPM6:p.R995H, TRPM7:p.R1862C, TRPM7:p.R843Q, TRPS1:p.R1125W, TRPV5:p.R492H, TRRAP:p.R3515W, TSHZ1:p.R881M, TTC21A:p.S270Y, TTN:p.R22795C, TTN:p.R3193Q, TTN:p.R328H, TUBA3D:p.R243Q, TUFT1:p.A340T, TXNDC15:p.R343Q, UBE2NL:p.R86I, UBIAD1:p.A97T, UGT2A1:p.N97fs, USH2A:p.F2369L, USP11:p.A286T, USP25:p.R1119Q, USP26:p.R861Q, USP29:p.F81L, USP31:p.D391N, USP40:p.S851L, UTP14A:p.V148I, VAV3:p.E685K, VCAN:p.R1125H, VPS13C:p.D1359Y, WBSCR17:p.R228C, WDR3:p.E841K, WDR52:p.A157T, XKR6:p.R268Q, XPOT:p.R541W, YTHDC1:p.R267Q, YTHDC2:p.E634K, ZBBX:p.R596I, ZBTB24:p.L607I, ZC3H13:p.R103Q, ZCWPW2:p.D144N, ZEB2:p.R156H, ZFHX4:p.E237D, ZFP14:p.R386C, ZFP28:p.R525I, ZFP2:p.R150I, ZFP3:p.R273I, ZFP90:p.R330Q, ZHX2:p.V790I, ZIC4:p.S305L, ZIM3:p.D352N, ZKSCAN4:p.R319Q, ZMYM4:p.R1446Q, ZNF117:p.R185I, ZNF167:p.R683I, ZNF180:p.R401I, ZNF19:p.R349I, ZNF205:p.R384C, ZNF236:p.S1480L, ZNF248:p.R568I, ZNF259:p.R174I, ZNF266:p.R512Q, ZNF266:p.R344Q, ZNF280B:p.E363K, ZNF283:p.R392Q, ZNF32:p.S62L, ZNF345:p.R82Q, ZNF345:p.R334I, ZNF350:p.R310Q, ZNF434:p.R306C, ZNF439:p.E239D, ZNF439:p.R262I, ZNF443:p.R301I, ZNF445:p.L682M, ZNF470:p.R641I, ZNF471:p.R282I, ZNF484:p.R138C, ZNF528:p.R279Q, ZNF563:p.K26N, ZNF573:p.R350I, ZNF583:p.R344I, ZNF585A:p.E638K, ZNF585A:p.E491D, ZNF625:p.R235Q, ZNF652:p.K327N, ZNF677:p.R451I, ZNF678:p.R368I, ZNF699:p.R41I, ZNF70:p.R244I, ZNF770:p.S441P, ZNF774:p.R423Q, ZNF782:p.K247T, ZNF7:p.R337I, and ZNF831:p.E949D.

Paragraph 50. The pharmaceutical composition according to Paragraph 49, wherein at least 56.65% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 51. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from DLBCL; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of EZH2:p.Y641F, MYD88:p.L273P, BCL2:p.G33R, CARD11:p.E626K, ADCY2:p.A87V, BCL2:p.N172S, BCL2:p.H20Q, BRAF:p.K601E, BTG1:p.L31F, CACNA1E:p.R1458C, CARD11:p.E93D, CD79B:p.Y197D, CD79B:p.Y197H, CREBBP:p.R1446H, GRID1:p.E622K, HIST1H1C:p.A65V, HIST1H1E:p.G133A, HIST1H3B:p.A48S, KRAS:p.G13D, MYD88:p.S251N, PABPC1:p.R94C, PIM1:p.L164F,

PIM1:p.L184F, POU2F2:p.T239A, POU2F2:p.T239S, RELN:p.R2971Q, SLC25A48:p.A67T, STAT6:p.D468H, TNF:p.L47F, and TRAF7:p.R11H.

Paragraph 52. The pharmaceutical composition according to Paragraph 51, wherein at least 13.79% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 53. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from KICH; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ACR:p.W279C, AGRN:p.1284_1285VT>A, C7orf25:p.R384fs, CAMSAP1:p.T466fs, CBWD6:p.E102fs, DOCK8:p.L1111fs, EBPL:p.Q196P, EBPL:p.L189V, GFM1:p.A17fs, GOLGA6L6:p.D570E, ITGA5:p.A48D, LUZP2:p.S154fs, MTMR9:p.K193fs, MUC16:p.P10452fs, MUC4:p.S2832P, ODF2L:p.K407fs, RHBDD3:p.G34fs, RILPL1:p.S358R, TAS2R30:p.L236fs, TRRAP:p.A973S, UBR5:p.K2120fs, URGCP:p.G639fs, ZNF98:p.A222T, and ZSWIM6:p.Q610fs.

Paragraph 54. The pharmaceutical composition according to Paragraph 53, wherein at least 50% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 55. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from KIRP; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, ZNF598:p.E25G, NEFH:p.E645K, EEF1B2:p.S43G, NEFH:p.AKSPEKEE652del, OBP2B:p.K61N, SKI:p.A62G, C14orf126:p.R6W, KRT8:p.S59A, ACSBG2:p.I250M, ASIC2:p.R46L, CSGALNACT2:p.L362F, FRG1B:p.A50P, IDUA:p.H33Q, KRTAP4-5:p.S74C, SCAF11:p.E926fs, SYN2:p.A34del, ZNF814:p.R322K, BMS1:p.E878D, JMY:p.P822T, KIF1A:p.E917D, KRTAP4-7:p.S57P, LAMA5:p.L2223R, LRP1:p.P1058T, MED16:p.H449Q, MUC2:p.T1488P, MUC5B:p.D682G, NACA2:p.R75K, NEFH:p.665_666insEE, OR2L8:p.S201fs, RGPD5:p.P1760A, RRN3:p.P11S, RRN3:p.R9C, STAG3L2:p.L81fs, ZNF814:p.G320E, ACP6:p.V29G, AHNAK2:p.S2166F, AHNAK2:p.P1215S, AP1G1:p.I782fs, AQP2:p.N68T, BAIAP2L2:p.V396M, BMP6:p.Q118L, BST1:p.G36A, CDR1:p.V31A, CLDN7:p.S172A, CLIP1:p.S1018fs, COL18A1:p.G884fs, CROCC:p.A355P, CTAGE15P:p.A364V, CUBN:p.I2816M, DMRT2:p.T106S, DPY19L1:p.V249L, DSPP:p.D1047N, EBPL:p.L189V, EIF4G1:p.E465del, EXOSC2:p.R11P, FAM216A:p.P36S, FCGR2A:p.V222G,

FMOD:p.S331R, FOLR2:p.Q112R, FRG1B:p.L20P, GAGE2B:p.9_10insY, GDPD5:p.G593fs, GIMAP8:p.A544S, GLUD2:p.R300G, GLUD2:p.S496R, GPR135:p.Q5P, HOXD8:p.Q67H, IER5:p.R194G, IL25:p.C168fs, JSRP1:p.V92A, KRAS:p.G12D, KRTAP1-1:p.Y86C, KRTAP4-11:p.L161V, LTBP1:p.L163P, MAML2:p.Q591K, MAPK7:p.A501D, MEF2A:p.P99S, MET:p.H1094Y, MET:p.M1250T, MST1:p.N435fs, MUC2:p.T1582R, MUC2:p.T1722I, MUC4:p.A4222T, MUC4:p.T2335M, MUC4:p.P1138L, MUC5B:p.S1098A, MUC5B:p.S3431N, MYH7:p.A1487T, NBPF10:p.R39fs, NBPF10:p.Y638S, NEFH:p.654_654S>SPEKAKS, PARG:p.A584T, PBX2:p.Y262F, PIP4K2A:p.R219K, RLIM:p.S471P, RUNX2:p.Q71E, SGK223:p.R63S, SMARCB1:p.L365fs, SRCAP:p.Q1875fs, TBC1D2B:p.R920Q, TCF7L2:p.R482fs, TMEM131:p.K640fs, TMEM60:p.K77fs, TPPP:p.R30K, TRPV3:p.A218E, TTBK2:p.C83W, UBXN11:p.S510G, UGT1A1:p.T4A, UTS2R:p.A289E, YBX1:p.P250L, ZNF514:p.V81G, ZNF516:p.A256D, ZNF681:p.K405Q, ZNF814:p.D404E, ZNF814:p.P323H, ZXDB:p.G206R.

Paragraph 56. The pharmaceutical composition according to Paragraph 55, wherein at least 42.24% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 57. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from LIHC; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R249S, CTNNB1:p.D32V, CTNNB1:p.D32G, CTNNB1:p.S33P, CTNNB1:p.K335I, CTNNB1:p.H36P, EEF1A1:p.T432L, GNAS:p.R844C, OR2T4:p.V137L, TP53:p.H193R, ATXN1:p.Q217H, CSMD3:p.F2383fs, CTNNB1:p.D32N, CTNNB1:p.S33C, CTNNB1:p.G34V, CTNNB1:p.S45P, CTNNB1:p.N387K, DHRS4:p.I218T, DNM2:p.E378D, F5:p.Q426L, GALNTL5:p.A45T, GPX1:p.P77R, GRM8:p.R852C, IDH1:p.R132C, KIF26B:p.A2033T, KRT8:p.S59A, LOC100132247:p.T532P, NEB:p.D3854H, PIK3CA:p.H1047R, SOLH:p.R714H, TP53:p.R158H, TP53:p.V157F, and ZNF638:p.D400N.

Paragraph 58. The pharmaceutical composition according to Paragraph 57, wherein at least 6.57% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 59. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from MM; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting

of NRAS:p.Q61R, KRAS:p.Q61H, KRAS:p.G13D, NRAS:p.Q61K, BRAF:p.V600E, NRAS:p.Q61H, NRAS:p.G13R, ZNF717:p.W315C, ATP13A4:p.V431G, DNAJC12:p.R135K, IRF4:p.K123R, KRAS:p.A146T, KRAS:p.Q61R, KRAS:p.G12A, KRAS:p.G12D, ZNF717:p.N594I, ACTG1:p.A22P, ARL6IP1:p.M75L, BEND2:p.E630K, BRAF:p.G469A, CDHR1:p.R218G, DIS3:p.R780K, DMXL2:p.D2412E, DNAJC10:p.I80K, EGR1:p.Q9H, FGFR3:p.*807S, IDH1:p.R132C, IL6ST:p.P216H, INTS12:p.M1V, KRAS:p.K117N, KRAS:p.A59G, KRAS:p.G12R, MAX:p.R36W, MLL5:p.G492E, NBPF1:p.E810K, NRAS:p.Q61L, NRAS:p.G12D, ODF2L:p.E294K, PADI2:p.T114P, PNLIP:p.T37M, PRDM1:p.S588C, PTPN11:p.E76K, PTPN14:p.E286K, RBM6:p.V675G, SCN10A:p.R1142H, SRGAP1:p.T61M, SUSD1:p.T168P, TAS2R16:p.V231I, TINAG:p.E403K, TRIP12:p.L1775P, and ZNF717:p.C844S.

Paragraph 60. The pharmaceutical composition according to Paragraph 59, wherein at least 23.9% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 61. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from PRAD; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, RGPD5:p.P1760A, FRG1B:p.L52S, EEF1B2:p.S43G, FRG1B:p.I10T, FRG1B:p.A53T, LRRC37A2:p.T102S, NBPF10:p.E3455K, PTH2:p.L22V, CYP2D7P1:p.S32A, FAM47C:p.N648D, MAP3K9:p.E38del, MUC4:p.H4205Q, CHEK2:p.K373E, FRG1B:p.A11T, FRG1B:p.A50P, HLA-J:p.R124W, KRTAP1-5:p.I88T, KRTAP4-9:p.D18V, NPIP:p.A271V, PDGFRA:p.R483fs, ZNF780A:p.Q600H, ZNF845:p.R925H, ZNF91:p.R333H, ARFGAP3:p.N299fs, BTN2A3P:p.P3S, FNBP4:p.TT58del, HLA-A:p.Q78R, LOC554223:p.RAPWMEQ147del, PODXL:p.28_30PSP>P, POLI:p.D17del, SPOP:p.F133L, SYN2:p.A34del, TMEM52:p.23_26LLPL>L, UBC:p.L149R, ZNF208:p.I647S, ZNF799:p.E589G, ZNF814:p.D404E, ASTN2:p.L221del, B4GALNT1:p.G88fs, C16orf74:p.S21del, CCDC15:p.H458P, CD209:p.R129W, CNTNAP1:p.S1029I, DBR1:p.541_542DD>D, FAM22F:p.S691del, FRG1B:p.D32V, FRG1B:p.I34T, FRG1B:p.N55D, FRG1B:p.I59V, FRG1B:p.S71N, KIF25:p.W3R, KRTAP4-11:p.L161V, KRTAP4-11:p.M93V, KRTAP4-11:p.R51K, KRTAP4-6:p.S153Y, LILRB5:p.S598P, LMOD2:p.E124del, LOC645752:p.L40P, LRP1:p.P1058T, LRRIQ3:p.K244fs, LURAP1L:p.55_56insGGG, MLLT10:p.V463E, MYOCD:p.Q310del, NBPF10:p.N1369D, OTUD4:p.T909I,

PARG:p.A584T, PEX1:p.I370fs, POTEC:p.K507E, POTEC:p.R477Q, POU4F2:p.68_69insG, PRG4:p.T417P, SDHAP2:p.R31C, SPOP:p.F133C, SPOP:p.W131G, TIMD4:p.T152del, TMEM121:p.P299del, TP53:p.G245S, UBC:p.R73L, UBC:p.I191T, WASH3P:p.G175S, ZMIZ1:p.D1048fs, ZNF709:p.T413I, ACADS:p.R330H, ADAMTS7:p.K1357fs, AFF2:p.R597H, AGAP6:p.S127I, AK302238:p.A44T, AK302879:p.Q191R, ALDH1A2:p.R85C, ANAPC1:p.T537A, ANKRD36C:p.H438R, AP4B1:p.R276W, ARFGAP2:p.S38N, BBS9:p.F268fs, BC139719:p.L133R, BRAF:p.G469A, C22orf43:p.D171del, CANT1:p.K131R, CHD3:p.E35del, CLEC4A:p.R209H, CNOT3:p.E20K, CNPY3:p.17_18LL>L, CNTNAP3B:p.S317T, CNTNAP3B:p.M1247I, CTNNB1:p.T41A, DDX10:p.D788del, DLC1:p.S741T, DPY19L2:p.M210V, EDC4:p.S617del, EFCAB6:p.R379K, ERC2:p.927_928HH>H, FAM111B:p.S269fs, FEM1A:p.L620M, FHOD3:p.A632fs, FLJ43860:p.L850fs, FMN2:p.G59del, FNBP4:p.914_915PP>P, FRG1:p.E86del, FRG1B:p.K13N, FRG1B:p.P42Q, GABRB1:p.R416C, GABRR2:p.A368V, GAGE2B:p.9_10insY, GOLGA8DP:p.N84H, GOT2:p.R355W, GPATCH4:p.K210fs, HDGFL1:p.188_189insA, HLA-DQB2:p.G250S, HLA-DQB2:p.R247H, IDH1:p.R132H, IL27:p.E176del, IRF2BPL:p.123_125QQQ>Q, KANK3:p.DGDS489del, KIAA1462:p.858_859SS>S, KRTAP4-11:p.S48R, KRTAP4-7:p.S57P, KRTAP4-8:p.C95S, LPHN3:p.R826H, LRP10:p.L11del, LRP5:p.S1609P, LRRC16B:p.R787W, MAS1L:p.R324G, MECOM:p.R915Q, MED12:p.L1224F, MED12L:p.Q2115del, MESP2:p.GQGQGQGQ195del, MGAT4C:p.T345M, MLEC:p.E238del, MSLNL:p.T68P, MUC7:p.S173P, MYC:p.Q37del, NBPF10:p.N440D, NLRP6:p.E611del, NOX3:p.C404fs, OR1M1:p.V69I, OR7E24:p.L7fs, OTUD4:p.A153del, PANK2:p.T417fs, PCLO:p.S496P, PCNT:p.S162G, PCSK9:p.23_24insL, PHOSPHO1:p.S32del, POU4F1:p.H108del, PRAMEF8:p.R319H, PRDM7:p.M387L, PRG4:p.T597P, PTPRD:p.R1323C, PTPRF:p.R1174Q, ROBO3:p.RS1367del, ROCK1:p.T518S, RPTN:p.G296S, RTL1:p.152_152E>EE, SIRPA:p.V233I, SLC2A6:p.A230D, SLC8A2:p.E710del, SMG7:p.E846fs, SNAPC4:p.S542del, SP8:p.G165del, SPOP:p.F133I, SPOP:p.F133V, SPOP:p.F102C, SPOP:p.F102V, SRSF11:p.G17fs, SRSF4:p.K396del, SSPO:p.S4198fs, STAG3L2:p.L81fs, STK19:p.R18fs, TBC1D2B:p.R920Q, TBC1D9:p.P1233T, TCHH:p.P1158R, TCOF1:p.K1366del, TNRC18:p.2664_2665SS>S, TP53:p.R248Q, TP53:p.R175H, TP53:p.C141G, TSPAN4:p.L92V, UBXN11:p.GPGPGPSP504del, UTP3:p.E81del, WASH3P:p.L187V, ZAN:p.P717L, ZAN:p.L878P, ZFP90:p.R591fs, ZNF761:p.H373R, and ZNF91:p.H305R.

Paragraph 62. The pharmaceutical composition according to Paragraph 61, wherein at least 39.85% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 63. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from STAD; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RNF43:p.G659fs, BZRAP1:p.P1416fs, XYLT2:p.Y526fs, LARP4B:p.T163fs, PGM5:p.I98V, ZBTB20:p.P692fs, ARID1A:p.G1848fs, FHOD3:p.P334fs, KIAA0182:p.T120fs, ATP6V1B1:p.Y383fs, PIK3CA:p.H1047R, FRMD4A:p.P1005fs, PIK3CA:p.E545K, CDC14A:p.N123fs, KRAS:p.G13D, MLL2:p.T172fs, BCORL1:p.S1679fs, PLEKHA6:p.V328fs, C9orf131:p.P342fs, CD4:p.Q164fs, FBXW7:p.R465C, GNG12:p.T68fs, IRS4:p.G591fs, JARID2:p.V422fs, KIAA0195:p.I902fs, MBD6:p.P732fs, MVK:p.P138fs, PAMR1:p.G101fs, WNT16:p.W165fs, ZNF43:p.N251fs, ABCA6:p.L306fs, ADAM28:p.K73fs, AOC3:p.L79fs, ATP2A1:p.R819fs, B2M:p.L13fs, C6orf89:p.P58fs, CNTLN:p.K1305fs, CR2:p.V206fs, DYRK4:p.K468fs, ERBB3:p.V104M, GLI1:p.W272fs, KRAS:p.G12D, MLL2:p.T172fs, MSH6:p.T1085fs, NLK:p.C190fs, OR5M3:p.T89fs, PAX6:p.P375fs, PTEN:p.L265fs, RABGAP1:p.K928fs, RAD51AP2:p.T316fs, SVIL:p.G1862fs, TP53:p.R273H, WNK4:p.G606fs, ARID1A:p.P2139fs, AXIN2:p.G665fs, C13orf33:p.R67fs, C1QTNF5:p.P308fs, CELSR1:p.G614fs, CRYGD:p.G159fs, DCHS1:p.R235fs, DDC:p.I433fs, EDNRB:p.Y383fs, EPHA2:p.P460fs, FOXN3:p.P96fs, HDAC4:p.P901fs, INF2:p.S527fs, KIRREL2:p.V649fs, KLF3:p.I104fs, KLHL14:p.P231fs, MAP7D3:p.Q308fs, OTX2:p.R44fs, PAFAH1B1:p.K302fs, PLAGL2:p.P10fs, POLM:p.P97fs, PRPF40B:p.I31fs, RALGAPB:p.T379fs, SBNO1:p.N1139fs, SERPINI1:p.L81fs, SH3KBP1:p.L574fs, SLC12A7:p.H686fs, SLC27A3:p.P643fs, TBX4:p.S370fs, TP53:p.R273C, TP53:p.R175H, TRAM1L1:p.R345fs, WBP1:p.P138fs, ABCC4:p.L883fs, AKAP13:p.K2785fs, ALDH3A1:p.P562fs, ALPK2:p.L356fs, ARFGEF1:p.P1552fs, ARID1A:p.G1848fs, AVPR1A:p.F351fs, BAX:p.M38fs, C14orf43:p.P313fs, C1QTNF5:p.G194fs, C7orf50:p.L179fs, CDC25C:p.K322fs, CETN3:p.K63fs, CHD3:p.P597fs, CTCF:p.K202fs, CTSC:p.F105fs, DDX17:p.G163fs, DLGAP3:p.G377fs, EBF3:p.G255fs, FHDC1:p.F100fs, FILIP1L:p.K749fs, FLNB:p.W529fs, GBP7:p.G431fs, GCC2:p.E700fs, GPR161:p.G517fs, IWS1:p.S802fs, KIAA0240:p.K895fs, KIAA1967:p.P415fs, LRRC43:p.D558fs, MACF1:p.R707fs, MBD6:p.G780fs, MLL3:p.F4496fs, MPRIP:p.A351fs, MUC6:p.2129_2130SS>S, NOX5:p.P467fs, OPTN:p.P24fs, OR4K5:p.F177fs,

PIK3CA:p.N345K, PIK3CA:p.E542K, PLXNA1:p.P1016fs, PNPLA7:p.P1199fs, PODN:p.I301fs, PPP2R3B:p.T389fs, PRSS36:p.L680fs, RGL2:p.G203fs, RHOQ:p.V190fs, RNF111:p.R771fs, RTN2:p.P313fs, SALL4:p.V995fs, SBF1:p.P1076fs, SETDB2:p.R715fs, SNAPC2:p.T292fs, SPG20:p.F232fs, SRCAP:p.P1876fs, STAT2:p.P489fs, TCHP:p.E172fs, TP53:p.R282W, TP53:p.R248Q, USP21:p.K474fs, WDR7:p.G262fs, ZBTB7C:p.E157fs, ZFC3H1:p.K385fs, ZNF124:p.T339fs, ZNF626:p.K115fs, ADNP2:p.S322fs, AGAP1:p.G127fs, ALDH2:p.L286fs, ARHGAP5:p.D890fs, ARHGEF17:p.A615fs, ARID1A:p.Y1324fs, ART1:p.I243fs, ASCL4:p.D35fs, ATXN2L:p.G998fs, B3GNT5:p.F30fs, BCKDHA:p.H37fs, BCL9L:p.P1127fs, BEND3:p.D265fs, BNC2:p.S575R, BRD3:p.P24fs, C12orf51:p.P4235fs, C1R:p.P216fs, C7orf49:p.G130fs, CA2:p.I145fs, CABP5:p.R145fs, CASD1:p.F781fs, CASP8:p.R471fs, CCDC153:p.P200fs, CD93:p.D280fs, CROT:p.L32fs, CSF3R:p.P468fs, CTCF:p.K202fs, ERBB2:p.S310F, FAM46D:p.S69R, FBN3:p.G601fs, FBXO21:p.F144fs, GAS6:p.G150fs, GLYR1:p.G380fs, GXYLT1:p.L223fs, HAUS6:p.S530fs, IGF2R:p.T1314fs, ITGB1:p.L378I, KDM3B:p.P1316fs, KIF13A:p.K1115fs, KLF3:p.S224fs, LARP1:p.A223fs, LRP1:p.G1488fs, LRP1:p.G1488fs, MAGEE2:p.Q45fs, MAMSTR:p.P162fs, MAPK15:p.Q511fs, MLL2:p.P647fs, MOCS2:p.P22fs, MTG1:p.L105fs, MTG1:p.H327fs, MTIF2:p.N109fs, NID2:p.R1035fs, PAX2:p.P395fs, PCCA:p.R230H, PDZD2:p.R101fs, PFKP:p.M593fs, PIK3CA:p.R88Q, PLA2G1B:p.L53fs, PLAU:p.R201fs, PMEPA1:p.P208fs, POP1:p.K750fs, PTCH1:p.P1307fs, PTPRT:p.P1075fs, RDBP:p.P6fs, RNMT:p.K392fs, ROBO2:p.P1080fs, RUNDC3B:p.L6fs, SDAD1:p.K275fs, SLC10A6:p.G109fs, SNAPC1:p.D211fs, SPATA5L1:p.C685fs, SPTA1:p.K1732T, STAT5B:p.P367fs, SYT4:p.M1fs, TAF1L:p.K851fs, TAP2:p.L75fs, TBL1XR1:p.N126fs, THEMIS:p.K406fs, TMEM79:p.P161fs, TP53:p.C176F, TP53BP2:p.K69fs, TP53RK:p.L174fs, UBQLN2:p.A523fs, UHRF1BP1:p.I1330fs, VPRBP:p.K939fs, VPS13B:p.T56fs, WASF3:p.P305fs, YLPM1:p.E1178fs, ZC3H13:p.K1006fs, ZC3H18:p.P825fs, ZC3H4:p.E779Q, ZNF48:p.P247fs, ZNF608:p.A465fs, ZNF878:p.S238fs, ZSCAN18:p.P225fs, ABCB1:p.R527fs, ABCB6:p.G318fs, ACACB:p.G255fs, ACP1:p.Q123fs, ACTL6A:p.L88fs, ADAMTSL4:p.G778fs, AGBL5:p.I420fs, AHI1:p.K303fs, AKAP9:p.M3743fs, AKD1:p.R1209fs, ANKRD40:p.D99E, ARHGEF5:p.S1512fs, ARID1A:p.K1071fs, ARID3A:p.S557G, ARPP21:p.I130fs, ASPN:p.F67fs, ASXL3:p.E873fs, ATP6V1C2:p.R312fs, BEST3:p.P444fs, BRAF:p.P403fs, BRMS1:p.G107fs, BTBD11:p.T451fs, BTBD11:p.A561V, C11orf9:p.S261fs, C14orf102:p.R90fs,

C14orf43:p.Q36fs, C15orf52:p.G98fs, C19orf21:p.R262C, C19orf70:p.P50fs, C20orf160:p.P46fs, C3:p.P890fs, CADPS2:p.N468fs, CASC3:p.S232F, CASC3:p.P603L, CASC3:p.P645L, CASC3:p.S658L, CASKIN2:p.P727fs, CBLL1:p.E138fs, CBLN3:p.P69fs, CCDC108:p.P1164fs, CCDC148:p.K420fs, CCDC153:p.P200fs, CCDC169-SOHLH2:p.K162R, CCDC88A:p.K677fs, CD1E:p.F85V, CD3EAP:p.K218fs, CDH11:p.K357T, CDH1:p.D254Y, CDH23:p.V403I, CFI:p.K37fs, CHPF2:p.D645fs, CIC:p.R507fs, CIC:p.A1114fs, CIC:p.A1114fs, CLSTN1:p.T615M, CNBD1:p.L396P, CNGA4:p.K510T, CNOT6:p.S248fs, CNTROB:p.R920fs, COL9A1:p.P283fs, CPAMD8:p.P784fs, CR1L:p.L79fs, CRB1:p.F630V, CSMD1:p.L3410V, CTNNA3:p.K856fs, CTNND1:p.I447fs, CTSD:p.P89fs, CUX1:p.A439fs, CYP7B1:p.K332T, DAB2IP:p.D994fs, DNAH11:p.T871fs, DNAH8:p.K1688fs, DNAJC1:p.K193fs, DNM2:p.P791fs, DSTN:p.F101fs, DYRK1B:p.Q545fs, EAF2:p.V109fs, EDNRB:p.A104V, EEA1:p.N570fs, EFHA1:p.F290fs, EGR1:p.P332fs, EIF4G3:p.K563fs, ELK3:p.S173fs, ENTPD2:p.G204fs, EOMES:p.G332fs, EPHA10:p.P868fs, EPHB6:p.G54fs, EPHX1:p.P132fs, EPPK1:p.G2015fs, ERBB4:p.M1fs, ESF1:p.T99fs, EXOSC8:p.L160fs, FAM113B:p.R51fs, FAM116A:p.L441fs, FAM135B:p.S645R, FAM151A:p.P117fs, FAM193A:p.D428fs, FAM193A:p.D428fs, FAM214B:p.A42fs, FAM40B:p.R740C, FAM70B:p.S19L, FASTKD1:p.K3fs, FBXW7:p.R479Q, FBXW9:p.G298fs, FER:p.L474fs, FERMT2:p.K152fs, FGGY:p.G138fs, FIGNL1:p.K309fs, FLG:p.K159fs, FLNB:p.W529fs, FOLH1:p.S501fs, FYB:p.G324fs, GABRD:p.Q412fs, GALNTL1:p.W317fs, GANAB:p.L23fs, GCDH:p.L389fs, GIMAP7:p.V276fs, GIPC3:p.G227fs, GLI3:p.P1033fs, GLIPR1L2:p.G92fs, GNPNAT1:p.F54fs, GON4L:p.M134fs, GPATCH4:p.K210fs, GRK4:p.K22fs, GTF3C1:p.S767fs, GTF3C4:p.E562fs, H2AFY2:p.K144fs, HCFC1R1:p.P83fs, HCRTR2:p.S9fs, HCRTR2:p.S9fs, HDLBP:p.G747fs, HECA:p.R333fs, HIVEP3:p.H554fs, HIVEP3:p.P534fs, HLA-C:p.P209fs, HOOK1:p.L361fs, HOXD8:p.P122fs, HTT:p.G697fs, IBTK:p.K1213fs, IDE:p.K37fs, IFT172:p.A837T, INPPL1:p.A974fs, INPPL1:p.P1154fs, INSM2:p.T533fs, INTS12:p.L14fs, INVS:p.R815fs, IPO11:p.S844fs, IRX6:p.A425V, ISG20L2:p.P288fs, ITGB8:p.A7fs, JARID2:p.G394fs, JHDM1D:p.R97fs, KBTBD6:p.G442fs, KCNC1:p.K455fs, KCNH2:p.G149A, KCNJ10:p.P102fs, KCNMB2:p.N151K, KCTD21:p.T6M, KIAA0586:p.A1592fs, KIAA1009:p.F406fs, KIAA1109:p.E1588fs, KIAA2026:p.K690fs, KIF26B:p.S1065fs, KIF6:p.L204fs, KIRREL:p.P335fs, KLC2:p.T568fs, KRAS:p.Q61H, KRAS:p.G12S, MAN1C1:p.G431fs, MAP1A:p.P2063fs, MAP2:p.K1472fs, MAP3K12:p.R449del, MAP7D1:p.A80fs,

MGST2:p.K102fs, MKI67:p.T1664fs, MKL1:p.P307fs, MLL2:p.P2354fs, MLL2:p.L656fs, MLL2:p.P647fs, MLL2:p.L1877fs, MMP3:p.I64fs, MPDZ:p.K1582fs, MTUS2:p.R1005W, MUC16:p.A6156T, MYB:p.R481fs, MYEOV:p.L269fs, MYH11:p.K1263del, MYO18A:p.P209fs, MYO7A:p.I539fs, MYOCD:p.G226fs, NAA16:p.H514fs, NBEA:p.V2247fs, NCAPD3:p.Q909fs, NCAPH:p.T466fs, NCOR2:p.P1308fs, NEFM:p.A213V, NEK8:p.V690fs, NF1:p.T676fs, NHLRC1:p.F204fs, NKD1:p.P286fs, NPR3:p.Y138H, NT5M:p.P206fs, NUFIP2:p.R224fs, NUP210:p.L135fs, NYNRIN:p.G113fs, OBSCN:p.G997fs, OGDH:p.Y948fs, OR4C16:p.S135R, OR51A7:p.L124R, OR7C1:p.C179fs, OSBP2:p.H627fs, OTOF:p.E1304K, P2RX1:p.R20fs, PALB2:p.M296fs, PALB2:p.N280fs, PANK1:p.K400fs, PAPD4:p.C225fs, PAPPA2:p.I1683fs, PARP15:p.K461fs, PARP4:p.K847fs, PCDH10:p.N118fs, PCDH10:p.P225fs, PCGF3:p.H63fs, PELI2:p.G197fs, PHACTR1:p.V251fs, PHACTR2:p.S237fs, PHACTR4:p.S354fs, PHKB:p.K642fs, PIAS3:p.H116fs, PIGO:p.P787fs, PIGT:p.A346fs, PIK3R3:p.M341fs, PITPNM1:p.P295fs, PKN2:p.K76fs, PLA2G15:p.W230fs, PLAG1:p.K184fs, PLEKHO1:p.T254fs, PLOD3:p.R297fs, PLOD3:p.P296fs, PLXNA2:p.P464fs, POLQ:p.L1430fs, PPARGC1B:p.P135fs, PPL:p.P454fs, PPM1H:p.P226fs, PPP1R12C:p.P372fs, PREX2:p.R562fs, PRICKLE4:p.Q109fs, PRKAR1B:p.P87fs, PRKCG:p.R345C, PRMT8:p.S28fs, PROX1:p.F592fs, PRRG3:p.R163fs, PSD2:p.G256fs, PTCHD3:p.F588fs, PTPN4:p.N319fs, PTPRC:p.Q895H, PWWP2B:p.S84fs, PYGO2:p.Q150fs, RABGAP1:p.K928fs, RB1CC1:p.N1171fs, RBM6:p.R96fs, RHOA:p.Y42C, RIMS1:p.R71G, RIMS2:p.V401fs, RING1:p.G171fs, RINT1:p.L107fs, RNF43:p.P116fs, ROBO2:p.K1293fs, RPS6KA6:p.K109fs, RRS1:p.N45fs, RSF1:p.K386fs, RUSC2:p.P486fs, RXFP3:p.A60V, SAFB:p.W798fs, SCARF1:p.R614Q, SCLT1:p.K109fs, SERPINB12:p.Q168fs, SGK3:p.L61fs, SGOL2:p.E407fs, SIGLEC1:p.P318fs, SIK1:p.Q678fs, SLC16A6:p.G98fs, SLC25A17:p.F28fs, SLC26A7:p.I629fs, SLC32A1:p.V494I, SLC4A3:p.L1061fs, SLC7A10:p.P157fs, SLC9A2:p.T746fs, SLITRK1:p.K45fs, SND1:p.H721fs, SOAT1:p.F64fs, SORBS2:p.E1158fs, SOX7:p.L309fs, SPAG17:p.Q1264fs, SPTY2D1:p.P485fs, SRCIN1:p.P865fs, SREBF2:p.H763fs, SRRT:p.G102fs, STAB1:p.P1120fs, STRADA:p.R333fs, STX2:p.K252fs, SV2A:p.E138fs, SYCP2:p.M176fs, SYNJ2:p.P1111fs, TAS2R10:p.L196fs, TBC1D22B:p.A175fs, TEAD2:p.P298fs, TFE3:p.G482fs, TGM6:p.T358fs, TIMM44:p.K83fs, TIMP3:p.A199fs, TLR4:p.L498V, TMEM132D:p.P206fs, TMEM41A:p.F156fs, TMEM41B:p.F230fs, TMTC4:p.R611C, TNK2:p.P632fs, TOPBP1:p.I1381fs, TP53:p.E286K, TP53:p.P152fs,

TRIP11:p.K541fs, TRPA1:p.T673fs, TRPM8:p.H765fs, TTF1:p.K336fs, TTI1:p.R707H, TTN:p.E15192D, U2AF2:p.L175fs, UBC:p.G684fs, UBR4:p.P2802fs, UPF2:p.E1033D, UPK2:p.P49fs, USP13:p.I116fs, USP15:p.K782fs, VASH1:p.G3fs, VEZF1:p.355_356insN, VPS13A:p.F2883fs, WAPAL:p.R522fs, WDFY3:p.L1842fs, WDR59:p.N160fs, WDR5:p.N214fs, WDR60:p.Q412fs, WDTC1:p.M287fs, WHSC1L1:p.K418fs, WNT1:p.W167fs, XIRP2:p.E1007D, YBX2:p.P226fs, YIF1A:p.R131fs, ZBBX:p.E151del, ZBTB40:p.L262fs, ZBTB7C:p.G342fs, ZBTB7C:p.D154fs, ZC3H18:p.T701fs, ZDHHC5:p.E651del, ZDHHC7:p.P316fs, ZFHX3:p.R1893fs, ZFHX3:p.E763fs, ZFHX4:p.L408fs, ZHX3:p.N249K, ZIM3:p.I384fs, ZKSCAN5:p.D13fs, ZMYM4:p.K345fs, ZNF236:p.T1410M, ZNF23:p.F122fs, ZNF334:p.K426fs, ZNF358:p.T130fs, ZNF701:p.L296fs, ZNF711:p.L737fs, and ZNF831:p.A49fs.

Paragraph 64. The pharmaceutical composition according to Paragraph 63, wherein at least 48.79% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 65. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from TGCT; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, BTN2A3P:p.P3S, MUC2:p.G1715S, NBPF10:p.L44V, SP8:p.G156S, DCP1B:p.Q252H, DEK:p.E41D, ERC1:p.K692R, FAM104B:p.D75H, FRG1B:p.M49V, KRTAP10-10:p.V234M, LRRCC1:p.A6V, NRAS:p.Q61R, PNPLA4:p.L223P, ANKLE1:p.C644fs, ANKLE1:p.C644fs, KIT:p.D816H, KIT:p.D816Y, MUC2:p.T1597I, PSMD11:p.A5V, RHPN2:p.V73M, RUNX2:p.Q71E, SP4:p.E7K, TUBA1C:p.L146F, ZNF814:p.Y324H, ADAMTS17:p.N572T, ATRX:p.K1936R, BCL11B:p.E535D, BMP2K:p.Q460H, BMP2K:p.H487Q, C12orf32:p.D60V, C22orf43:p.K19E, CDC27:p.N571I, CDC27:p.P242S, DDX11:p.K208fs, EBPL:p.L189V, EZH2:p.K510R, FAM86A:p.A141T, GAS2L2:p.D189A, GRID2IP:p.LS754del, HGC6.3:p.E171G, KIT:p.D816V, KIT:p.N822Y, KIT:p.N822K, KRAS:p.Q61R, KRAS:p.G12V, KRTAP1-1:p.I116V, LRRC37BP1:p.Y166D, MEF2A:p.R127Q, MFF:p.S7F, MST1:p.R347W, MUC4:p.S3048L, MUC6:p.H2000Q, MUC6:p.P1977H, NAT10:p.I393T, OPLAH:p.A900D, PIEZO1:p.Q749E, PRAMEF4:p.F300V, RBM10:p.E184D, SERINC2:p.T121P, SPIN2A:p.M150V, SRRM2:p.A2257S, SSBP3:p.K6R, ZNF680:p.R501W, ABCC8:p.Y512C, ABCC9:p.L466P, ABCD1:p.H169Q, ABL2:p.P19T, ACVR2B:p.R48C, AHDC1:p.P33fs, AHNAK2:p.L1640M, ALPPL2:p.W31S, AMMECR1:p.G77C, ANK3:p.D1322E, ANKHD1-

EIF4EBP3:p.G60S, ANKRD11:p.Y2015S, ANKRD11:p.K369R, ANKRD50:p.V637M, APBB3:p.L450P, ARHGAP24:p.T35A, ARID4B:p.G1076A, ARMC3:p.A514T, ARRB2:p.T99P, ATAD5:p.I305V, ATXN3:p.305_306insQQQQQQQ, AVPR1B:p.G39R, AXDND1:p.E994Q, BAI2:p.A231G, BEST3:p.P383L, BIRC6:p.V414L, BIRC8:p.A225M, BRWD1:p.K1319R, BTN2A2:p.L15F, C12orf51:p.A2644T, C12orf65:p.K143T, C16orf62:p.L244I, C1QBP:p.T225I, C1orf167:p.S123G, C5orf25:p.Y4F, CACNA1E:p.G2080S, CAPNS1:p.LV303del, CCDC159:p.A332S, CDKAL1:p.P409L, CDYL:p.V48A, CDYL:p.A60G, CELSR2:p.L17P, CHD4:p.E138D, CKAP5:p.G576A, CLCC1:p.K52R, CMTM8:p.S26T, CNKSR2:p.P249L, CNTN5:p.I501T, COG5:p.H617R, COL15A1:p.K708R, COL6A3:p.A2378D, CRYGB:p.R143G, CSGALNACT2:p.L362F, CUL4A:p.I438F, CXXC1:p.Q156H, CYP19A1:p.F406L, DCLRE1B:p.F28I, DDX11:p.A376T, DDX11:p.E680D, DEPDC5:p.R1525Q, DLC1:p.S741T, DNMT1:p.R995Q, DOCK11:p.Q169E, DSPP:p.D1047N, E2F7:p.I91S, EBF1:p.D353G, ECI2:p.K55R, EEF1A2:p.Y418S, EIF3J:p.A8G, EML6:p.K805R, EPAS1:p.S474T, EPRS:p.L1335I, ERICH1:p.E327K, FAM101B:p.L5P, FAM104A:p.M1R, FAM110D:p.R71H, FAM155A:p.Q95R, FAM186A:p.G1492E, FAM194B:p.Y139H, FAM21B:p.P1231S, FAM32A:p.K9R, FAM46B:p.H416R, FAM48B1:p.I499V, FAM48B1:p.A516P, FAM5C:p.S425W, FAM86C2P:p.C120Y, FBXL14:p.V48G, FRMPD3:p.Q832del, FRS2:p.L47S, GDF5:p.E105fs, GPNMB:p.C3fs, GPT2:p.R10P, H2AFV:p.Q125R, HDLBP:p.R503C, HERC2:p.R2129C, HIST1H2BJ:p.K13R, HLX:p.N231K, HMGB3:p.E198D, HSF4:p.R169W, HSF4:p.S491P, HYAL4:p.D222N, INO80E:p.P206fs, INTS4:p.S460A, IQCF6:p.R3H, ITPR1:p.M1569I, ITPR3:p.R1698G, KANSL3:p.G376E, KCNA4:p.E627del, KDM5A:p.P423S, KDM6A:p.Y362fs, KIAA0020:p.K63R, KIDINS220:p.N851S, KIT:p.W557G, KLHDC2:p.W321S, KRAS:p.A146T, KRAS:p.Q61H, KRAS:p.Q61L, KRAS:p.G12A, KRAS:p.G12R, KRBA1:p.R839G, KRTAP4-8:p.T63S, L2HGDH:p.P441del, LAMC3:p.P174Q, LHCGR:p.L16Q, LOC401296:p.L144M, LPHN2:p.F906I, LRP12:p.G310C, LTB4R:p.F73L, LTBP3:p.L35del, LUC7L3:p.S148T, LYPD4:p.T64K, MAMLD1:p.Q572L, MAP4K2:p.R341G, MAPK7:p.A501D, MAT2A:p.E166G, MED12L:p.C1292Y, MESP2:p.Q182E, MEX3C:p.R534S, MIER2:p.L131F, MLL5:p.Y66C, MLLT3:p.177_178SS>S, MMS19:p.D1005N, MRPS25:p.E119del, MSH6:p.D576A, MTIF3:p.G65E, MUC17:p.M1807T, MUC17:p.T2279N, MUC17:p.G2474S, MUC2:p.TTPSPP1475del, MUC2:p.T1568M, MUC2:p.T1580N, MUC2:p.T1704I,

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Paragraph 66. The pharmaceutical composition according to Paragraph 65, wherein at least 51.61% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 67. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from THCA; and (b) the at least one

tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, HRAS:p.Q61R, NRAS:p.Q61K, OTUD4:p.T909I, HRAS:p.Q61K, NLRP6:p.E611G, AKT1:p.E17K, ANKMY1:p.N302I, ATP6V1A:p.L237P, CYP19A1:p.S113I, DCUN1D4:p.L275P, DGCR8:p.E518K, DLC1:p.S741T, DNAH10:p.C1853F, EIF1AX:p.G9D, FAM75D5:p.L222P, FCGRT:p.P40A, KRAS:p.Q61K, LMX1B:p.Q285del, MAS1L:p.R324G, MED15:p.S35I, MEGF6:p.Y393C, ODZ2:p.A1529V, OR5L1:p.R122H, OR6K6:p.F311L, OTX1:p.D315N, POTEE:p.S75G, SCN5A:p.D1978H, TOP2A:p.K1199E, and TSG101:p.K265R.

Paragraph 68. The pharmaceutical composition according to Paragraph 67, wherein at least 69.88% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 69. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from UCS; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R248Q, ZNF814:p.D404E, BTN2A3P:p.P3S, FBXW7:p.R465C, FRG1B:p.G65E, MUC4:p.H4205Q, NBPF10:p.V99F, PIK3CA:p.E545K, PIK3CA:p.H1047R, PPP2R1A:p.P179R, DDX11L2:p.*128Q, FBXW7:p.R479Q, FRG1B:p.K13N, FRG1B:p.L52S, HSD17B7P2:p.N175S, KRAS:p.G12V, LOC283788:p.S37G, TP53:p.R273H, TP53:p.S241Y, ADAMTS12:p.E359K, BCL2L11:p.L187fs, CDC27:p.L460fs, CHEK2:p.K373E, ESPNP:p.W122fs, FBXW7:p.R689W, FBXW7:p.R505G, FBXW7:p.R465H, FCGBP:p.V4019M, FRG1B:p.I10T, FRG1B:p.D32V, FRG1B:p.R37K, KRAS:p.G12D, LOC100233156:p.R21C, LOC283788:p.I46M, LRP1B:p.L1392F, MAMLD1:p.Q572L, MST1P9:p.L319P, MUC4:p.A2390T, MUC4:p.G2172S, NBPF10:p.E3455K, PIK3CA:p.G106V, PODXL:p.28_30PSP>P, POTEC:p.R477Q, PPP2R1A:p.R183W, PPP2R1A:p.S219L, PTPN18:p.TG378del, RGPD3:p.N756D, RPL13AP20:p.G107R, SAMD4B:p.R477W, SMAP1:p.E169fs, TP53:p.H193R, TP53:p.H179R, TP53:p.R175H, TUBBP5:p.R119H, and U2AF1:p.S34F.

Paragraph 70. The pharmaceutical composition according to Paragraph 69, wherein at least 16.07% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 71. The pharmaceutical composition according to any of Paragraphs 1 to 7, wherein: (a) the population of subjects is suffering from PAAD; and (b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group

consisting of RBM14:p.AAAAAAA286del, KRAS:p.G12D, JMY:p.PPPPPPPPPPP811del, RIOK1:p.D69del, LCE2A:p.SSGGCCGSSSGGCC47del, KRAS:p.G12V, C1QB:p.GPKGPMGPKGGPGAPGAP90del, ZFHX3:p.V777del, DBR1:p.541_542DD>D, AEBP1:p.K1133del, KRAS:p.G12R, RBM47:p.495_502AAAAAAAA>A, , AP3S1:p.K41fs, MLL2:p.AEGPHLSPQPEELHLSPQ792del, RFX1:p.386_401GGGGGGGGGGGGGGSG>G, AXDND1:p.EQ991del, HERC2P3:p.A803V, RGPD3:p.N756D, FNDC1:p.D1180del, ANAPC1:p.T537A, IRS4:p.21_22AA>A, GIGYF2:p.Q1005del, NCOA3:p.Q1253fs, SIK3:p.950_951QQ>Q, GPR6:p.AAAAATAAGGPDTGEWGPPA36del, NBPF12:p.D1323fs, SHROOM4:p.1156_1157EE>E, ZMIZ2:p.VAAAAATATATATAT153del, DGKK:p.PAPP41del, LZTS1:p.RTQDLEGALRTKGLEL432del, CASQ2:p.395_396DD>D, DCP1B:p.251_252insH, ESPNP:p.296_317PPPPSFPPPPPPPGTQLPPPPP>P, KBTBD6:p.T403K, NBPF16:p.D449fs, ANKRD36C:p.H438R, ESPN:p.PPPPPPSFPPPPPPPGTQLPP430del, FCGBP:p.A2493V, KRAS:p.Q61H, NCOA3:p.Q1276del, OR2T2:p.C203fs, TMCC1:p.Q565L, BCKDHA:p.G129fs, ESPNP:p.H64fs, GNAS:p.R844H, NBPF14:p.R25C, OGFOD1:p.G477fs, RBM12:p.P693S, SLC38A10:p.1071_1072II>I, SORBS2:p.P866S, TP53:p.R248W, TP53:p.R175H, and UBAC1:p.E269del.

Paragraph 72. The pharmaceutical composition according to Paragraph 71, wherein at least 50% of subjects in the population have the at least one tumor-specific mutation.

Paragraph 73. The pharmaceutical composition according to any of Paragraphs 1 to 72, wherein the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 neoantigenic peptides.

Paragraph 74. The pharmaceutical composition according to Paragraph 73, wherein the composition comprises 15 to 20 neoantigenic peptides.

Paragraph 75. The pharmaceutical composition according to any of Paragraphs 1 to 74, wherein each neoantigenic peptide is from about 5 to about 50 amino acids in length.

Paragraph 76. The pharmaceutical composition according to any of Paragraphs 1 to 75, wherein each tumor-specific neoepitope binds to HLA-A, -B or –C with a K_D of less than 500 nM.

Paragraph 77. The pharmaceutical composition according to any of Paragraphs 1 to 76, which is an immunogenic or vaccine composition.

Paragraph 78. The pharmaceutical composition according to Paragraph 77, further comprising an immunomodulator or adjuvant.

Paragraph 79. The pharmaceutical composition according to Paragraph 78, wherein the immunodulator or adjuvant is selected from the group consisting of poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryllipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel®, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon.

Paragraph 80. A method of treating or preventing a tumor in a subject in need thereof, comprising administering to the subject a pharmaceutical composition according to any of Paragraphs 1 to 79.

Paragraph 81. The method of Paragraph 80, wherein the pharmaceutical composition is administered as a combination therapy with an additional cancer therapy.

Paragraph 82. The method of Paragraph 81, wherein the additional thereapy is a check point inhibitor.

Paragraph 83. The method of Paragraph 81, wherein the additional therapy is surgery, chemotherapy, or a targeted therapy.

Paragraph 84. A method of prophylactic cancer treatment comprising: (a) selecting a cancer drug for a patient in need thereof, the drug selected from the group consisting of ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitors, and antiestrogen therapy; and (b) administering prophylactically to the subject, a pharmaceutical composition according to any of Paragraphs 1 to 79 wherein the at least one neoantigenic peptide is derived from drug resistant mutations associated with the selected cancer drug.

Paragraph 85. A method of treating or preventing a tumor in a population of subjects in need thereof, comprising administering to a subject an agent comprising an extracellular ligand-binding domain recognizing a tumor-specific neoepitope comprising a tumor-specific mutation having an incidence of at least 1% of subjects in the population.

Paragraph 86. The method according to Paragraph 85, wherein the agent comprises an antibody, antibody fragment, antibody drug conjugate, aptamer, CAR, or T cell receptor.

Paragraph 87. The method according to Paragraph 86, wherein the antibody or antibody fragment is humanized, fully humanized, or chimeric.

Paragraph 88. The method according to Paragraphs 86 or 87, wherein the antibody fragment comprises a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment.

Paragraph 89. The method according to any of Paragraphs 85 to 88, wherein the tumor-specific mutation comprises a mutation listed for any population in Table 9.

Paragraph 90. The method according to any of Paragraphs 85 to 88, wherein the tumor-specific mutation is within a gene containing an extracellular domain.

Paragraph 91. The method according to Paragraph 90, wherein the tumor-specific mutation comprises FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

Paragraph 92. The method according to Paragraph 90, wherein the tumor-specific mutation is within the extracellular domain.

Paragraph 93. The method according to Paragraph 92, wherein the tumor-specific mutation comprises FGFR3 S249C or ERBB3 V104M.

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<400> 17
Val Ile Pro Gly Asn Ile Leu Asn Val
1 5

<210> 18
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<220>
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<400> 18
Val Ile Pro Gly Asn Ile Leu Asn Val
1 5

<210> 19
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 19
His Thr Ala Glu Leu Val Ile Pro Gly
1 5

<210> 20
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 20
Asn Ile Leu Asn Val Ser Ile Lys Ile
1 5

<210> 21
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 21
Lys Ile Cys Leu Thr Leu Ser Pro
1 5

<210> 22
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<220>
<221> source
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<400> 22
Val Ser Ile Lys Ile Cys Leu Thr Leu
1 5

<210> 23
<211> 9
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<220>
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<400> 23
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1 5

<210> 24
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<400> 24
Arg Val Phe Gly Val Ser Glu Trp Leu
1 5

<210> 25
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<400> 25
Gly Met Thr Leu Gly Ala Val Val Val
1 5

<210> 26
<211> 9
<212> PRT
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<220>
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<400> 26
Met Thr Leu Gly Glu Lys Phe Arg Val
1 5

<210> 27
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<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 27

Arg Val Gly Asn Cys Lys His Leu Lys
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 28
Arg Val Gly Asn Cys Lys His Leu Lys
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 29
Val Val Val Ser Glu Arg Ile Leu Arg
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 30
Arg Val Gly Asn Cys Lys His Leu Lys
1 5

<210> 31
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<400> 31
Lys Phe Arg Val Gly Asn Cys Lys His

1 5

<210> 32
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32
Lys Phe Arg Val Gly Asn Cys Lys His Leu
1 5 10

<210> 33
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 33
Arg Val Gly Asn Cys Lys His
1 5

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 34
Thr Leu Gly Ala Val Val Val
1 5

<210> 35
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 35
Val Val Val Ser Glu Arg Ile Leu
1 5

<210> 36
<211> 7
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<213> Artificial Sequence

<220>
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<400> 36
Gly Met Thr Leu Gly Glu Lys
1 5

<210> 37
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 37
Ala Val Val Val Ser Glu Arg
1 5

<210> 38
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 38
Ala Gly Met Thr Leu Gly Glu
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 39
Gly Asn Cys Lys His Leu Lys
1 5

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 40
Leu Gly Ala Val Val Val Ser
1 5

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 41
Arg Val Phe Gly Val Ser Glu
1 5

<210> 42
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 42
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1 5

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 43
Asn Cys Lys His Leu Lys Met
1 5

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 44
Thr Leu Gly Ala Val Val Val
1 5

<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 45
Val Val Val Ser Glu Arg Ile Leu
1 5

<210> 46
<211> 7
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 46
Thr Leu Gly Ala Val Val Val
1 5

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 47
Glu Ala Gly Met Thr Leu Gly
1 5

<210> 48

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 48
Leu Gly Ala Val Val Val Ser
1 5

<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 49
Ala Val Val Val Ser Glu Arg
1 5

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 50
Ser Leu Leu Asn Tyr Leu Arg Glu Met
1 5

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 51
Glu Tyr Met Ala Asn Gly Ser Leu Leu
1 5

<210> 52
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 52
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 53
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 54
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 54
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 55
<211> 9
<212> PRT
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<220>
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<400> 55
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 56
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 56
Leu Leu Asn Tyr Leu Arg Glu Met Arg
1 5

<210> 57
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 57
Glu Tyr Met Ala Asn Gly Ser Leu Leu
1 5

<210> 58
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 58
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 59
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 60
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 61
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<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 61
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 62
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 62
Leu Leu Asn Tyr Leu Arg Glu Met Arg
1 5

<210> 63
<211> 9
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 63
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 64
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 64
Glu Tyr Met Ala Asn Gly Ser Leu Leu
1 5

<210> 65
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 65
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 66
<211> 9
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 66
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 67
<211> 9
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 67
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 68
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 69
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 69
Leu Leu Asn Tyr Leu Arg Glu Met Arg
1 5

<210> 70
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 70
Glu Tyr Met Ala Asn Gly Ser Leu Leu
1 5

<210> 71
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 71
Met Ala Asn Gly Ser Leu Leu Asn Tyr
1 5

<210> 72
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 72
Thr Glu Tyr Met Ala Asn Gly Ser Leu
1 5

<210> 73
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 73
Val Gln Leu Ile Met Gln Leu Met Pro Phe
1 5 10

<210> 74
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 74
Ser Thr Val Gln Leu Ile Met Gln Leu Met
1 5 10

<210> 75
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 75
Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 76
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 76
Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 77
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 77
Val Gln Leu Ile Met Gln Leu Met Pro Phe
1 5 10

<210> 78
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 78
Met Gln Leu Met Pro Phe Gly Cys Leu Leu
1 5 10

<210> 79
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 79
Met Gln Leu Met Pro Phe Gly Cys Leu
1 5

<210> 80
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 80
Gln Leu Ile Met Gln Leu Met Pro Phe
1 5

<210> 81
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R732Q"

<400> 81
Phe Tyr Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu Val His
1 5 10 15

Val Glu Glu Pro His Thr Glu Thr Val Gln Gln Lys Tyr Phe Pro Glu
20 25 30

Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala Glu
35 40 45

Val Gly Val Thr
50

<210> 82
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S654fs"

<400> 82
Tyr Asp Gln Cys Pro Val Ser Gly Pro Trp Asp Phe Pro Gln Pro Leu
1 5 10 15

Ile Asp Pro Met Pro Gln Gly His Ser Glu Pro Ala Phe His Tyr Leu
20 25 30

Glu Ala Leu Val Leu
35

<210> 83
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A266T"

<400> 83
Val Pro Leu Leu Ser Arg Lys Phe Met Val Thr Ser Leu Cys Asn Tyr
1 5 10 15

Leu Ala Ile Asp Leu Ser Trp Arg Asp Thr Thr Ile Leu Asn Gly Thr
20 25 30

Cys Val Pro Pro Asp Val Trp Arg Lys Tyr Glu Lys Trp Leu Ser Pro
35 40 45

Asp Asn Ile Pro
50

<210> 84
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T878fs"

<400> 84
Lys Thr Ile Asp Leu Val Ala Tyr Gly Asp Ile Asn Gly Phe Ser Ala
1 5 10 15

Met Ala Lys Thr Val Gly Leu Pro Thr Arg His Gly Ser Gln Asn Val
20 25 30

Ala

<210> 85
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R385I"

<400> 85
Thr Gly Glu Lys Pro Tyr Thr Cys Gly Glu Cys Gly Lys Thr Phe Arg
1 5 10 15

Gln Ser Ala Asn Leu Tyr Val His Arg Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Glu Asp Cys Gly Lys Ala Phe Gly Arg Tyr Thr
35 40 45

Ala Leu Asn Gln
50

<210> 86
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E95D"

<400> 86
Thr Phe Pro Pro Pro Gly Asp Thr Trp Glu Leu Ala Tyr Ile Pro Ser
1 5 10 15

His Ser Asp Ala Ala Lys Thr Val Thr Asp Asp Thr Val Arg Arg Ala
20 25 30

Leu Val Ile Asn Met Arg Val Arg Gly Phe Pro Ser Glu Lys Asp Phe

35 40 45

Glu Asp Tyr Ile
50

<210> 87
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1476Q"

<400> 87
Pro Gln Ile Thr Leu Leu Asp Glu Pro Ser Thr Gly Met Asp Pro Lys
1 5 10 15

Ala Lys Gln His Met Trp Arg Ala Ile Gln Gln Thr Ala Phe Lys Asn
20 25 30

Arg Lys Arg Ala Ala Ile Leu Thr Thr His Tyr Met Glu Glu Ala Glu
35 40 45

Ala Val Cys Asp
50

<210> 88
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L306fs"

<400> 88
Phe Val Thr Ile Ile Ile Thr Phe Thr Gln Ile Ile Val Met Thr Gly
1 5 10 15

Phe Met Val Ile Phe Ile Leu Phe Phe Tyr Met Ala Tyr Leu Trp
20 25 30

<210> 89
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A696T"

<400> 89
Ser Thr Gln Phe Met Asp Glu Ala Asp Ile Leu Ala Asp Arg Lys Val
1 5 10 15

Phe Leu Ser Gln Gly Lys Leu Lys Cys Thr Thr Gly Ser Ser Leu Phe
20 25 30

Leu Lys Lys Lys Trp Gly Ile Gly Tyr His Leu Ser Leu Gln Leu Asn
35 40 45

Glu Ile Cys Val
50

<210> 90
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R842Q"

<400> 90
Arg Leu Val Glu Met Glu Gln Val Leu Ser Ser Leu Asn Lys Met Arg
1 5 10 15

Lys Thr Ile Gly Gly Val Ala Leu Trp Gln Gln Gln Gln Ile Cys Ala
20 25 30

Ile Ala Arg Val Arg Leu Leu Lys Leu Lys His Glu Arg Lys Ala Leu
35 40 45

Leu Ala Leu Leu
    50

<210> 91
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.E1158K"

<400> 91
Asn Ser Gly Ile Trp Ser Phe Cys Phe Tyr Val Val Thr Val Phe Ser
1   5   10   15

Val Ala Gly Phe Ala Phe Ser Ile Phe Lys Lys Ser Asp Ile Pro Phe
            20   25   30

Ile Phe Thr Phe Leu Ile Pro Pro Ala Thr Met Ile Gly Cys Leu Phe
        35   40   45

Leu Ser Ser His
    50

<210> 92
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R467L"

<400> 92
Arg Leu Tyr Asp Pro Thr Glu Gly Met Val Ser Val Asp Gly Gln Asp
1   5   10   15

Ile Arg Thr Ile Asn Val Arg Phe Leu Leu Leu Glu Ile Ile Gly Val
            20   25   30

Val Ser Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile
35 40 45

Arg Tyr Gly Arg
50

<210> 93
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R527fs"

<400> 93
Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro His Lys
1 5 10 15

Phe Asp Thr Leu Val Gly Glu Arg Gly Pro Val Glu Trp Trp Ala Glu
20 25 30

Ala Glu Asp Arg His Cys Thr Cys Pro Gly Ser Gln Pro Gln Asp Pro
35 40 45

Pro Ala Gly
50

<210> 94
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G318fs"

<400> 94
Leu Thr Glu Lys Ala Pro Trp Asn Ser Leu Ala Trp Thr Val Thr Ser
1 5 10 15

Tyr Val Phe Leu Lys Phe Leu Gln Gly Val Ala Leu Ala Val Gln Ala

20 25 30

Ser

<210> 95
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R345H"

<400> 95
Ser Arg Gln Cys Gln Glu Gln Ile Ala Arg Ala Met Gly Val Ala Asp
1 5 10 15

Glu Ala Leu Gly Asn Val Arg Thr Val His His Ala Phe Ala Met Glu
20 25 30

Gln Arg Glu Glu Glu Arg Tyr Gly Ala Glu Leu Glu Ala Cys Arg Cys
35 40 45

Arg Ala Glu Glu
50

<210> 96
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R570W"

<400> 96
Arg Met Leu Ile Leu Pro Leu Asn Asn Phe Pro Trp Val Ile Asn Gly
1 5 10 15

Leu Leu Glu Ala Lys Val Ser Leu Asp Trp Trp Ile Gln Leu Phe Leu
20 25 30

Asp Leu Pro Asn His Asn Pro Gln Ala Tyr Tyr Ser Pro Asp Pro Pro
35 40 45

Ala Glu Pro Ser
50

<210> 97
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L883fs"

<400> 97
Val Ala Val Ile Pro Trp Ile Ala Ile Pro Leu Val Pro Leu Gly Ile
1 5 10 15

Ile Phe Ile Phe Leu Arg Arg Tyr Phe Trp Lys Arg Gln Glu Met
20 25 30

<210> 98
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1090fs"

<400> 98
His Ala Tyr Asn Lys Gly Gln Glu Phe Leu His Arg Tyr Gln Glu Leu
1 5 10 15

Leu Asp Asp Asn Gln Ala Pro Phe Phe Cys Leu Arg Val Arg Cys Gly
20 25 30

Gly Trp Leu Cys Gly Trp Thr Ser Ser Ala Ser Pro Ser Ser Pro Pro
35 40 45

Arg Gly
    50

<210> 99
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.Y512C"

<400> 99
Ser Thr Leu Glu Tyr Ser Asn Glu Arg Leu Lys Gln Thr Asn Glu Met
1   5   10   15

Leu Arg Gly Ile Lys Leu Leu Lys Leu Cys Cys Ala Trp Glu Asn Ile
            20   25   30

Phe Arg Thr Arg Val Glu Thr Thr Arg Arg Lys Glu Met Thr Ser Leu
        35   40   45

Arg Ala Phe Ala
    50

<210> 100
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.L466P"

<400> 100
Ile Ile Met Gly Val Ile Leu Leu Tyr Asn Leu Leu Gly Ser Ser Ala
1   5   10   15

Leu Val Gly Ala Ala Val Ile Val Leu Pro Pro Ala Pro Ile Gln Tyr
            20   25   30

Phe Ile Ala Thr Lys Leu Ala Glu Ala Gln Lys Ser Thr Leu Asp Tyr
35 40 45

Ser Thr Glu Arg
50

<210> 101
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S606P"

<400> 101
Asp Val Val His Leu His His Ile Leu Gln Arg Glu Gly Gly Trp Glu
1 5 10 15

Ala Met Cys Asp Trp Lys Asp Val Leu Pro Pro Gly Gly Glu Lys Gln
20 25 30

Arg Ile Gly Met Ala Arg Met Phe Tyr His Arg Pro Lys Tyr Ala Leu
35 40 45

Leu Asp Glu Cys
50

<210> 102
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H169Q"

<400> 102
Ala Thr Phe Val Asn Ser Ala Ile Arg Tyr Leu Glu Gly Gln Leu Ala
1 5 10 15

Leu Ser Phe Arg Ser Arg Leu Val Ala Gln Gln Ala Tyr Arg Leu Tyr

20 25 30

Phe Ser Gln Gln Thr Tyr Tyr Arg Val Ser Asn Met Asp Gly Arg Leu
35 40 45

Arg Asn Pro Asp
50

<210> 103
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K445N"

<400> 103
Asp Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr
1 5 10 15

Ala Asp Gly Asp Pro Ala Trp Ala Pro Asn Asn Asn Tyr Ile Glu Lys
20 25 30

Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser
35 40 45

Phe Met Glu Gly
50

<210> 104
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P19T"

<400> 104
Met Gly Gln Gln Val Gly Arg Val Gly Glu Ala Pro Gly Leu Gln Gln
1 5 10 15

Pro Gln Thr Thr Arg Gly Ile Arg Gly Ser Ser Ala Ala Arg Pro Ser
20 25 30

Gly Arg Arg Arg Asp Pro Ala Gly Arg Thr Thr Glu Thr
35 40 45

<210> 105
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.L249fs"

<400> 105
Thr Ile Glu Pro Pro Pro Ala Asp Pro Arg Leu Arg Glu Asp Met Ala
1 5 10 15

Leu Leu Ala Asp Cys Ala Leu Pro Pro Arg Ala Pro Arg
20 25

<210> 106
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1731C"

<400> 106
Ala Arg Ala Glu Gly Ile Pro Arg Ile Tyr Val Ser Ala Asn Ser Gly
1 5 10 15

Ala Arg Ile Gly Leu Ala Glu Glu Ile Cys Cys His Met Phe His Val
20 25 30

Ala Trp Val Asp Pro Glu Asp Pro Tyr Lys Gly Tyr Arg Tyr Leu Tyr
35 40 45

Leu Thr Pro Gln
50

<210> 107
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E2318Q"

<400> 107
Val Ala Val Gln Phe Ala Asp Phe His Asp Thr Pro Gly Arg Met Leu
1 5 10 15

Glu Lys Gly Val Ile Ser Asp Ile Leu Gln Gln Trp Lys Thr Ala Arg
20 25 30

Thr Phe Leu Tyr Trp Arg Leu Arg Arg Leu Leu Leu Glu Asp Gln Val
35 40 45

Lys Gln Glu Ile
50

<210> 108
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G255fs"

<400> 108
Glu His Lys Lys Leu Asp Leu His Arg Asp Phe Thr Val Ala Ser Pro
1 5 10 15

Ala Glu Phe Val Thr Arg Phe Gly Gly Ile Gly Ser Ser Arg Arg Cys
20 25 30

Leu Leu Pro Thr Thr Gly Leu Pro Pro
35 40

<210> 109
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F48C"

<400> 109
Gln His Thr Lys Ala Asn Arg Gln Arg Glu Pro Gly Leu Gly Phe Ser
1 5 10 15

Phe Glu Phe Thr Glu Gln Gln Lys Glu Cys Cys Gln Ala Thr Ala Arg
20 25 30

Lys Phe Ala Arg Glu Glu Ile Ile Pro Val Ala Ala Glu Tyr Asp Lys
35 40 45

Thr Gly Glu Tyr
50

<210> 110
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R330H"

<400> 110
Thr Lys Leu Gln Val Ile Gln Phe Lys Leu Ala Asp Met Ala Leu Ala
1 5 10 15

Leu Glu Ser Ala Arg Leu Leu Thr Trp His His Ala Ala Met Leu Lys
20 25 30

Asp Asn Lys Lys Pro Phe Ile Lys Glu Ala Ala Met Ala Lys Leu Ala

35 40 45

Ala Ser Glu Ala
50

<210> 111
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R224L"

<400> 111
Arg Glu Glu Glu Glu Arg Glu Arg Leu Gln Lys Glu Glu Glu Lys Arg
1 5 10 15

Arg Arg Glu Glu Glu Glu Arg Leu Arg Leu Leu Glu Glu Glu Glu Arg
20 25 30

Arg Arg Ile Glu Glu Glu Arg Leu Arg Leu Glu Gln Gln Lys Gln Gln
35 40 45

Ile Met Ala Ala
50

<210> 112
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R50Q"

<400> 112
Gly Pro Gln Asn Pro Lys Lys Gln Gly Ile Phe His Ile His Glu Ala
1 5 10 15

Cys Ser Ser Ile His Val Asn His Val Gln Gln Asp Lys Leu Arg Glu
20 25 30

Ile Val Gly Ala Ser Thr Asn Trp Arg Asp His Val Lys Ala Met Glu
35 40 45

Glu Arg Lys Leu
50

<210> 113
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q123fs"

<400> 113
Asp Leu Asn Arg Lys Ser Asn Gln Val Lys Thr Cys Lys Ala Lys Ile
1 5 10 15

Glu Leu Leu Gly Ser Tyr Asp Pro Gln Asn Asn Leu Leu Leu Lys Ile
20 25 30

Pro Ile Met Gly Met Thr Leu Thr Leu Arg Arg Cys Thr Ser Ser Val
35 40 45

Ser Gly Ala Ala Glu Arg Ser Trp Arg Arg Pro Thr Glu Ala Gly Ser
50 55 60

Cys Pro Ala Ala Ala Ser Leu Thr Arg Pro His Pro Glu Val Leu His
65 70 75 80

Phe Ser Val Gly Val
85

<210> 114
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V29G"

<400> 114
Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val Leu Thr Ser
1 5 10 15

Leu Ala Tyr Cys Leu His Gln Arg Arg Gly Gly Ala Leu Ala Glu Leu
20 25 30

Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu Lys Leu
35 40 45

Lys Met Val Gln
50

<210> 115
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R43W"

<400> 115
Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala Lys
1 5 10 15

Glu Leu Lys Phe Val Thr Leu Val Phe Trp Trp His Gly Asp Arg Ser
20 25 30

Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
35 40 45

Gln Gly Phe Gly
50

<210> 116
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R105Q"

<400> 116
Glu Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu
1 5 10 15

Ser Tyr Lys His Glu Gln Val Tyr Ile Gln Gln Ser Thr Asp Val Asp
20 25 30

Arg Thr Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro
35 40 45

Glu Gly Val Ser
50

<210> 117
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E321K"

<400> 117
Leu Gln Met Ala Leu Asp Val Tyr Asn Gly Leu Leu Pro Pro Tyr Ala
1 5 10 15

Ser Cys His Leu Thr Glu Leu Tyr Phe Lys Lys Lys Gly Glu Tyr Phe
20 25 30

Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln His Glu Pro Tyr Pro Leu
35 40 45

Met Leu Pro Gly
50

<210> 118
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.W279C"

<400> 118
Tyr Val Val Val Gly Ile Thr Ser Trp Gly Val Gly Cys Ala Arg Ala
1 5 10 15

Lys Arg Pro Gly Ile Tyr Thr Ala Thr Cys Cys Pro Tyr Leu Asn Trp
20 25 30

Ile Ala Ser Lys Ile Gly Ser Asn Ala Leu Arg Met Ile Gln Ser Ala
35 40 45

Thr Pro Pro Pro
50

<210> 119
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I250M"

<400> 119
Ala Val Leu Ile Tyr Thr Ser Gly Thr Thr Gly Ile Pro Lys Gly Val
1 5 10 15

Met Leu Ser His Asp Asn Ile Thr Trp Met Met Ala Gly Ala Val Thr
20 25 30

Lys Asp Phe Lys Leu Thr Asp Lys His Glu Thr Val Val Ser Tyr Leu
35 40 45

Pro Leu Ser His
50

<210> 120
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T188S"

<400> 120
Ala Ile Phe Cys Glu Thr Arg Ala Glu Trp Met Ile Ala Ala Gln Ala
1 5 10 15

Cys Phe Met Tyr Asn Phe Gln Leu Val Ser Ser Leu Tyr Ala Thr Leu
20 25 30

Gly Gly Pro Ala Ile Val His Ala Leu Asn Glu Thr Glu Val Thr Asn
35 40 45

Ile Ile Thr Ser
50

<210> 121
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L402fs"

<400> 121
Pro Gly Tyr Met Gly Thr Ala Ala Ser Cys Tyr Asp Val Gln Ile Ile
1 5 10 15

Asp Asp Lys Gly Asn Val Leu Pro Pro Arg His Arg Arg Arg His Trp
20 25 30

His Gln Gly Gln Thr His Gln Ala Tyr Arg His Leu Leu Trp Leu Cys
35 40 45

Gly Gln Ser Arg Gln Asp Ser Ser Gln His Ser Arg Arg Leu Leu Ala
50 55 60

Pro Trp Arg Pro Gly Asn Gln Arg
65 70

<210> 122
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K195N"

<400> 122
Val Ala Ser Glu Cys Pro Ser Leu Arg Ile Lys Leu Leu Val Ser Glu
1 5 10 15

Lys Ser Cys Asp Gly Trp Leu Asn Phe Asn Asn Lys Leu Leu Asn Glu
20 25 30

Ala Ser Thr Thr His His Cys Val Glu Thr Gly Ser Gln Glu Ala Ser
35 40 45

Ala Ile Tyr Phe
50

<210> 123
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G275C"

<400> 123
Ile Thr Ile Gly Asn Glu Arg Phe Arg Cys Pro Glu Thr Leu Phe Gln
1 5 10 15

Pro Ser Phe Ile Gly Met Glu Ser Ala Cys Cys Ile His Glu Thr Thr
20 25 30

Tyr Asn Ser Ile Met Lys Cys Asp Ile Asp Ile Arg Lys Asp Leu Tyr
35 40 45

Ala Asn Asn Val
50

<210> 124
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A22P"

<400> 124
Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1 5 10 15

Cys Lys Ala Gly Phe Pro Pro Gly Asp Asp Ala Pro Arg Ala Val Phe
20 25 30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met
35 40 45

<210> 125
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L88fs"

<400> 125
Gly Pro Thr Tyr Tyr Ile Asp Thr Asn Ala Leu Arg Val Pro Arg Glu
1 5 10 15

Asn Met Glu Ala Ile Ser Pro Leu Lys Met Gly Trp Leu Lys Thr Gly
20 25 30

Ile Val Ser Lys Leu Phe Trp Ile Ile Pro Thr Lys Cys Met Ser Asn

35 40 45

Gln Lys Pro Val Ser Ile Leu Phe Ser Cys Gln Arg His Arg Gly Ile
50 55 60

Leu Glu Gln Arg Glu Arg Asn
65 70

<210> 126
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R354H"

<400> 126
Thr Gly Phe Lys Glu Glu Met Ala Ala Asn Val Leu Leu Cys Gly Gly
1 5 10 15

Cys Thr Met Leu Asp Gly Phe Pro Glu His His Phe Gln Arg Glu Leu
20 25 30

Ser Leu Leu Cys Pro Gly Asp Ser Pro Ala Val Ala Ala Ala Pro Glu
35 40 45

Arg Lys Thr Ser
50

<210> 127
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E211K"

<400> 127
Ile Tyr Ser Tyr Gly Lys Thr Ser Gly Leu Val Val Glu Ser Gly His
1 5 10 15

Gly Val Ser His Val Val Pro Ile Ser Lys Lys Gly Asp Val Leu Pro
20 25 30

Gly Leu Thr Ser Arg Ala Asp Tyr Ala Gly Gly Asp Leu Thr Asn Tyr
35 40 45

Leu Met Gln Leu
50

<210> 128
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R331H"

<400> 128
Glu Val Pro Gly Leu Ser Pro Val Gly Leu Ser Thr Met Ala Lys Gln
1 5 10 15

Ser Leu Arg Lys Leu Ser Leu Glu Met His His Ala Asp Leu Ala Gln
20 25 30

Asn Val Leu Leu Cys Gly Gly Ser Ser Leu Phe Thr Gly Phe Glu Gly
35 40 45

Arg Phe Arg Ala
50

<210> 129
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.D893Y"

<400> 129
Ala Tyr Ser Gly Pro Gly Ser Val Pro Gly Ala Leu Asp Tyr Ala Ala
1 5 10 15

Phe Ser Ser Ala Leu Tyr Gly Glu Ser Tyr Tyr Leu
20 25

<210> 130
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R206H"

<400> 130
Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
1 5 10 15

Pro Phe Leu Val Gln Arg Thr Val Ala His His Gln Ile Thr Leu Leu
20 25 30

Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp
35 40 45

Gln Gly Glu Asn
50

<210> 131
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S290L"

<400> 131
Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser Thr Gln Leu Trp
1 5 10 15

Leu Ile Thr His Tyr His Glu Met Gly Leu Leu Leu Tyr Asp Tyr Leu
20 25 30

Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile Val Leu Ser
35 40 45

Ile Ala Ser Gly
50

<210> 132
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S11L"

<400> 132
Met Ala Ser Asn Asn His Trp Phe Gln Ser Leu Leu Gln Val Pro Ser
1 5 10 15

Phe Ala Gln Met Leu Lys Lys Asn Leu Pro Val Gln Pro Ala Thr Lys
20 25 30

Thr Ile Thr Thr Pro
35

<210> 133
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G44E"

<400> 133
Leu Ala Ala Ser Leu Gln Ile Ser Pro Gln Pro Arg Pro Trp Arg Pro
1 5 10 15

Leu Pro Ala Gln Ala Gln Ser Ala Trp Glu Glu Pro Ala Pro Ala Pro

20 25 30

Ala Thr Tyr Arg Ala Glu Gly Gly Trp Pro Gln Val Ser Val Leu Arg
35 40 45

Asp Ser Gly Pro
50

<210> 134
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K380M"

<400> 134
Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met Leu His
1 5 10 15

Glu Phe Ser Lys Tyr Arg Gln Arg Ile Met Met Gln His Ala Asp Ala
20 25 30

Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser Leu
35 40 45

Ser Tyr Phe Gly
50

<210> 135
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K73fs"

<400> 135
Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn Gly
1 5 10 15

Lys Ile Ala Val Leu Tyr Leu Lys Lys Lys Gln Glu Pro Pro Cys Thr
20 25 30

Arg Leu His Gly Asn Ile Leu
35

<210> 136
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V205I"

<400> 136
Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly Trp Trp Ile
1 5 10 15

His Phe Arg Ile Val Glu Ile Val Val Ile Ile Ile Asp Asn Tyr Leu
20 25 30

Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp Leu Tyr
35 40 45

Val Ile Val Asn
50

<210> 137
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q741H"

<400> 137
Leu Lys Pro Lys Gln Glu Lys Met Pro Leu Ser Lys Ala Lys Thr Glu
1 5 10 15

Gln Glu Glu Ser Lys Thr Lys Thr Val His His Glu Glu Ser Lys Thr
20 25 30

Lys Thr Gly Gln Glu Glu Ser Glu Ala Lys Thr Gly Gln Glu Glu Ser
35 40 45

Lys Ala Lys Thr
50

<210> 138
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G97L"

<400> 138
Lys His Val Leu His Leu Trp Pro Lys Arg Leu Leu Leu Pro Arg His
1 5 10 15

Leu Arg Val Phe Ser Phe Thr Glu His Leu Leu Glu Leu Leu Glu Asp
20 25 30

His Pro Tyr Ile Pro Lys Asp Cys Asn Tyr Met Gly Ser Val Lys Glu
35 40 45

Ser Leu Asp Ser Lys
50

<210> 139
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S314Y"

<400> 139

Ser Ser Asp Trp Ala His Leu Tyr Leu Gln Arg Lys Tyr Asn Asp Ala
1 5 10 15

Leu Ala Trp Ser Phe Gly Lys Val Cys Tyr Tyr Leu Glu Tyr Ala Gly
20 25 30

Ser Val Ser Thr Leu Leu Asp Thr Asn Ile Leu Ala Pro Ala Thr Trp
35 40 45

Ser Ala His Glu
50

<210> 140
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R559Q"

<400> 140
Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp Arg Asn Leu Ile Cys
1 5 10 15

Gly Arg Leu Val Cys Thr Tyr Pro Thr Gln Gln Lys Pro Phe His Gln
20 25 30

Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp Ser Val Cys Ile
35 40 45

Thr Val Asp Tyr
50

<210> 141
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.R256Q"

<400> 141
Asn Gln Thr Ala Val Arg Glu Glu Met Ile Leu Leu Ala Asn Tyr Leu
1 5 10 15

Asp Ser Met Tyr Ile Met Leu Asn Ile Gln Gln Ile Val Leu Val Gly
20 25 30

Leu Glu Ile Trp Thr Asn Gly Asn Leu Ile Asn Ile Val Gly Gly Ala
35 40 45

Gly Asp Val Leu
50

<210> 142
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E359K"

<400> 142
Leu Asn Pro Val His His Asp Val Ala Val Leu Leu Thr Arg Lys Asp
1 5 10 15

Ile Cys Ala Gly Phe Asn Arg Pro Cys Lys Lys Thr Leu Gly Leu Ser
20 25 30

His Leu Ser Gly Met Cys Gln Pro His Arg Ser Cys Asn Ile Asn Glu
35 40 45

Asp Ser Gly Leu
50

<210> 143
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1053A"

<400> 143
Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met Ser Thr
1 5 10 15

Ser Thr Pro Ala Ile Ser Ser Pro Ser Ala Ala Thr Thr Ala Ser Lys
20 25 30

Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln Pro
35 40 45

Glu Leu Ser Ser
50

<210> 144
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G238C"

<400> 144
Gln Gln Glu Trp Ala Glu Pro Asp Gly Asp Leu His Asn Glu Ala Phe
1 5 10 15

Gly Leu Gly Asp Leu Pro Asn Leu Leu Cys Cys Leu Val Gly Asp Gln
20 25 30

Leu Gly Asp Thr Glu Arg Lys Arg Arg His Ala Lys Pro Gly Ser Tyr
35 40 45

Ser Ile Glu Val
50

<210> 145
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D817N"

<400> 145
Leu Arg Arg Tyr Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly
1 5 10 15

Arg Tyr Lys Phe Ser Gly Thr Thr Phe Asn Asn Tyr Arg Arg Ser Tyr
20 25 30

Asn Glu Pro Glu Asn Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu
35 40 45

Ile Val Glu Leu
50

<210> 146
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.N572T"

<400> 146
Ser Pro Trp Gly Ala Trp Ser Met Cys Ser Arg Thr Cys Gly Thr Gly
1 5 10 15

Ala Arg Phe Arg Gln Arg Lys Cys Asp Thr Thr Pro Pro Pro Gly Pro
20 25 30

Gly Gly Thr His Cys Pro Gly Ala Ser Val Glu His Ala Val Cys Glu
35 40 45

Asn Leu Pro Cys
50

<210> 147
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D948N"

<400> 147
Trp Glu Pro Cys Ser Gln Thr Cys Gly Arg Thr Gly Met Gln Val Arg
1 5 10 15

Ser Val Arg Cys Ile Gln Pro Leu His Asn Asn Asn Thr Thr Arg Ser
20 25 30

Val His Ala Lys His Cys Asn Asp Ala Arg Pro Glu Ser Arg Arg Ala
35 40 45

Cys Ser Arg Glu
50

<210> 148
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R541L"

<400> 148
Lys Leu His Lys Gly Cys Phe Thr Gln His Val Pro Pro Ala Asp Gly
1 5 10 15

Thr Asp Cys Gly Pro Gly Met His Cys Leu Leu His Gly Leu Cys Val
20 25 30

Asn Lys Glu Thr Glu Thr Arg Pro Val Asn Gly Glu Trp Gly Pro Trp
35 40 45

Glu Pro Tyr Ser
50

<210> 149

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1251S"

<400> 149
Gly Lys Thr Thr Arg Gln Val Leu Cys Met Asn Tyr His Gln Pro Ile
1 5 10 15

Asp Glu Asn Tyr Cys Asp Pro Glu Val Ser Ser Pro Leu Met Glu Gln
20 25 30

Glu Cys Ser Leu Ala Ala Cys Pro Pro Ala His Ser His Phe Pro Ser
35 40 45

Ser Pro Val Gln
50

<210> 150
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R156W"

<400> 150
Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly
1 5 10 15

Gly Ala Leu Leu Gly Val Leu Gln Tyr Trp Trp Gly Ala Glu Leu His
20 25 30

Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly
35 40 45

Ala His Ile Leu
50

<210> 151
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L549M"

<400> 151
Gln Gly Gln Met Val Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly
1 5 10 15

Thr Pro Cys Gly Lys Gly Arg Ile Cys Met Met Gln Gly Lys Cys Val
20 25 30

Asp Lys Thr Lys Lys Lys Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp
35 40 45

Gly Ser Trp Gly
50

<210> 152
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V524M"

<400> 152
Thr Pro Cys Gly Pro Gly His Leu Cys Ser Glu Gly Ser Cys Leu Pro
1 5 10 15

Glu Glu Glu Val Glu Arg Pro Lys Pro Met Met Ala Asp Gly Gly Trp
20 25 30

Ala Pro Trp Gly Pro Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly Gly
35 40 45

Val Gln Phe Ser
    50

<210> 153
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="p.G659W"

<400> 153
Phe Lys Ser Cys Asn Thr Glu Pro Cys Leu Lys Gln Lys Arg Asp Phe
1   5   10   15

Arg Asp Glu Gln Cys Ala His Phe Asp Trp Trp Lys His Phe Asn Ile
            20   25   30

Asn Gly Leu Leu Pro Asn Val Arg Trp Val Pro Lys Tyr Ser Gly Ile
        35   40   45

Leu Met Lys Asp
    50

<210> 154
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G778fs"

<400> 154
Thr Ser Cys Ser Arg Ser Cys Gly Pro Gly Thr Gln His Arg Gln Leu
1   5   10   15

Gln Cys Arg Gln Glu Phe Gly Gly Gly Trp Leu Leu Gly Ala Pro Gly
            20   25   30

Ala Leu Trp Thr Ser Pro Pro Ala Gln His His Pro Val Leu Pro Ala
35 40 45

Ala Pro Leu Trp Pro Leu Gly Ser Trp Leu Ser Leu Glu Pro Val Leu
50 55 60

Arg Ala Val Arg Pro Gly Pro Glu Lys Pro Ala Gly Ser Leu Cys Trp
65 70 75 80

Glu Gln Trp

<210> 155
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A87V"

<400> 155
Leu Ala Val Phe Phe Ala Leu Gly Leu Glu Val Glu Asp His Val Ala
1 5 10 15

Phe Leu Ile Thr Val Pro Thr Ala Leu Val Val Ile Phe Phe Ala Ile
20 25 30

Phe Ile Leu Val Cys Ile Glu Ser Val Phe Lys Lys Leu Leu Arg Leu
35 40 45

Phe Ser Leu Val
50

<210> 156
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.V888I"

<400> 156
His Val Ala Glu His Phe Leu Ala Arg Ser Leu Lys Asn Glu Glu Leu
1 5 10 15

Tyr His Gln Ser Tyr Asp Cys Val Cys Ile Ile Met Phe Ala Ser Ile
20 25 30

Pro Asp Phe Lys Glu Phe Tyr Thr Glu Ser Asp Val Asn Lys Glu Gly
35 40 45

Leu Glu Cys Leu
50

<210> 157
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P1016T"

<400> 157
Ser Phe Asn Asp Phe Lys Leu Arg Val Gly Ile Asn His Gly Pro Val
1 5 10 15

Ile Ala Gly Val Ile Gly Ala Gln Lys Thr Thr Gln Tyr Asp Ile Trp
20 25 30

Gly Asn Thr Val Asn Val Ala Ser Arg Met Asp Ser Thr Gly Val Leu
35 40 45

Asp Lys Ile Gln
50

<210> 158
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R661H"

<400> 158
Ser Ile Glu Thr Phe Leu Ile Leu Arg Cys Thr Gln Lys Arg Lys Glu
1 5 10 15

Glu Lys Ala Met Ile Ala Lys Met Asn His His Gln Arg Thr Asn Ser
20 25 30

Ile Gly His Asn Pro Pro His Trp Gly Ala Glu Arg Pro Phe Tyr Asn
35 40 45

His Leu Gly Gly
50

<210> 159
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E570K"

<400> 159
His Gly Pro Pro Ala Pro Pro Asn Pro Phe Ser His Leu Thr Glu Gly
1 5 10 15

Glu Leu Glu Glu Tyr Lys Arg Thr Ile Lys Lys Arg Lys Gln Gln Gly
20 25 30

Leu Glu Asp Ala Glu Gln Glu Leu Leu Ser Asp Asp Ala Ser Ser Val
35 40 45

Ser Gln Ile Gln
50

<210> 160
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S1124L"

<400> 160
Pro Cys Asn Ser Phe Ala Ile Lys Glu Ile Arg Asp Tyr Tyr Ile Pro
1 5 10 15

Asn Asp Lys Lys Ile Leu Phe Arg Tyr Leu Leu Val Lys Val Leu Thr
20 25 30

Pro Gln Pro Ala Thr Ile Gln Val Arg Thr Ser Lys Pro Asp Ala Phe
35 40 45

Ile Lys Leu Gln
50

<210> 161
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D154V"

<400> 161
Ser Arg Phe Thr Cys Arg Arg Lys Pro Ile His His Phe Leu Gly Ile
1 5 10 15

Ser Thr Phe Ser Gln Tyr Thr Val Val Val Val Glu Asn Ala Val Ala
20 25 30

Lys Ile Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys
35 40 45

Gly Phe Ser Thr
50

<210> 162
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S322fs"

<400> 162
Asn Ser Pro Ser Pro Ala Ala Gly Gln Pro Val Thr Val Ala Gln Gly
1 5 10 15

Ala Pro Gly Ser Leu Thr His Ser Pro Leu Leu Leu Ala Asn Pro Thr
20 25 30

<210> 163
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R597H"

<400> 163
Val Lys Thr Asn Ala Ser Gln Val Pro Ala Glu Pro Lys Glu Arg Pro
1 5 10 15

Leu Leu Ser Leu Ile Arg Glu Lys Ala His His Pro Arg Pro Thr Gln
20 25 30

Lys Ile Pro Glu Thr Lys Ala Leu Lys His Lys Leu Ser Thr Thr Ser
35 40 45

Glu Thr Val Ser
50

<210> 164
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E919K"

<400> 164
Ile Asn Lys Asn Glu Lys Met Leu Arg Ser Pro Ile Ser Pro Leu Ser
1   5   10   15

Asp Ala Ser Lys His Lys Tyr Thr Ser Lys Lys Asp Leu Thr Ser Ser
            20   25   30

Ser Arg Pro Asn Gly Asn Ser Leu Phe Thr Ser Ala Ser Ser Ser Lys
        35   40   45

Lys Pro Lys Ala
    50

<210> 165
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A182G"

<400> 165
Thr Phe Met Asn Lys Phe Ile Tyr Glu Ile Ala Arg Arg His Pro Phe
1   5   10   15

Leu Tyr Ala Pro Thr Ile Leu Leu Trp Gly Gly Ala Arg Tyr Asp Lys
            20   25   30

Ile Ile Pro Ser Cys Cys Lys Ala Glu Asn Ala Val Glu Cys Phe Gln
        35   40   45

Thr Lys Ala Ala
    50

<210> 166
<211> 46
<212> PRT
<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G127fs"

<400> 166
Gly Gly Arg Phe Lys Lys Glu Ile Val Val Asp Gly Gln Ser Tyr Leu
1 5 10 15

Leu Leu Ile Arg Asp Glu Gly Gly Pro Arg Arg Arg Ser Leu Pro Cys
20 25 30

Gly Trp Thr Leu Leu Tyr Leu Ser Ser Ala Trp Arg Met Lys
35 40 45

<210> 167
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R766W"

<400> 167
Val Trp Glu Gly Ala Leu Gly Gly Tyr Ser Lys Pro Gly Pro Asp Ala
1 5 10 15

Cys Arg Glu Glu Lys Glu Arg Trp Ile Trp Trp Ala Lys Tyr Glu Gln
20 25 30

Lys Leu Phe Leu Ala Pro Leu Pro Ser Ser Asp Val Pro Leu Gly Gln
35 40 45

Gln Leu Leu Arg
50

<210> 168
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D69fs"

<400> 168
Met Ala Ala Ala Val Gln Pro Ala Glu Val Thr Val Glu Val Gly Glu
1 5 10 15

Asp Leu His Met His His Val Arg Asp Gly Arg Cys Leu Lys Leu Trp
20 25 30

Ser Leu Thr Phe Leu Pro Ile Gln Ser Gln Ala Gln Tyr Ser Arg Gly
35 40 45

Thr Leu Lys Gln Lys Leu Trp Ser Leu Thr Leu Leu Pro Ile Gln Arg
50 55 60

Gln Ala Gln Tyr Ser Arg Gly Thr Leu Lys Gln Met Leu
65 70 75

<210> 169
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S127I"

<400> 169
Asn Pro Ser Ala Asn Pro Glu Ala Ser Thr Ile Phe Gln Arg Asn Ser
1 5 10 15

Gln Thr Asp Val Val Glu Ile Arg Arg Ile Ile Asn Cys Thr Asn His
20 25 30

Val Ser Ala Val Arg Phe Ser Gln Gln Tyr Ser Leu Cys Ser Thr Ile
35 40 45

Phe Leu Asp Asp
50

<210> 170
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E71fs"

<400> 170
Ala Ala Ala Val Gln Pro Ala Glu Val Thr Val Glu Val Gly Glu Asp
1 5 10 15

Leu His Met His His Val Arg Asp Arg Arg Cys Leu Lys Leu Trp Ser
20 25 30

Leu Thr Leu Leu Pro Ile Gln Arg Gln Ala Gln Tyr Ser Arg Gly Thr
35 40 45

Leu Lys Gln Met Leu
50

<210> 171
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M248V"

<400> 171
Ser Thr Ser Gln Glu Asp Pro Gln Phe Ser Val Pro Pro Thr Ala Asn
1 5 10 15

Thr Pro Thr Pro Val Cys Lys Leu Ser Val Val Arg Trp Ser Asn Leu
20 25 30

Phe Thr Ser Glu Lys Gly Ser Asp Pro Asp Lys Glu Arg Lys Ala Pro
35 40 45

Glu Asn His Ala

50

<210> 172
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I420fs"

<400> 172
Lys Leu Asn Ser Val Trp Ile Met Pro Gln Gln Ser Ala Gly Leu Glu
1 5 10 15

Glu Ser Ala Pro Asp Thr Ile Pro Pro Gln Arg Glu Trp Arg Cys Leu
20 25 30

Leu Cys Gly Pro Ala Trp Thr Cys Phe Gln Lys Gly Leu Leu His Val
35 40 45

Arg Lys Gln Leu
50

<210> 173
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V313M"

<400> 173
Thr Gly Thr Pro Glu Ile Ala Gly Leu Thr Pro Ser Gln Ala Leu Glu
1 5 10 15

Ile Ile Arg Gly Cys Gln Gly Leu Asn Met Met Met Gly Cys Asp Leu
20 25 30

Val Glu Val Ser Pro Pro Tyr Asp Leu Ser Gly Asn Thr Ala Leu Leu
35 40 45

Ala Ala Asn Leu
50

<210> 174
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A212T"

<400> 174
Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys His
1 5 10 15

His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ile Thr Val Arg Ser
20 25 30

Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn Phe Arg
35 40 45

Asn Asn Glu Asn
50

<210> 175
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.1284_1285VT>A"

<400> 175
Gly Ala Thr Ser Gly Ala Ile Ala Ala Gly Ala Thr Ala Arg Ala Thr
1 5 10 15

Thr Ala Ser Arg Leu Pro Ser Ser Ala Ala Ala Pro Arg Ala Pro His
20 25 30

Pro Ser His Thr Ser Gln Pro Val Ala Lys Thr Thr Ala Ala Pro Thr
35 40 45

Thr Arg Arg Pro Pro Thr
50

<210> 176
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R502C"

<400> 176
Phe Ser Gln Thr Phe Arg Ile Ala Pro Ser Met Cys Ile Thr Lys Pro
1 5 10 15

Glu Val Asp Phe Ala Val Glu Val Phe Cys Cys Ser Ala Leu Thr Gln
20 25 30

His Met Glu Arg Arg Ala Lys
35

<210> 177
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K303fs"

<400> 177
Asp Asp Glu Ile Ser Ser Met Glu Gln Ser Thr Glu Asp Ser Met Gln
1 5 10 15

Asp Asp Thr Lys Pro Lys Pro Lys Lys Asn Lys Lys Glu Asp
20 25 30

<210> 178
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S4150F"

<400> 178
Lys Ala Pro Lys Ile Ser Met Pro Glu Val Asp Leu Asn Leu Lys Gly
1 5 10 15

Pro Lys Met Lys Gly Asp Val Asp Val Phe Phe Leu Pro Lys Val Glu
20 25 30

Gly Asp Leu Lys Gly Pro Glu Val Asp Ile Lys Gly Pro Lys Val Asp
35 40 45

Ile Asp Val Pro
50

<210> 179
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.5_6insE"

<400> 179
Met Glu Lys Glu Glu Glu Glu Thr Thr Arg Glu Leu Leu Leu Pro Asn
1 5 10 15

Trp Gln Gly Ser Gly Ser His Gly Leu Thr Ile Ala Gln Arg Asp Asp
20 25 30

Gly Val

<210> 180

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V1220I"

<400> 180
Ile Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys
1 5 10 15

Gly Asp Val Asp Val Ser Val Pro Lys Ile Ile Glu Gly Glu Met Lys
20 25 30

Val Pro Asp Val Glu Ile Lys Gly Pro Lys Met Asp Ile Asp Ala Pro
35 40 45

Asp Val Glu Val
50

<210> 181
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A2114G"

<400> 181
Pro Asp Val Ser Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys
1 5 10 15

Leu Lys Met Pro Glu Met His Phe Lys Gly Gly Pro Lys Ile Ser Met
20 25 30

Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys Gly Asp Val
35 40 45

Asp Val Ser Leu
50

<210> 182
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D2889H"

<400> 182
Leu Lys Gly Pro Glu Val Asp Leu Lys Gly Pro Lys Val Asp Ile Asp
1 5 10 15

Val Pro Asp Val Asn Val Gln Gly Pro His His Trp His Leu Lys Met
20 25 30

Pro Lys Met Lys Met Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu
35 40 45

Gly Pro Glu Val
50

<210> 183
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P1215S"

<400> 183
Ala Pro Lys Val Glu Ala Asp Val Ser Leu Pro Ser Met Gln Gly Asp
1 5 10 15

Leu Lys Thr Thr Asp Leu Ser Ile Gln Ser Ser Pro Ser Ala Asp Leu
20 25 30

Glu Val His Ala Gly Gln Val Asp Val Lys Leu Leu Glu Gly His Val
35 40 45

Pro Glu Gly Ala
50

<210> 184
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1640M"

<400> 184
Pro Asp Val Lys Met Ser Leu Ser Ser Met Glu Val Asp Val Gln Ala
1 5 10 15

Pro Arg Ala Lys Leu Asp Gly Ala Gln Met Met Glu Gly Asp Leu Ser
20 25 30

Leu Ala Asp Lys Ala Val Thr Ala Lys Asp Ser Lys Phe Lys Met Pro
35 40 45

Lys Phe Lys Met
50

<210> 185
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S2166F"

<400> 185
Leu Ala Asn Lys Asp Leu Thr Thr Lys Asp Ser Lys Phe Lys Met Pro
1 5 10 15

Lys Phe Lys Met Pro Ser Phe Gly Val Phe Phe Ala Pro Gly Lys Ser
20 25 30

Ile Glu Ala Ser Val Asp Val Ser Pro Pro Lys Val Glu Ala Asp Met
35 40 45

Ser Leu Pro Ser
50

<210> 186
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R131G"

<400> 186
Leu Arg Ile Phe Thr Ala Arg Leu Tyr Phe Cys Glu Asp Arg Lys Ala
1 5 10 15

Glu Pro Glu Gly Leu Arg Arg Leu His Gly Gly Ala Gly Val Gln Ile
20 25 30

Ala Ile Met Thr Phe Lys Asp Tyr Phe Tyr Cys Trp Asn Thr Phe Val
35 40 45

Glu Asn His Glu
50

<210> 187
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y144F"

<400> 187
Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg Leu His Arg Ala Gly Val
1 5 10 15

Gln Ile Ala Ile Met Thr Phe Lys Asp Phe Phe Phe Tyr Cys Trp Asn

20 25 30

Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys Ala Trp Glu Gly Leu
35 40 45

His Glu Asn Ser
50

<210> 188
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K247M"

<400> 188
Val Asp Ile Glu Leu Gln Lys His Val Glu Lys Leu Thr Lys Gly Ala
1 5 10 15

Ala Ile Phe Phe Glu Phe Lys His Tyr Met Met Pro Lys Lys Arg Phe
20 25 30

Thr Ser Thr Lys Cys Phe Ala Phe Met Glu Met Asp Glu Ile Lys Pro
35 40 45

Gly Pro Ile Val
50

<210> 189
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.Q191R"

<400> 189
Ala Val Ser Thr Gln Gln Gln Glu Glu Asp Arg Ser Ser Ser Cys Arg
1 5 10 15

Glu Ala Val Leu Gln Trp Arg Leu Gln Arg Arg Thr Ile Lys Glu Gln
20 25 30

Ala Leu Leu Asn Ala His Val Thr Gln Val Thr Glu Ser Leu Lys Gln
35 40 45

Val Gln Leu Glu
50

<210> 190
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A159V"

<400> 190
Ser Ala Leu Ser Glu Glu Val Ser His Phe Glu Lys Arg Lys Leu Phe
1 5 10 15

Ile Leu Leu Ser Thr Val Met Thr Trp Val Val Arg Ser Lys Ala Leu
20 25 30

Asp Pro Glu Asp Ser Glu Val Pro Phe Thr Glu Glu Asp Tyr Arg Arg
35 40 45

Arg Lys Ser His
50

<210> 191
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D243A"

<400> 191
Lys Leu Leu Glu Tyr His Arg Asn Ile Val Arg Val Ile Pro Ser Tyr
1 5 10 15

Pro Lys Ile Leu Lys Val Ile Ser Ala Ala Ala Gln Pro Cys Val Asp
20 25 30

Val Phe Tyr Gln Ala Leu Thr Tyr Val Gln Ser Asn His Arg Thr Asn
35 40 45

Ala Pro Phe Thr
50

<210> 192
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E1282K"

<400> 192
Ile Leu Ser Lys Thr Glu Gly Thr Gln Glu Ala Asp Gln Tyr Ala Asp
1 5 10 15

Glu Lys Thr Lys Asp Val Pro Phe Phe Lys Lys Gly Leu Glu Gly Ser
20 25 30

Ile Asp Thr Gly Ile Thr Val Ser Arg Glu Lys Val Thr Glu Val Ala
35 40 45

Leu Lys Gly Glu
50

<210> 193
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.K2785fs"

<400> 193
Gln Ala Pro Ala Ser Thr Ser Ala Ser Thr Arg Leu Phe Gly Leu Thr
1 5 10 15

Lys Pro Lys Glu Lys Lys Glu Lys Lys Arg Arg Thr Lys Pro Ala Ala
20 25 30

Leu Ser Pro Val Met Val Pro Arg Gln Lys Tyr Gln Gln Arg Val Lys
35 40 45

Arg Ser Ser Ala Asp Pro Leu Pro Leu Cys
50 55

<210> 194
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L3482I"

<400> 194
Arg Arg Ile Leu Tyr Gln Asn Leu Asn Glu Pro Thr Thr Trp Ser Leu
1 5 10 15

Thr Ser Asp Arg Thr Arg Asn Trp Val Ile Ile Gln Gln Lys Ile Glu
20 25 30

Gly Glu Thr Lys Glu Ser Asn Tyr Ala Lys Leu Ile Glu Met Asn Gly
35 40 45

Gly Gly Thr Gly
50

<210> 195
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M3743fs"

<400> 195
Tyr Leu Leu Leu Leu Leu Gly Gly Phe Gln Glu Cys Glu Asp Ala Thr
1 5 10 15

Leu Ala Leu Leu Ala Arg Met Gly Gly Ser Gln Leu Ser Arg Ile
20 25 30

<210> 196
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1209fs"

<400> 196
Asp Met Lys Ala Lys Ile Arg Val Asp Thr Ile Ala Lys Arg Arg Ala
1 5 10 15

Glu Leu Ile Leu Glu Arg Asp Lys Lys Gly Gly Arg Met Leu Leu Glu
20 25 30

Met Met Lys Arg Leu Val Arg Lys Asn Leu Lys Lys Thr Met Met Ile
35 40 45

Leu Lys Thr Ser Leu Lys Met Ser Phe Gln Lys Met Arg Lys Arg
50 55 60

<210> 197
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K620R"

<400> 197
Ala Glu Met Thr Ala Pro Ser Pro Ser Cys Ala Phe Cys Arg Arg Leu
1 5 10 15

Leu Glu Trp Lys Gln Asn Val Glu Lys Arg Arg Gly His Gly Arg Ile
20 25 30

Asn Cys Gly Arg Phe Ser Ile Val Leu His Glu Lys Ala Pro His Ser
35 40 45

Asp Ser Thr Pro
50

<210> 198
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E17K"

<400> 198
Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
1 5 10 15

Lys Lys Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn
20 25 30

Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro
35 40

<210> 199
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I289M"

<400> 199
Glu Tyr Leu His Ser Arg Asp Val Val Tyr Arg Asp Ile Lys Leu Glu
1 5 10 15

Asn Leu Met Leu Asp Lys Asp Gly His Met Met Lys Ile Thr Asp Phe
20 25 30

Gly Leu Cys Lys Glu Gly Ile Ser Asp Gly Ala Thr Met Lys Thr Phe
35 40 45

Cys Gly Thr Pro
50

<210> 200
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G302R"

<400> 200
Pro Arg Val Cys Gly Ala Val Met Asp Thr Leu Lys Gln His Gly Ala
1 5 10 15

Gly Ala Gly Gly Thr Arg Asn Ile Ser Arg Arg Thr Ser Lys Phe His
20 25 30

Val Asp Leu Glu Arg Glu Leu Ala Asp Leu His Gly Lys Asp Ala Ala
35 40 45

Leu Leu Phe Ser
50

<210> 201
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.S294L"

<400> 201
Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu
1 5 10 15

Ala Lys Tyr Ile Cys Glu Asn Gln Asp Leu Leu Ile Ser Ser Lys Leu
20 25 30

Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala
35 40 45

Glu Val Glu Asn
50

<210> 202
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R85C"

<400> 202
Pro Ala Thr Gly Glu Gln Val Cys Glu Val Gln Glu Ala Asp Lys Ala
1 5 10 15

Asp Ile Asp Lys Ala Val Gln Ala Ala Cys Cys Leu Ala Phe Ser Leu
20 25 30

Gly Ser Val Trp Arg Arg Met Asp Ala Ser Glu Arg Gly Arg Leu Leu
35 40 45

Asp Lys Leu Ala
50

<210> 203
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A870T"

<400> 203
Lys Ala Leu Tyr Val Ser Asp Lys Leu Gln Ala Gly Thr Val Phe Val
1 5 10 15

Asn Thr Tyr Asn Lys Thr Asp Val Ala Thr Thr Pro Phe Gly Gly Phe
20 25 30

Lys Gln Ser Gly Phe Gly Lys Asp Leu Gly Glu Ala Ala Leu Asn Glu
35 40 45

Tyr Leu Arg Val
50

<210> 204
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L286fs"

<400> 204
Thr Glu Ile Gly Arg Val Ile Gln Val Ala Ala Gly Ser Ser Asn Leu
1 5 10 15

Lys Arg Val Thr Leu Glu Leu Gly Gly Arg Ala Pro Thr Ser Ser Cys
20 25 30

Gln Met Pro Ile Trp Ile Gly Pro Trp Asn Arg Pro Thr Ser Pro Cys
35 40 45

Ser Ser Thr Arg Ala Ser Ala Ala Val Pro Ala Pro Gly Pro Ser Cys
50 55 60

Arg Arg Thr Ser Met Met Ser Leu Trp Ser Gly Ala Leu Pro Gly Pro
65 70 75 80

Ser Leu Gly Trp Ser Gly Thr Pro Leu Ile Ala Arg Pro Ser Arg Gly
85 90 95

Arg Arg Trp Met Lys Leu Ser Leu Arg Arg Ser Ser Ala Thr Ser Thr
100 105 110

Arg Gly Ser Lys Arg Gly Arg Ser Cys Cys Val Val Gly Ala Leu Leu
115 120 125

Leu Thr Val Val Thr Ser Ser Ser Pro Leu Cys Leu Glu Met Cys Arg
130 135 140

Met Ala
145

<210> 205
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P562fs"

<400> 205
Glu Thr Phe Ser His Arg Arg Ser Cys Leu Val Arg Pro Leu Met Asn
1 5 10 15

Asp Glu Gly Leu Lys Val Arg Tyr Pro Arg Ala Arg Pro Arg
20 25 30

<210> 206
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S302Y"

<400> 206
Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val Gln Gln Ser Asp
1 5 10 15

Leu Gly Gln Tyr Val Thr Phe Leu Arg Tyr Tyr Phe Ser Asp Lys Gln
20 25 30

Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val Leu Tyr Thr Pro Ser
35 40 45

Asn Glu His Phe
50

<210> 207
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K137E"

<400> 207
Trp His Trp Val Lys Gln Cys Leu Lys Leu Tyr Ser Gln Lys Pro Asn
1 5 10 15

Val Cys Asn Leu Asp Lys His Met Ser Glu Glu Glu Glu Thr Gln Asp
20 25 30

Leu Trp Glu Gln Ser Lys Glu Phe Leu Arg Tyr Lys Glu Ala Thr Lys
35 40 45

Arg Arg Pro Arg
50

<210> 208
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.L356fs"

<400> 208

Glu Cys Ser Asp Val Met Thr Asp Tyr Ser Asn Ala Val Trp Gln Arg
1 5 10 15

Asn Leu Leu Gly Thr Glu His Val Phe Tyr
20 25

<210> 209
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K523fs"

<400> 209
Leu Leu Ser Gly Glu Ser Glu Asn Ser Gly Met Ser Gln Cys Trp Glu
1 5 10 15

Thr Ala Ala Asp Lys Arg Val Gly Gly Arg Thr Tyr Gly Ala Arg Gly
20 25 30

Val Gln Gly Asn Leu Pro Gly
35

<210> 210
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D53N"

<400> 210
Asp Ala Val Leu Arg Cys Ile Ile Ser Gly Gln Pro Lys Pro Glu Val
1 5 10 15

Thr Trp Tyr Lys Asn Gly Gln Ala Ile Asn Asn Gly Ser Gly Ile Ile
20 25 30

Ser Asn Tyr Glu Phe Phe Glu Asn Gln Tyr Ile His Val Leu His Leu

35 40 45

Ser Cys Cys Thr
50

<210> 211
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W31S"

<400> 211
Val Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu Gly Ile Ile
1 5 10 15

Pro Val Glu Glu Glu Asn Pro Asp Phe Ser Ser Asn Arg Gln Ala Ala
20 25 30

Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr Ala Ala
35 40 45

Lys Asn Leu Ile
50

<210> 212
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R126Q"

<400> 212
Pro Pro Pro Gln Pro Gln Pro Gln Gln Gln Gln Pro Gln Pro Gln Pro
1 5 10 15

Pro Ala Gln Pro His Leu Tyr Leu Gln Gln Gln Gly Ala Cys Lys Thr
20 25 30

Pro Pro Asp Gly Ser Leu Lys Leu Gln Glu Gly Ser Ser Gly His Ser
35 40 45

Ala Ala Leu Gln
50

<210> 213
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S225Y"

<400> 213
Gln Gly Pro Ser Leu Pro Gly Leu Asp Phe Ala Asp Pro Gln Gly Ser
1 5 10 15

Thr Ile Phe Gln Ile Ala Arg Leu Ile Tyr Tyr His Gly Pro Met Pro
20 25 30

Gln Asn Lys Gln Ser Pro Leu Tyr Pro Gly Met Leu Tyr Val Pro Phe
35 40 45

Gly Ala Asn Gln
50

<210> 214
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.S3G"

<400> 214
Met Ala Gly Gly Gly His Ser Leu Leu Leu Glu Asn Ala Gln Gln Val
1 5 10 15

Val Leu Val Cys Ala Arg Gly Glu Arg Phe Leu Ala Arg
20 25

<210> 215
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R292W"

<400> 215
Pro Ser Pro Leu Pro Ser Pro Thr Ala Ser Pro Asn His Thr Leu Ala
1 5 10 15

Pro Ala Ser Pro Ala Pro Ala Arg Pro Trp Trp Ser Pro Ser Gln Thr
20 25 30

Arg Lys Gly Pro Pro Val Pro Pro Leu Pro Lys Val Thr Pro Thr Lys
35 40 45

Glu Leu Gln Gln
50

<210> 216
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T537A"

<400> 216
Pro Gly Leu Pro Ala Pro Ser Leu Thr Met Ser Asn Thr Met Pro Arg
1 5 10 15

Pro Ser Thr Pro Leu Asp Gly Val Ser Ala Ala Pro Lys Pro Leu Ser
20 25 30

Lys Leu Leu Gly Ser Leu Asp Glu Val Val Leu Leu Ser Pro Val Pro
35 40 45

Glu Leu Arg Asp
50

<210> 217
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N453S"

<400> 217
Thr Glu Ser Gly Leu Thr Pro Ile His Val Ala Ala Phe Met Gly His
1 5 10 15

Leu Asn Ile Val Leu Leu Leu Leu Gln Ser Ser Gly Ala Ser Pro Asp
20 25 30

Val Thr Asn Ile Arg Gly Glu Thr Ala Leu His Met Ala Ala Arg Ala
35 40 45

Gly Gln Val Glu
50

<210> 218
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q3076L"

<400> 218
Asp Asp Glu Ala Phe Glu Ala Arg Val Lys Glu Glu Glu Gln Lys Ile
1 5 10 15

Phe Gly Leu Met Val Asp Arg Gln Ser Leu Leu Gly Thr Thr Pro Asp

20 25 30

Thr Thr Pro Ala Arg Thr Pro Thr Glu Glu Gly Thr Pro Thr Ser Glu
35 40 45

Gln Asn Pro Phe
50

<210> 219
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1322E"

<400> 219
Leu Ala Thr Gln Leu Tyr Arg Glu Leu Ile Cys Val Pro Tyr Met Ala
1 5 10 15

Lys Phe Val Val Phe Ala Lys Met Asn Glu Glu Pro Val Glu Ser Ser
20 25 30

Leu Arg Cys Phe Cys Met Thr Asp Asp Lys Val Asp Lys Thr Leu Glu
35 40 45

Gln Gln Glu Asn
50

<210> 220
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R24H"

<400> 220
Met Gln Glu Glu Leu Ala Trp Glu Thr Asp Gly Leu Leu Pro Leu Glu
1 5 10 15

Arg Gln Leu His Glu Ala Ala His His Gln Asn Asn Val Gly Arg Met
20 25 30

Gln Glu Leu Ile Gly Arg Arg Val Asn Thr Arg Ala Arg Asn His Val
35 40 45

Gly Arg
50

<210> 221
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M280I"

<400> 221
Tyr Arg Leu Tyr Arg Arg Met Lys Thr Gly Phe Glu His Ala Arg Ala
1 5 10 15

Pro Glu Met Pro Thr Asn Val Cys Leu Ile Ile Val Thr Ser Ser Thr
20 25 30

Ser Leu Thr Val Ser Phe Gln Glu Pro Leu Ser Val Asn Ala Ala Val
35 40 45

Val Thr Arg Tyr
50

<210> 222
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C644fs"

<400> 222
Thr Ala Ala Pro Ile Ser Gly Phe Arg Arg Gly Val Cys Val Cys Val
1 5 10 15

Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Arg
20 25 30

Glu His Pro Gly Arg Ser Pro Pro Gly
35 40

<210> 223
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C644fs"

<400> 223
Thr Ala Ala Pro Ile Ser Gly Phe Arg Arg Gly Val Cys Val Cys Val
1 5 10 15

Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val
20 25 30

Gly Ser Thr Gln Ala Asp Leu Pro Gln Ala Glu Arg Gly Leu Cys Tyr
35 40 45

Arg Trp Tyr Cys Trp Arg Gly Ser Lys
50 55

<210> 224
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N302I"

<400> 224

Lys Glu Leu Asp Ala Arg Ile Phe Leu Asn Glu Ile Pro Pro Phe Val
1 5 10 15

Glu Asp Gly Glu Pro Trp Phe Ile Ile Ile Glu Thr Pro Leu Leu
20 25 30

Val Lys Ile Gln Lys Gln Thr Tyr Lys Phe Arg Asn Lys Pro Ala His
35 40 45

Thr Ser Trp Asn
50

<210> 225
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K369R"

<400> 225
Lys Asp Glu Tyr Glu Phe Asp Glu Asp Asp Glu Gln Asp Arg Val Pro
1 5 10 15

Pro Val Asp Asp Lys His Leu Leu Lys Arg Arg Asp Tyr Arg Lys Glu
20 25 30

Thr Lys Ser Asn Ser Phe Ile Ser Ile Pro Lys Met Glu Val Lys Ser
35 40 45

Tyr Thr Lys Asn
50

<210> 226
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.Y2015S"

<400> 226
Ser Pro Lys Arg Phe Cys Pro Ala Asp Pro Leu His Ser Ala Ala Pro
1 5 10 15

Gly Pro Phe Ser Ala Ser Glu Ala Pro Ser Ser Pro Ala Pro Pro Ala
20 25 30

Ser Pro Ala Pro Tyr Ala Leu Pro Val Ala Glu Pro Gly Leu Glu Asp
35 40 45

Val Lys Asp Gly
50

<210> 227
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E627K"

<400> 227
His Lys Glu Lys Ser Lys His Gln Lys Asp Phe His Leu Glu Phe Gly
1 5 10 15

Glu Lys Ser Asn Ala Lys Ile Lys Asp Lys Lys Asp His Ser Pro Thr
20 25 30

Phe Glu Asn Ser Asp Cys Thr Leu Lys Lys Met Asp Lys Glu Gly Lys
35 40 45

Thr Leu Lys Lys
50

<210> 228
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E721Q"

<400> 228
Trp Lys Glu Asn Phe Phe Lys Ser Asp Glu Thr Glu Asp Leu Phe Leu
1 5 10 15

Asn Met Glu His Glu Ser Leu Thr Leu Gln Gln Lys Lys Ser Lys Leu
20 25 30

Glu Lys Asn Ile Lys Asp Asp Lys Ser Thr Lys Glu Lys His Val Ser
35 40 45

Lys Glu Arg Asn
50

<210> 229
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T999N"

<400> 229
Ser Glu Phe Ile Leu Ala Ser Lys Gly Leu Thr His Leu Asn Glu Leu
1 5 10 15

Leu Met Ala Cys Lys Ser His Lys Glu Asn Asn Thr Ser Val His Thr
20 25 30

Asp Trp Leu Leu Asp Leu Tyr Ala Gly Asn Ile Lys Thr Leu Gln Lys
35 40 45

Leu Pro His Ile
50

<210> 230
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P337R"

<400> 230
Thr Ser Asp Lys Asp Asp Ser Val Ser Asn Thr Ala Thr Glu Ile Lys
1 5 10 15

Asp Glu Gln Lys Ser Gly Thr Val Leu Arg Arg Ala Val Glu Gln Cys
20 25 30

Leu Asn Arg Ser Leu Tyr Arg Pro Asp Ala Val Ala Gln Pro Val Thr
35 40 45

Glu Asn Glu Phe
50

<210> 231
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K378R"

<400> 231
Val Ala Gln Pro Val Thr Glu Asn Glu Phe Ser Leu Glu Ser Glu Ile
1 5 10 15

Ile Ser Lys Leu Tyr Ile Pro Lys Arg Arg Arg Ile Ile Ser Pro Arg
20 25 30

Ser Ile Lys Asp Val Leu Pro Pro Val Glu Glu Ala Val Asp Arg Cys
35 40 45

Leu Tyr Leu Leu
50

<210> 232
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D1014Y"

<400> 232
Ser Glu Lys Pro Pro Gly Leu Lys Ala Thr Ser Asp Glu Lys Asp Ser
1 5 10 15

Val Leu Asn Ile Ala Arg Gly Lys Lys Tyr Tyr Gly Glu Lys Thr Arg
20 25 30

Thr Val Ser Ser Gln Lys Pro Pro Thr Leu Lys Ala Thr Ser Asp Glu
35 40 45

Glu Asp Ser Val
50

<210> 233
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M1144T"

<400> 233
Lys Ser Arg Thr Val Ser Ser Pro Lys Gln Pro Ala Leu Lys Ala Ile
1 5 10 15

Cys Asp Lys Glu Asp Ser Val Pro Asn Thr Thr Ala Thr Glu Lys Lys
20 25 30

Asp Glu Gln Ile Ser Gly Thr Val Ser Cys Gln Lys Gln Pro Ala Leu
35 40 45

Lys Ala Thr Ser
50

<210> 234

<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H438R"

<400> 234
Leu Glu Lys Asp Thr Ile Lys Asn Gln Asn Leu Glu Lys Lys Tyr Leu
1 5 10 15

Lys Asp Phe Glu Ile Val Lys Arg Lys Arg Arg Glu Asp Leu Gln Lys
20 25 30

Ala

<210> 235
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V637M"

<400> 235
Trp Thr Ala Leu Arg Ser Ala Ala Trp Gly Gly His Thr Glu Val Val
1 5 10 15

Ser Ala Leu Leu Tyr Ala Gly Val Lys Met Met Asp Cys Ala Asp Ala
20 25 30

Asp Ser Arg Thr Ala Leu Arg Ala Ala Ala Trp Gly Gly His Glu Asp
35 40 45

Ile Val Leu Asn
50

<210> 236
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R479C"

<400> 236
Thr Gln His Gln Met Arg Val Leu Asp Lys Leu Met Val Glu Arg Leu
1 5 10 15

Ser Ala Glu Arg Thr Glu Cys Leu Asn Cys Cys Leu Gln Gln His Ser
20 25 30

Asp Thr Glu Lys His Glu Gly Glu Lys Arg Gln Ile Ser Leu Val Asp
35 40 45

Glu Leu Lys Thr
50

<210> 237
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R334C"

<400> 237
Pro Leu His Asp Gly Glu Tyr Asp Ser Pro Glu Asp Asp Met Asn Asp
1 5 10 15

Arg Lys Leu Leu Tyr Gln Glu Trp Ala Cys Cys Tyr Gly Val Phe Tyr
20 25 30

Lys Phe Gln Pro Ile Asp Leu Ile Arg Lys Tyr Phe Gly Glu Lys Ile
35 40 45

Gly Leu Tyr Phe
50

<210> 238
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A41S"

<400> 238
Gly Met Asn Ile Ser Lys Ser Glu Ile Thr Lys Glu Thr Ser Leu Lys
1 5 10 15

Pro Ser Arg Arg Ser Leu Pro Cys Leu Ser Ser Gln Ser Tyr Ala Tyr
20 25 30

Ser Lys Ser Leu Ser Gln Ser Thr Ser Leu Phe Gln Ser Thr Glu Ser
35 40 45

Glu Ser Gln Ala
50

<210> 239
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M956I"

<400> 239
Ile Ala Tyr Leu Ile Pro Asp Val Pro Lys Gly Leu His Asp Arg Ile
1 5 10 15

Arg Arg Glu Lys Tyr Leu Val Gln Glu Ile Ile Met Tyr Glu Ala Glu
20 25 30

Leu Glu His Leu Gln Gln Gln Arg Arg Lys Ser Gly Gln Pro Val His
35 40 45

His Glu Trp Pro
    50

<210> 240
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R231Q"

<400> 240
Arg Ser Lys Gln His Leu Arg Leu Val Phe Asp Glu Tyr Leu Lys Thr
1   5   10   15

Thr Gly Lys Pro Ile Glu Ala Ser Ile Gln Gln Gly Glu Leu Ser Gly
            20   25   30

Asp Phe Glu Lys Leu Met Leu Ala Val Val Lys Cys Ile Arg Ser Thr
        35   40   45

Pro Glu Tyr Phe
    50

<210> 241
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.L79fs"

<400> 241
Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr Ala Val
1   5   10   15

Met Arg Phe Leu Thr Gln Arg Leu Gly Ala Arg Ala Gly Gly Cys Ser
            20   25   30

Pro Gly Pro Ala Leu Gly Gln Leu Cys Leu Leu Ser Gly Val Ala Ala

35 40 45

Ala Ser Gln Gly Cys Ser Pro Gly Ser Leu Gly Gln Gly Glu Pro Pro
50 55 60

Thr Cys Pro Gly Gly Thr Gly His Arg Leu Leu Trp Gln Ala Thr Pro
65 70 75 80

Ala Gln Arg Glu

<210> 242
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A507V"

<400> 242
Gly Arg His Trp Asn Glu Gln Met Leu Asp Ile Ala Cys Arg Leu Ile
1 5 10 15

Leu Asn Glu Val Ser Leu Leu Gly Ser Val Val Pro Gly Gly Lys Val
20 25 30

Glu Phe Lys Arg Thr Leu Ile Ile Ser Phe Leu Phe Lys Phe Tyr Leu
35 40 45

Glu Val Ser Gln
50

<210> 243
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R723L"

<400> 243
Asn Asp Ile Ala Ala Gly Ile Pro Ser Ile Thr Ala Tyr Ser Lys Asn
1 5 10 15

Gly Leu Lys Ile Glu Phe Thr Phe Glu Leu Leu Ser Asn Thr Asn Pro
20 25 30

Ser Val Thr Val Ile Thr Ile Gln Ala Ser Asn Ser Thr Glu Leu Asp
35 40 45

Met Thr Asp Phe
50

<210> 244
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D243N"

<400> 244
Pro Gln Leu Val His Ile Leu Arg Thr Leu Val Thr Met Gly Tyr Ser
1 5 10 15

Thr Glu His Ser Ile Ser Gly Val Ser Asn Asn Pro Phe Leu Gln Val
20 25 30

Gln Ile Leu Arg Leu Leu Arg Ile Leu Gly Arg Asn His Glu Glu Ser
35 40 45

Ser Glu Thr Met
50

<210> 245
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K41fs"

<400> 245
Leu Ser Lys Phe Tyr Gln Pro Tyr Ser Glu Asp Thr Gln Gln Gln Ile
1 5 10 15

Ile Arg Glu Thr Phe His Leu Val Ser Glu Met Lys Met Phe Val Ile
            20 25 30

Ser

<210> 246
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R276W"

<400> 246
Val Val Met Gly Ala Thr Lys Leu Phe Leu Ile Leu Ala Lys Met Phe
1 5 10 15

Pro His Val Gln Thr Asp Val Leu Val Trp Trp Val Lys Gly Pro Leu
            20 25 30

Leu Ala Ala Cys Ser Ser Glu Ser Arg Glu Leu Cys Phe Val Ala Leu
        35 40 45

Cys His Val Arg
    50

<210> 247
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>

<221> source
<223> /note="p.E624K"

<400> 247
Leu Ile Ala Gln Ser Ile Gly Gln Ala Phe Ser Val Ala Tyr Gln Glu
1 5 10 15

Phe Leu Arg Ala Asn Gly Ile Asn Pro Lys Lys Asp Leu Ser Gln Lys
20 25 30

Glu Tyr Ser Asp Leu Leu Asn Thr Gln Asp Met Tyr Asn Asp Asp Leu
35 40 45

Ile His Phe Ser
50

<210> 248
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K730N"

<400> 248
Gln Ile Met Ser Ile Asn Gly Thr Ser Leu Val Gly Leu Pro Leu Ser
1 5 10 15

Thr Cys Gln Ser Ile Ile Lys Gly Leu Asn Asn Asn Gln Ser Arg Val
20 25 30

Lys Leu Asn Ile Val Arg Cys Pro Pro Val Thr Thr Val Leu Ile Arg
35 40 45

Arg Pro Asp Leu
50

<210> 249
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T243fs"

<400> 249
Glu Asp Gly Gln Val Ala Thr Val Ser Ser Ser Pro Glu Thr Lys Lys
1 5 10 15

Asp His Pro Lys Thr Gly Ala Lys Thr Arg Leu Cys Thr Ala Pro Asp
20 25 30

Pro Glu Pro Gly Thr Glu Arg
35

<210> 250
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E847fs"

<400> 250
Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Ser Arg Gly
1 5 10 15

Ser Leu Asp Ser Ser Arg Ser Glu Lys Ile Glu Val Trp Arg Glu Asn
20 25 30

Ala Glu Leu Val
35

<210> 251
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F1354fs"

<400> 251
Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu
1 5 10 15

Ser Ala Arg His Lys Ala Val Glu Phe Leu Gln Glu Arg Asn Leu Pro
20 25 30

Pro Lys Val Val Leu Arg His Pro Lys Val His Leu Asn Thr Met Phe
35 40 45

Arg Arg Pro His Ser Cys Leu Ala Asp Val Leu Leu Ser Val His Leu
50 55 60

Ile Val Leu Arg Val Val Arg Leu Pro Ala Pro Phe Arg Val Asn His
65 70 75 80

Ala Val Glu Trp

<210> 252
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A43V"

<400> 252
Leu Leu Leu Leu Leu Ala Gly Ala Arg Ala Glu Glu Glu Met Leu Glu
1 5 10 15

Asn Val Ser Leu Val Cys Pro Lys Asp Val Val Thr Arg Phe Lys His
20 25 30

Leu Arg Lys Tyr Thr Tyr Asn Tyr Glu Ala Glu Ser Ser Ser Gly Val
35 40 45

Pro Gly Thr Ala
50

<210> 253
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L973M"

<400> 253
Thr Lys Thr Glu Val Ile Pro Pro Leu Ile Glu Asn Arg Gln Ser Trp
1 5 10 15

Ser Val Cys Lys Gln Val Phe Pro Gly Met Met Asn Tyr Cys Thr Ser
20 25 30

Gly Ala Tyr Ser Asn Ala Ser Ser Thr Asp Ser Ala Ser Tyr Tyr Pro
35 40 45

Leu Thr Gly Asp
50

<210> 254
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.F3102L"

<400> 254
Phe Leu Ser Pro Ser Ala Gln Gln Ala Ser Trp Gln Val Ser Ala Arg
1 5 10 15

Phe Asn Gln Tyr Lys Tyr Asn Gln Asn Leu Leu Ser Ala Gly Asn Asn
20 25 30

Glu Asn Ile Met Glu Ala His Val Gly Ile Asn Gly Glu Ala Asn Leu
35 40 45

Asp Phe Leu Asn
50

<210> 255
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R3136C"

<400> 255
Met Glu Ala His Val Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu
1 5 10 15

Asn Ile Pro Leu Thr Ile Pro Glu Met Cys Cys Leu Pro Tyr Thr Ile
20 25 30

Ile Thr Thr Pro Pro Leu Lys Asp Phe Ser Leu Trp Glu Lys Thr Gly
35 40 45

Leu Lys Glu Phe
50

<210> 256
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R840L"

<400> 256
Ser Gln Val Glu Ala Phe Glu Ser Arg Glu Gly Gly Pro Trp Gly Gly
1 5 10 15

Arg Val Glu Ala Glu Glu Ser Ala Gly Leu Val Glu Asp Ser Cys Gly
20 25 30

Leu Asp Pro Ala Gly Ser Gln Thr Ala Arg Ala Glu Gly Met Gly Ala
35 40 45

Met Val Glu Ala

50

<210> 257
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S115L"

<400> 257
Ile Glu Gly Glu Ala Thr Pro Val Asn Leu Thr Glu Pro Ala Lys Leu
1 5 10 15

Glu Val Lys Phe Ser Trp Phe Met Pro Leu Leu Ala Pro Tyr Trp Ile
20 25 30

Leu Ala Thr Asp Tyr Glu Asn Tyr Ala Leu Val Tyr Ser Cys Thr Cys
35 40 45

Ile Ile Gln Leu
50

<210> 258
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C130R"

<400> 258
Glu Glu Thr Arg Ala Arg Leu Ser Lys Glu Leu Gln Ala Ala Gln Ala
1 5 10 15

Arg Leu Gly Ala Asp Met Glu Asp Val Arg Arg Gly Arg Leu Val Gln
20 25 30

Tyr Arg Gly Glu Val Gln Ala Met Leu Gly Gln Ser Thr Glu Glu Leu
35 40 45

Arg Val Arg Leu
    50

<210> 259
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.I138L"

<400> 259
Pro Lys Met Gly Val Ile Thr Val Ser Gly Leu Ala Gly Leu Val Ser
1   5   10   15

Ala Arg Lys Gly Ser Lys Phe Lys Lys Leu Leu Thr Tyr Pro Leu Gly
            20   25   30

Leu Ala Thr Leu Gly Ala Thr Val Cys Tyr Pro Val Gln Ser Val Ile
        35   40   45

Ile Ala Lys Val
    50

<210> 260
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R668W"

<400> 260
Glu Arg Val Lys Glu Lys Gln Gln Lys Glu Leu Asn Lys Gln Lys Gln
1   5   10   15

Ile Glu Lys Asp Leu Glu Glu Gln Ser Trp Trp Leu Ile Ala Ala Ser
            20   25   30

Ser Arg Pro Asn Gln Ala Ser Ser Glu Gly Gln Phe Val Val Leu Ser
35 40 45

Ser Ser Gln Ser
50

<210> 261
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q261L"

<400> 261
Ser Ala Gly Asn Gly Trp Trp Trp Val Pro Val Val Ala Pro Leu Val
1 5 10 15

Gly Ala Thr Val Gly Thr Ala Thr Tyr Leu Leu Leu Leu Val Ala Leu
20 25 30

His His Pro Glu Gly Pro Glu Pro Ala Gln Asp Leu Val Ser Ala Gln
35 40 45

His Lys Ala Ser
50

<210> 262
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N68T"

<400> 262
Gln Ile Ala Met Ala Phe Gly Leu Gly Ile Gly Thr Leu Val Gln Ala
1 5 10 15

Leu Gly His Ile Ser Gly Ala His Ile Thr Thr Pro Ala Val Thr Val
20 25 30

Ala Cys Leu Val Gly Cys His Val Ser Val Leu Arg Ala Ala Phe Tyr
35 40 45

Val Ala Ala Gln
50

<210> 263
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A309T"

<400> 263
Lys Glu Asp Val Asn Gly Ser Lys Trp Thr Val Thr Thr Phe Ser Thr
1 5 10 15

Thr Pro His Met Pro Thr Tyr Leu Val Thr Thr Phe Val Ile Cys Asp
20 25 30

Tyr Asp His Val Asn Arg Thr Glu Arg Gly Lys Glu Ile Arg Ile Trp
35 40 45

Ala Arg Lys Asp
50

<210> 264
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1226L"

<400> 264
Ala Ser Leu Leu Leu Lys Lys Val Pro Leu Ala Gln Ala Gly Cys Leu

1 5 10 15

Phe Thr Gly Ile Arg Arg Glu Ser Pro Leu Leu Val Gly Leu Leu Arg
20 25 30

Cys Arg Glu Glu Pro Pro Arg Leu Leu Gly Ser Arg Phe Gln Glu Arg
35 40 45

Phe Phe Leu Leu
50

<210> 265
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R149H"

<400> 265
Phe Ala Asn Lys Gln Asp Leu Pro Asn Ala Met Ala Ile Ser Glu Met
1 5 10 15

Thr Asp Lys Leu Gly Leu Gln Ser Leu His His Asn Arg Thr Trp Tyr
20 25 30

Val Gln Ala Thr Cys Ala Thr Gln Gly Thr Gly Leu Tyr Glu Gly Leu
35 40 45

Asp Trp Leu Ser
50

<210> 266
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S38N"

<400> 266
Leu Phe Lys Arg Leu Arg Ala Val Pro Thr Asn Lys Ala Cys Phe Asp
1 5 10 15

Cys Gly Ala Lys Asn Pro Ser Trp Ala Asn Asn Ile Thr Tyr Gly Val
20 25 30

Phe Leu Cys Ile Asp Cys Ser Gly Val His Arg Ser Leu Gly Val His
35 40 45

Leu Ser Phe Ile
50

<210> 267
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N299fs"

<400> 267
Ser Leu Arg Leu Ala Tyr Lys Asp Leu Glu Ile Gln Met Lys Lys Asp
1 5 10 15

Glu Lys Met Asn Ile Ser Gly Lys Lys Met Leu Thr Gln Thr Asp Ser
20 25 30

Ala Trp Asp Leu Glu Ile Ala Glu Val Leu Phe His Ile Gln
35 40 45

<210> 268
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1552fs"

<400> 268
Leu Asp Ile Phe Lys Thr Thr Ile Pro His Ala Leu Leu Thr Trp Arg
1 5 10 15

Pro Asn Ser Gly Glu Thr Ala Pro Pro Thr Ser Ile Ser Cys Lys
20 25 30

<210> 269
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1632N"

<400> 269
Lys Phe Pro Glu Gln Lys Leu Phe Ala Ala Leu Leu Ile Lys Cys Val
1 5 10 15

Val Gln Leu Glu Leu Ile Gln Thr Ile Asn Asn Asn Ile Val Phe Phe
20 25 30

Pro Ala Thr Ser Lys Lys Glu Asp Ala Glu Asn Leu Ala Ala Ala Gln
35 40 45

Arg Asp Ala Val
50

<210> 270
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R86L"

<400> 270
Gly Leu Ile Pro Thr Gly Ser Gly Arg His Pro Ser His Ser Thr Thr
1 5 10 15

Pro Ser Gly Pro Gly Asp Glu Val Ala Leu Leu Gly Ile Ala Gly Glu
20 25 30

Lys Phe Asp Ile Val Lys Lys Trp Gly Ile Asn Thr Tyr Lys Cys Thr
35 40 45

Lys Gln Leu Leu
50

<210> 271
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T35A"

<400> 271
Asn Pro Gln Gln Gly Gln Gly Arg Gln Asn Ala Ile Lys Cys Gly Trp
1 5 10 15

Leu Arg Lys Gln Gly Gly Phe Val Lys Ala Ala Trp His Thr Arg Trp
20 25 30

Phe Val Leu Lys Gly Asp Gln Leu Tyr Tyr Phe Lys Asp Glu Asp Glu
35 40 45

Thr Lys Pro Leu
50

<210> 272
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1253K"

<400> 272
Leu Glu Phe Ala Asp Lys Ser Pro Thr Pro Pro Asn Leu Pro Ser Asp

120

1 5 10 15

Lys Ile Tyr Pro Pro Ser Gly Ser Pro Lys Lys Glu Asn Thr Ser Thr
20 25 30

Ala Thr Met Thr Tyr Met Thr Thr Thr Pro Ala Thr Ala Gln Met Ser
35 40 45

Thr Lys Glu Ala
50

<210> 273
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R128C"

<400> 273
Gly Gln Gln Arg Ala Val Ser His Lys Thr Phe Gly Ile Ser Leu Glu
1 5 10 15

Glu Val Leu Val Asn Glu Phe Thr Arg Cys Cys Lys His Leu Glu Leu
20 25 30

Thr Ala Thr Met Gln Val Glu Glu Ala Thr Gly Gln Ala Ala Gly Arg
35 40 45

Arg Arg Gly Asn
50

<210> 274
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A147V"

<400> 274
Val Asn Glu Phe Thr Arg Arg Lys His Leu Glu Leu Thr Ala Thr Met
1 5 10 15

Gln Val Glu Glu Ala Thr Gly Gln Ala Val Val Gly Arg Arg Arg Gly
20 25 30

Asn Val Val Arg Arg Val Phe Gly Arg Ile Arg Arg Phe Phe Ser Arg
35 40 45

Arg Arg Asn Glu
50

<210> 275
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P16H"

<400> 275
Met Gly Gly Cys Ile Pro Phe Leu Lys Ala Ala Arg Ala Leu Cys His
1 5 10 15

His Arg Ile Met Pro Pro Leu Leu Leu Leu Ser Ala Phe Ile Phe Leu
20 25 30

Val Ser Val Leu Gly Gly Ala Pro Gly His
35 40

<210> 276
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M691L"

<400> 276
Glu Ser Leu Ser Phe Ile Gly Glu Phe Ile Gly Lys Ile Arg Thr Glu
1 5 10 15

Ala Ser Gln Ile Arg Lys Asp Lys Tyr Leu Leu Ala Asn Leu Pro Phe
20 25 30

Thr Leu Ile Leu Ala Asn Gln Arg Asp Ser Ile Ser Lys Asn Leu Pro
35 40 45

Ile Leu Arg His
50

<210> 277
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D890fs"

<400> 277
Arg Ala Phe Leu Ser Glu Val Gln Asp Thr Ile Pro Val Gln Leu Val
1 5 10 15

Ala Val Thr Asp Ser Gln Ala Asp Phe Leu Lys Met Arg Leu Ser Lys
20 25 30

Ser

<210> 278
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R137C"

<400> 278

Gln Gln Val Ser Leu Ala Glu Gly Asp Arg Phe Leu Leu Leu Arg Lys
1 5 10 15

Thr Asn Ser Asp Trp Trp Leu Ala Arg Cys Cys Leu Glu Ala Pro Ser
20 25 30

Thr Ser Arg Pro Ile Phe Val Pro Ala Ala Tyr Met Ile Glu Glu Ser
35 40 45

Ile Pro Ser Gln
50

<210> 279
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 279
Val Gln Glu Ala Arg Gln Val Phe Glu Lys Ile Gln Arg Met Gly Ala
1 5 10 15

Gln Gln Asp Asp Gly Ser Asp Ala Pro Leu Glu Ala Leu Thr Gly Gln
20 25 30

Gly Met

<210> 280
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E487G"

<400> 280
Pro Ile Ser Leu Leu Gly Ser Phe Leu Thr Glu Glu Ser Pro Asp Lys

1 5 10 15

Glu Ile Asp Gln Asn Ser Gln Gln Glu Gly Gly Ser Arg Leu Arg Lys
20 25 30

Gly Thr Val Ser Ser Gln Gly Thr Glu Val Val Phe Ala Ser Ala Ser
35 40 45

Val Thr Pro Pro
50

<210> 281
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S1512fs"

<400> 281
Glu Lys Leu Arg Trp Ile Ser Ala Leu Ala Met Pro Arg Glu Glu Leu
1 5 10 15

Asp Leu Leu Glu Cys Tyr Asn Ser Pro Arg Tyr Ser Ala Phe Glu Pro
20 25 30

Thr Ser Pro Glu Arg Met Met Asn Trp His Trp Arg Lys Pro Thr Trp
35 40 45

<210> 282
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S614L"

<400> 282
Gln Thr Ala Tyr Ser Gln Gln Arg Phe Pro Pro Pro Gln Glu Leu Ser
1 5 10 15

Gln Asp Ser Phe Gly Ser Gln Ala Ser Leu Leu Ala Pro Ser Met Thr
20 25 30

Ser Ser Lys Gly Gly Gln Glu Asp Met Asn Leu Ser Leu Gln Ser Arg
35 40 45

Pro Ser Ser Leu
50

<210> 283
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K1071fs"

<400> 283
Lys Pro Leu Asp Leu Tyr Arg Leu Tyr Val Ser Val Lys Glu Ile Gly
1 5 10 15

Gly Leu Thr Gln Val Asn Lys Asn Lys Asn Gly Gly Asn Leu Gln Pro
20 25 30

Thr Ser Met Trp Ala His Gln Ala Val Leu Pro Ala Pro
35 40 45

<210> 284
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Y1324fs"

<400> 284
Ser Thr Gly Ala Pro Gln Pro Asn Leu Met Pro Ser Asn Pro Asp Ser
1 5 10 15

Gly Met Tyr Ser Pro Ser Arg Tyr Pro Arg Ser Ser Ser Ser Ser Ser
20 25 30

Ser Asn Asp Met Ile Pro Met Ala Ile Ser Ser Pro Pro Lys Ala Pro
35 40 45

Leu Leu Ala Ala Pro Ser Pro Ala Ser Arg Leu Gln Cys Ile Asn Ser
50 55 60

Asn Ser Arg Ile Thr Ser Gly Gln Trp Met Ala His Met Ala Leu Leu
65 70 75 80

Pro Ser Gly Thr Lys Gly Arg Cys Thr Ala Cys His Thr Ala Leu Gly
85 90 95

Arg Gly Ser Leu Ser Ser Ser Ser Cys Pro Gln Pro Ser Pro Ser Leu
100 105 110

Pro Ala Ser Asn Lys Leu Pro Ser Leu Pro Leu Ser Lys Met Tyr Thr
115 120 125

Thr Ser Met Ala Met Pro Ile Leu Pro Leu Pro Gln Leu Leu Leu Ser
130 135 140

Ala Asp Gln Gln Ala Ala Pro Arg Thr Asn Phe His Ser Ser Leu Ala
145 150 155 160

Glu Thr Val Ser Leu His Pro Leu Ala Pro Met Pro Ser Lys Thr Cys
165 170 175

His His Lys

<210> 285
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G1848fs"

<400> 285

Val Asp Cys Ser Asp Lys Leu Gly Arg Val Gln Glu Phe Asp Ser Gly
1 5 10 15

Leu Leu His Trp Arg Ile Gly Gly Gly Thr Pro Leu Ser Ile Ser Arg
20 25 30

Pro Thr Ser Arg Ala Arg Gln Ser Cys Cys Leu Pro Gly Leu Thr His
35 40 45

Pro Ala His Gln Pro Leu Gly Ser Met
50 55

<210> 286
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P2139fs"

<400> 286
Arg Leu Val Leu Glu Thr Leu Ser Lys Leu Ser Ile Gln Asp Asn Asn
1 5 10 15

Val Asp Leu Ile Leu Ala Thr Pro Pro Ser Ala Ala Trp Arg Ser Cys
20 25 30

Ile Ala Leu Trp Cys Ala Ser Ser Val Thr Glu Arg Thr Arg Cys Ala
35 40 45

Gly Arg Trp Leu Trp Tyr Cys Trp Pro Thr Trp Leu Arg Gly Thr Ala
50 55 60

Trp Gln Leu Val Pro Leu Gln Cys Arg Arg Ala Val Ser Ala Thr Ser
65 70 75 80

Trp Ala Ser

<210> 287
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G550fs"

<400> 287
Asn Gly Ile Met Tyr Thr Gly Val Leu Phe Ala Gln Pro Pro Ala Pro
1 5 10 15

Thr Pro Thr Ser Ala Pro Asn Lys Gly Arg Arg Arg Arg Gln Gln
20 25 30

Gln Gln Arg Arg Arg Pro Gly Arg Lys His Arg Asn Gln Arg Arg Pro
35 40 45

Gly Trp Ala Ser Gly Ala Val His Thr Leu His Ile Tyr Leu Lys
50 55 60

<210> 288
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D1154E"

<400> 288
Leu Asn Val Ser Lys Pro Gln Lys Leu Ala Arg Ser Pro Ala Arg Ile
1 5 10 15

Ser Pro His Ile Lys Asp Gly Glu Lys Glu Glu Lys His Arg Glu Lys
20 25 30

His Pro Asn Ser Ser Pro Arg Thr Tyr Lys Trp Ser Phe Gln Leu Asn
35 40 45

Glu Leu Asp Asn
50

<210> 289
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R358L"

<400> 289
Glu Thr Asp Arg Pro Ser Leu Glu Ser Ala Asn Gly Lys Lys Lys Thr
1 5 10 15

Lys Lys Leu Arg Met Lys Arg Asn His Leu Leu Val Glu Pro Leu Asn
20 25 30

Ile Asp Asp Cys Ala Pro Glu Ser Pro Thr Pro Pro Pro Pro Pro Pro
35 40 45

Pro Val Gly Trp
50

<210> 290
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G6R"

<400> 290
Met Arg Val Ala Gly Arg Arg Arg Ala Leu Ser Arg Gly Ala Glu Leu
1 5 10 15

Arg Val Pro Gly Gly Ala Lys His Gly Met Cys Leu Leu Leu Gly Ala
20 25 30

<210> 291
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M75L"

<400> 291
Gly Val Val Ser Leu Val Phe Leu Ile Ile Tyr Tyr Leu Asp Pro Ser
1 5 10 15

Val Leu Ser Gly Val Ser Cys Phe Val Leu Leu Phe Leu Cys Leu Ala
20 25 30

Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg Ile Phe Gly Ser Asn Lys
35 40 45

Trp Thr Thr Glu
50

<210> 292
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A514T"

<400> 292
Leu Arg Ser Lys Asn Asp Glu Val Arg Lys His Ala Ser Trp Ala Val
1 5 10 15

Met Val Cys Ala Gly Asp Glu Leu Thr Thr Thr Asn Glu Leu Cys Arg
20 25 30

Leu Gly Ala Leu Asp Ile Leu Glu Glu Val Asn Val Ser Gly Thr Arg
35 40 45

Lys Asn Lys Phe
50

<210> 293
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E22K"

<400> 293
Met Gly Val Ala Leu Arg Lys Leu Thr Gln Trp Thr Ala Ala Gly His
1 5 10 15

Gly Thr Gly Ile Leu Lys Lys Ile Thr Pro Leu Asn Glu Ala Ile Leu
20 25 30

Lys Glu Ile Ile Val Phe Val Glu Ser Phe Ile Tyr Lys His Pro Gln
35 40 45

<210> 294
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T395M"

<400> 294
Gly Thr Ser Cys Tyr Glu Tyr Phe His Gln Asp Asp Ile Gly His Leu
1 5 10 15

Ala Glu Cys His Arg Gln Val Leu Gln Met Met Arg Glu Lys Ile Thr
20 25 30

Thr Asn Cys Tyr Lys Phe Lys Ile Lys Asp Gly Ser Phe Ile Thr Leu
35 40 45

Arg Ser Arg Trp
50

<210> 295
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F212L"

<400> 295
Ser Lys Met Pro Phe Gly Gln Leu Met Ser Glu Phe Gly Gly Ser Gly
1 5 10 15

Thr Gly Gly Trp Val His Gly Val Ser Leu Leu Ser Ala Ser Gly Ser
20 25 30

Arg Leu Ala Trp Val Ser His Asp Ser Thr Val Ser Val Ala Asp Ala
35 40 45

Ser Lys Ser Val
50

<210> 296
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R338H"

<400> 296
Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser Asp His Gln Arg Ala Trp
1 5 10 15

Ser Ser Thr Asp Ser Asp Ser Ser Asn His His Asn Leu Lys Pro Ala
20 25 30

Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr Val Leu Thr Arg Gly
35 40 45

Asp Ser Thr Ser
50

<210> 297
<211> 100

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I130fs"

<400> 297
His Asn Val Glu Lys Gln Asp Ile Ala Thr Tyr Tyr Cys Ala Leu Trp
1 5 10 15

Glu Val His Ser Lys Leu Gly Lys Lys Ser Arg Tyr Leu Val Pro Glu
20 25 30

Gln Ser Leu Ser Leu Gln Ile Asn Asn Leu Met Gln Met Phe Pro Pro
35 40 45

Ser Pro Leu Phe Phe Phe Leu Gln Leu Leu Lys Gln Ser Ser Arg Arg
50 55 60

Leu Glu His Thr Phe Val Phe Leu Arg Asn Phe Ser Leu Met Leu Leu
65 70 75 80

Arg Tyr Ile Gly Lys Lys Arg Arg Ala Thr Arg Phe Trp Asp Pro Arg
85 90 95

Arg Gly Thr Pro
100

<210> 298
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T99P"

<400> 298
Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
1 5 10 15

Pro Val Pro Asn Pro Pro Arg Pro Pro Pro Pro Arg Leu Gln Asp Arg
20 25 30

Leu Leu Arg Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Val
35 40 45

Arg Met Pro Leu
50

<210> 299
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T79A"

<400> 299
Ala Leu Arg Leu Glu Ala Gln Gly Arg Ala Thr Ala Ala Trp Gly Pro
1 5 10 15

Ser Thr Cys Pro Arg Ala Ser Ala Ser Ala Ala Ala Ala Leu Ala Val
20 25 30

Phe Ser Glu Val Glu Tyr Leu Asn Val Arg Leu Ser Leu Arg Glu Pro
35 40 45

Pro Ala Gly Glu
50

<210> 300
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A234G"

<400> 300

Leu Gly Ile Leu Thr Leu Ala Ala Gly Gln Thr Cys Gly Phe Phe Ser
1 5 10 15

Val Ser Ala Arg Ala Val Thr Gly Met Gly Gly Gly Val Gly Cys Leu
20 25 30

Phe Phe Ile Ser Trp Tyr Ser Ser Phe Gly Phe Val Arg Arg Trp Asn
35 40 45

Cys Ile Leu Met
50

<210> 301
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.AGV234del"

<400> 301
Leu Gly Ile Leu Thr Leu Ala Ala Gly Gln Thr Cys Gly Phe Phe Ser
1 5 10 15

Val Ser Ala Arg Ala Val Thr Gly Met Gly Cys Leu Phe Phe Ile Ser
20 25 30

Trp Tyr Ser Ser Phe Gly Phe Val Arg Arg Trp Asn Cys Ile Leu Met
35 40 45

Arg Asn His Asp Val Thr Glu Gln Pro Met Val
50 55

<210> 302
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.V131I"

<400> 302
Phe Ala Val Thr Ser Val Gly Gly Leu Pro Leu Asn Glu Thr Thr Leu
1 5 10 15

Ala Glu Val Leu Gln Gln Ala Gly Tyr Ile Ile Thr Gly Ile Ile Gly
20 25 30

Lys Trp His Leu Gly His His Gly Ser Tyr His Pro Asn Phe Arg Gly
35 40 45

Phe Asp Tyr Tyr
50

<210> 303
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I243fs"

<400> 303
Ile Trp Thr Cys Leu Gly Ala Pro Ile Lys Gly Tyr Ser Phe Phe Pro
1 5 10 15

Gly Glu Glu Glu Val Leu Ile Pro Pro Leu Arg Pro Ser Lys
20 25 30

<210> 304
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T249A"

<400> 304
Gln His Val Ala Leu Tyr Leu Glu His Gly Ala Asp Val Gly Leu Arg
1 5 10 15

Thr Ser Gln Gly Glu Thr Ala Leu Asn Ala Ala Ala Cys Ala Gly Ala
20 25 30

Glu Gly Pro Gly Ser Cys Arg Arg His Gln Ala Ala Ala Arg Arg Leu
35 40 45

Leu Glu Ala Gly
50

<210> 305
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H207Y"

<400> 305
Gln Glu Glu Val Leu Ala Lys Cys Ser Met Asp His Gly Val Asp Ser
1 5 10 15

Ser Ile Phe Gln Asn Pro Lys Lys Leu Tyr Tyr Leu Thr Ile Gly Met
20 25 30

Leu Val Leu Leu Ser Glu Glu Glu Ile Gln Gln Thr Cys Glu Met Leu
35 40 45

Gln Gln Cys Lys
50

<210> 306
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R365L"

<400> 306
Cys Asp Asn Ile Gln Gly Phe Ile Glu Glu Phe Leu Gln Ile Phe Ser
1 5 10 15

Ser Leu Leu Gln Glu Lys Arg Phe Leu Leu Leu Asp Tyr Asp Ala Leu
20 25 30

Phe Pro Val Ala Glu Asp Ile Ser Leu Leu Gln Gln Ala Ser Ser Val
35 40 45

Leu Asp Glu Thr
50

<210> 307
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1197Q"

<400> 307
Val Lys Gln Cys Val His Gln Ile Pro Ser Val Met Met Glu Ala Ser
1 5 10 15

Ile Gln Pro Ile Thr Arg Thr Val Leu Gln Gln Val Thr Leu Ser Ile
20 25 30

Tyr Ala Asp Phe Thr Trp Asn Asp Gln Val His Gly Thr Val Gly Glu
35 40 45

Pro Trp Trp Ile
50

<210> 308
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R136Q"

<400> 308
Glu Thr Lys Ala Ile Lys Gln Met Phe Gly Pro Phe Pro Ser Ser Ser
1 5 10 15

Ala Thr Ala Ala Cys Asn Ala Thr Asn Gln Gln Ile Ile Ser His Phe
20 25 30

Ser Gln Asp Asp Leu Thr Ala Leu Val Gln Met Thr Glu Lys Glu His
35 40 45

Gly Asp Arg Val
50

<210> 309
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D35fs"

<400> 309
Ala Leu Pro Tyr Ser Leu Arg Thr Ala Pro Leu Gly Val Pro Gly Thr
1 5 10 15

Leu Pro Gly Leu Pro Arg Arg Asp Pro Ser Gly Ser Pro Cys Val Trp
20 25 30

Thr Pro Arg Ala Gly Ser Gly Arg Ala Ala Ala Ala His Gly Asp Gly
35 40 45

Ser Thr Cys Pro Cys Arg Trp Thr Ala Pro Ser Ser Pro Pro Ser Ser
50 55 60

Ala Ser Ala Thr Ser Ala Ser Gly Ser Gly Cys Ala Ala
65 70 75

<210> 310
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R46L"

<400> 310
Arg Met Ala Arg Glu Glu Pro Ala Pro Ala Ala Leu Ala Ala Ala Gly
1 5 10 15

Gln Pro Gly Gly Gly Arg Gly Gly Glu Leu Leu Ala Leu Gln Gly Pro
20 25 30

Gly Val Ala Arg Arg Gly Arg Pro Ser Leu Ser Arg Ala Lys Leu His
35 40 45

Gly Leu Arg His
50

<210> 311
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q266R"

<400> 311
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr
1 5 10 15

Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Arg Ser Leu Leu Ala Cys
20 25 30

Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
35 40

<210> 312
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S240F"

<400> 312
Glu Glu Asn Lys Ile Pro Ile Ser Pro Ile Ser Pro Ala Phe Asn Glu
1 5 10 15

Cys His Gly Ala Thr Cys Leu Pro Leu Phe Phe Val Arg Arg Ser Thr
20 25 30

Thr Tyr Ser Ser Leu His Ala Ser Glu Asn Arg Glu Leu Leu Asn Val
35 40 45

His Ser Ala Asn
50

<210> 313
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F67fs"

<400> 313
Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro
1 5 10 15

Thr Arg Glu Pro Arg Ser His Phe Phe His Leu Ile Cys Phe Gln Cys
20 25 30

Val His Leu Asp Val Ser Ala Ile His Glu Leu Tyr Ile Ala Gln Ile
35 40 45

<210> 314
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L221del"

<400> 314
Glu Ile Val Glu Glu Gln Met His Ile Leu His Ile Ser Val Met Gly
1 5 10 15

Gly Leu Ile Ala Leu Leu Leu Leu Leu Val Phe Thr Val Ala Leu Tyr
20 25 30

Ala Gln Arg Arg Trp Gln Lys Arg Arg Arg Ile Pro Gln Lys Ser Ala
35 40 45

Ser Thr Glu Ala Thr
50

<210> 315
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S1081L"

<400> 315
Glu Gly Leu Ser Lys Ala Thr Gln Asp Gln Ile Leu Gln Thr Leu Ile
1 5 10 15

Gln Arg Val Arg Arg Gln Asn Leu Leu Leu Leu Val Val Pro Pro Ser
20 25 30

Gln Phe Asn Phe Ala His Ser Gly Phe Gln Leu Glu Asp Ile Ser Thr
35 40 45

Ser Gln Arg Phe
50

<210> 316
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E873fs"

<400> 316
Ser Ile Pro Glu Leu Ala Ser Thr Glu Met Ile Lys Val Lys Asn His
1 5 10 15

Ser Val Leu Gln Arg Thr Glu Lys Lys Cys Tyr Leu His His Trp Asn
20 25 30

Tyr Leu Ser Phe Leu Lys Gly Gln Ile Ile Arg Glu Met Ser Phe His
35 40 45

Leu Leu Asn Tyr Arg Thr Ser Asn Ile Ser His Gln Trp Ile Arg Leu
50 55 60

His Phe Gln Lys Ala Leu Glu Ile Lys His Ile Ser Lys Gly Val His
65 70 75 80

Arg Val Gly

<210> 317
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P1470Q"

<400> 317
Asn Arg Ala Asp Asn Ser Gly Lys Pro Gln Gln Pro Pro Gly Gly Phe
1 5 10 15

Ala Pro Ala Ala Ile Asn Arg Ser Ile Gln Gln Cys Lys Val Ile Val
20 25 30

Asp His Ser Thr Thr Leu Thr Ser Ser Leu Ser Leu Thr Val Ser Val

35 40 45

Glu Ser Ser Glu
50

<210> 318
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I305V"

<400> 318
Glu Ile Pro Asp Ser Thr Met Ser Ile Cys Val Pro Ser Glu Thr Val
1 5 10 15

Asp Glu Ile Val Lys Ser Gly Tyr Ile Val Gly Glu Ser Glu Asn Ser
20 25 30

Glu Ile Ser Gln Gln Val Arg Phe Lys Thr Val Thr Val Leu Ala Gln
35 40 45

Val His Pro Ile
50

<210> 319
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S800F"

<400> 319
Ser Leu Arg Asn Met Met Gln Leu Cys Thr Arg Cys Leu Ser Asn Cys
1 5 10 15

Thr Lys Lys Ser Pro Asn Lys Ile Ala Phe Phe Gly Phe Phe Leu Arg
20 25 30

Leu Leu Thr Ser Lys Leu Met Asn Asp Ile Ala Asp Ile Cys Lys Ser
35 40 45

Leu Ala Ser Phe
50

<210> 320
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1304I"

<400> 320
Cys Asn Ser Pro Thr Asn Pro Tyr Trp Val Met Glu Gly Gln Leu Ser
1 5 10 15

Asn Pro Thr Phe Tyr Leu Val Cys Phe Ile Ile Thr Pro Val Val Ala
20 25 30

Leu Leu Pro Arg Tyr Phe Phe Leu Ser Leu Gln Gly Thr Cys Gly Lys
35 40 45

Ser Leu Ile Ser
50

<210> 321
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R311H"

<400> 321
Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu Thr Lys Ala Met
1 5 10 15

Leu Asn Asn Ser Gly Pro Arg Tyr Lys His His Ser Lys Leu Glu Arg
20 25 30

Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu Val Ile Met
35 40 45

Cys Leu Thr Gly
50

<210> 322
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R858C"

<400> 322
Leu Gly Thr Asp Ile Ile Pro Ser Ile Ala Leu Ala Tyr Glu Lys Ala
1 5 10 15

Glu Ser Asp Ile Met Asn Arg Lys Pro Cys Cys His Lys Asn Lys Asp
20 25 30

Arg Leu Val Asn Gln Pro Leu Ala Val Tyr Ser Tyr Leu His Ile Gly
35 40 45

Leu Met Gln Ala
50

<210> 323
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G704C"

<400> 323

Val Glu Pro Ser His Lys Ser Lys Ile Val Glu Tyr Leu Gln Ser Tyr
1 5 10 15

Asp Glu Ile Thr Ala Met Thr Gly Asp Cys Cys Val Asn Asp Ala Pro
20 25 30

Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly Ser Gly Thr Ala
35 40 45

Val Ala Lys Thr
50

<210> 324
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R819fs"

<400> 324
Leu Val Thr Asp Gly Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro
1 5 10 15

Asp Leu Asp Ile Met Asp Arg Pro Pro Pro Glu Pro Gln Gly Ala Pro
20 25 30

His Gln Trp Leu Ala Leu Leu Pro Leu His Gly Asn Arg Gly Leu Cys
35 40 45

Gly Cys Ser His Arg Gly Ser Ser Cys Leu Val Val Pro Val Arg
50 55 60

<210> 325
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R183H"

<400> 325
Ser Val Ile Ile Val Val Leu Val Thr Ala Phe Asn Asp Trp Ser Lys
1 5 10 15

Glu Lys Gln Phe Arg Gly Leu Gln Cys His His Ile Glu Gln Glu Gln
20 25 30

Lys Phe Ser Ile Ile Arg Asn Gly Gln Leu Ile Gln Leu Pro Val Ala
35 40 45

Glu Ile Val Val
50

<210> 326
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E724K"

<400> 326
Gly Thr Asp Val Cys Lys Glu Ala Ala Asp Met Ile Leu Val Asp Asp
1 5 10 15

Asp Phe Gln Thr Ile Met Ser Ala Ile Lys Lys Glu Gly Lys Gly Ile
20 25 30

Tyr Asn Asn Ile Lys Asn Phe Val Arg Phe Gln Leu Ser Thr Ser Ile
35 40 45

Ala Ala Leu Thr
50

<210> 327
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E119Q"

<400> 327
Ile Ser Tyr Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val
1 5 10 15

Ala Asn Ser Ile His Ser Leu Phe Ser Gln Gln Glu Thr Pro Val Val
20 25 30

Leu Gln Leu Ala Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala
35 40 45

Asn Ser Val Phe
50

<210> 328
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R191Q"

<400> 328
Met Thr Gly Lys Leu Gly Phe Ile Ala Gly Val Ile Asn Arg Glu Arg
1 5 10 15

Met Ala Ser Phe Glu Arg Leu Leu Trp Gln Gln Ile Cys Arg Gly Asn
20 25 30

Val Tyr Leu Lys Phe Ser Glu Met Asp Ala Pro Leu Glu Asp Pro Val
35 40 45

Thr Lys Glu Glu
50

<210> 329
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.L237P"

<400> 329
Arg Gln Val Arg Pro Val Thr Glu Lys Leu Pro Ala Asn His Pro Leu
1 5 10 15

Leu Thr Gly Gln Arg Val Leu Asp Ala Pro Pro Phe Pro Cys Val Gln
20 25 30

Gly Gly Thr Thr Ala Ile Pro Gly Ala Phe Gly Cys Gly Lys Thr Val
35 40 45

Ile Ser Gln Ser
50

<210> 330
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.Y383fs"

<400> 330
Asp Leu Thr Gly Phe Ile Thr Glu Gly Gln Ile Tyr Val Asp Arg Gln
1 5 10 15

Leu His Asn Arg Gln Ile Tyr Pro Pro Ser Thr Cys Ser Leu Pro Cys
20 25 30

Arg Gly

<210> 331
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.R312fs"

<400> 331
Ser Thr Phe Pro Asp His Lys Val Lys Val Thr Pro Leu Gly Asn Pro
1 5 10 15

Asp Arg Pro Ala Ala Gly Gln Thr Asp Lys Glu Arg Glu Arg Val Arg
20 25 30

Ala Arg Val Arg Ala Pro Cys Cys Ala Gly Ser Arg
35 40

<210> 332
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q990fs"

<400> 332
Ile Val Glu Thr Tyr Phe Pro Gly Tyr Asn Arg Ser Ile Ser Arg Thr
1 5 10 15

Glu Thr Ile Ile Arg Phe Ala Phe Gln Ser Leu Tyr His Ser Ser Val
20 25 30

Tyr Cys Met Ser Leu Phe Thr Gly Thr Gly His Ser Asn Cys Cys Asp
35 40 45

Gly Gly Tyr Arg Ser Arg Cys Ser Lys Trp His Thr Asn Lys Arg Trp
50 55 60

Arg Ala Ile Gly Asp Gly Ser
65 70

<210> 333
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R519Q"

<400> 333
Val Tyr Gln Ala Ser Ser Pro Asp Glu Val Ala Leu Val Gln Trp Thr
1 5 10 15

Glu Ser Val Gly Leu Thr Leu Val Gly Gln Gln Asp Gln Ser Ser Met
20 25 30

Gln Leu Arg Thr Pro Gly Asp Gln Ile Leu Asn Phe Thr Ile Leu Gln
35 40 45

Ile Phe Pro Phe
50

<210> 334
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R290Q"

<400> 334
Ala Ser Gly Thr Val Val Gly Val Val Leu Tyr Thr Gly Arg Glu Leu
1 5 10 15

Arg Ser Val Met Asn Thr Ser Asn Pro Gln Gln Ser Lys Ile Gly Leu
20 25 30

Phe Asp Leu Glu Val Asn Cys Leu Thr Lys Ile Leu Phe Gly Ala Leu
35 40 45

Val Val Val Ser
50

<210> 335
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S39G"

<400> 335
Ala Ala Ala Ala Ala Asn Arg Lys Arg Ala Ala Tyr Tyr Ser Ala Ala
1 5 10 15

Gly Pro Arg Pro Gly Ala Asp Arg His Gly Gly Arg Tyr Gln Leu Glu
20 25 30

Asp Glu Ser Ala His Leu Asp Glu Met Pro Leu Met Met Ser Glu Glu
35 40 45

Gly Phe Glu Asn
50

<210> 336
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1814fs"

<400> 336
Asn Tyr Leu Ala Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg Leu
1 5 10 15

Gly Gln Leu Leu Leu Ser Ala Lys Lys Glu Ile Ser Gln Leu Phe Met
20 25 30

Thr His

<210> 337
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P197Q"

<400> 337
Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu Tyr
1 5 10 15

Val Tyr Asp Gly Asp Ser Ile Tyr Ala Gln Gln Leu Val Ala Ala Phe
20 25 30

Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu
35 40 45

Val Val Ala Thr
50

<210> 338
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L1244F"

<400> 338
Ile Ala Phe Ser Gln His Asn Thr Ile Met Asp Leu Val Gln Phe Phe
1 5 10 15

Val Thr Phe Phe Ser Cys Phe Leu Ser Phe Phe Leu Leu Val Ala Ala
20 25 30

Val Val Trp Lys Ile Lys Gln Thr Cys Trp Ala Ser Arg Arg Arg Glu
35 40 45

Gln Leu Leu Arg
50

<210> 339
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K1936R"

<400> 339
Ile Ala Ser Asp Ser Asp Glu Thr Ser Met Ser Leu Ser Ser Asp Asp
1 5 10 15

Tyr Thr Lys Lys Lys Lys Lys Gly Lys Arg Arg Gly Lys Lys Asp Ser
20 25 30

Ser Ser Ser Gly Ser Gly Ser Asp Asn Asp Val Glu Val Ile Lys Val
35 40 45

Trp Asn Ser Arg
50

<210> 340
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q217H"

<400> 340
Gly His Lys Ala Glu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15

Gln His Gln His Gln Gln Gln Gln Gln His His Gln Gln Gln Gln Gln
20 25 30

Gln Gln Gln His Leu Ser Arg Ala Pro Gly Leu Ile Thr Pro Gly Ser
35 40 45

Pro Pro Pro Ala

50

<210> 341
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S387L"

<400> 341
Arg Leu Leu Lys His Asn Pro Ser Gln Arg Pro Met Leu Arg Glu Val
1 5 10 15

Leu Glu His Pro Trp Ile Thr Ala Asn Leu Leu Ser Lys Pro Ser Asn
20 25 30

Cys Gln Asn Lys Glu Ser Ala Ser Lys Gln Ser
35 40

<210> 342
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G64W"

<400> 342
Glu Gly Asp Cys Tyr Val Ile Leu Ser Thr Arg Arg Val Ala Ser Leu
1 5 10 15

Leu Ser Gln Asp Ile His Phe Trp Ile Trp Trp Lys Asp Ser Ser Gln
20 25 30

Asp Glu Gln Ser Cys Ala Ala Ile Tyr Thr Thr Gln Leu Asp Asp Tyr
35 40 45

Leu Gly Gly Ser
50

<210> 343
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G299fs"

<400> 343
Asp Leu Leu Asn His Asp Asp Cys Tyr Ile Leu Asp Gln Ser Gly Thr
1 5 10 15

Lys Ile Tyr Val Trp Lys Gly Lys Gly Ser His Lys Gly
20 25

<210> 344
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F34L"

<400> 344
Asp Gly Val Pro Arg Gly Pro Val Leu His Ile Val Val Val Gly Phe
1 5 10 15

His His Lys Lys Gly Cys Gln Val Glu Leu Leu Ser Tyr Pro Pro Leu
20 25 30

Ile Pro Gly Asp Gly His Asp Ser His Thr Leu Pro Glu Glu Trp Lys
35 40 45

Tyr Leu Pro Phe
50

<210> 345
<211> 32
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G7fs"

<400> 345
Met Glu Lys Ala Arg Arg Gly Gly Gly Trp Arg Pro Pro Gly Ala Arg
1 5 10 15

Thr Ala His Arg Gly Gly Arg Ile Ser Pro Gln Glu Gly Leu Pro Gly
20 25 30

<210> 346
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F351fs"

<400> 346
Glu Asn Pro Thr Ile Thr Ile Thr Ala Leu Leu Gly Ser Leu Asn Ser
1 5 10 15

Cys Cys Asn Pro Trp Ile Tyr Met Phe Leu Val Ala Ile Ser Phe Lys
20 25 30

Thr Val Phe Lys Ala Ser His Ala Ala Lys Thr
35 40

<210> 347
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

<221> source
<223> /note="p.G39R"

<400> 347
Arg Gly Thr Leu Ser Ala Pro Asn Ala Thr Thr Pro Trp Leu Gly Arg
1 5 10 15

Asp Glu Glu Leu Ala Lys Val Glu Ile Arg Arg Val Leu Ala Thr Val
20 25 30

Leu Val Leu Ala Thr Gly Gly Asn Leu Ala Val Leu Leu Thr Leu Gly
35 40 45

Gln Leu Gly Arg
50

<210> 348
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E930D"

<400> 348
Trp Arg Glu Ser Ala Lys Gln Gly Thr Leu Ala Gln Lys Tyr Leu Glu
1 5 10 15

Ala Met Ala Val Ile Glu His Met Gln Asp Asp Lys Leu Leu Glu Val
20 25 30

Glu Asn Arg Ala Arg Gln Ala Glu Glu Lys Phe Glu Asp Ala Tyr Glu
35 40 45

Lys Leu His His
50

<210> 349
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W101R"

<400> 349
Cys Pro Glu Asn Leu Leu Pro Pro Lys Lys Ile Lys Thr Pro Lys Gly
1 5 10 15

Thr Leu Pro Arg Leu Val Asp His Val Arg Arg His His Pro Val Arg
20 25 30

Arg Asn Lys Phe Lys Tyr Leu Ile Asp His Pro Val Ser Leu Thr Gly
35 40 45

Ala Gly Arg Asp
50

<210> 350
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W663fs"

<400> 350
Gln Ser Thr Lys Lys Ala Tyr Pro Leu Glu Ser Ala Arg Ser Ser Pro
1 5 10 15

Gly Glu Arg Ala Ser Arg His His Leu Ser Thr Ala Gly Thr Pro Ala
20 25 30

Pro Pro Pro Val Pro Thr Cys Ser Pro Arg Thr Leu Arg Cys Leu Pro
35 40 45

<210> 351
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G665fs"

<400> 351
Lys Lys Ala Tyr Pro Leu Glu Ser Ala Arg Ser Ser Pro Gly Glu Arg
1 5 10 15

Ala Ser Arg His His Leu Trp Gly Gly Gln Gln Arg Ala Pro Pro His
20 25 30

His Pro Pro Cys Pro Pro Val His Pro Gly Pro Cys Asp Ala Ser Pro
35 40 45

Asp Pro Thr Gln His Ala Gly Ser Ala Gly Gly Gly Leu Ser Gln Ala
50 55 60

Ser
65

<210> 352
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G665fs"

<400> 352
Thr Lys Lys Ala Tyr Pro Leu Glu Ser Ala Arg Ser Ser Pro Gly Glu
1 5 10 15

Arg Ala Ser Arg His His Leu Trp Gly Ala Thr Ala Gly Thr Pro Ala
20 25 30

Pro Pro Pro Val Pro Thr Cys Ser Pro Arg Thr Leu Arg Cys Leu Pro
35 40 45

<210> 353
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.M1V"

<400> 353
Val Val Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu
1 5 10 15

Ser Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys
20 25

<210> 354
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L13fs"

<400> 354
Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Phe Trp
1 5 10 15

Pro Gly Gly Tyr Pro Ala Tyr Ser Lys Asp Ser Gly Leu Leu Thr Ser
20 25 30

Ser Ser Arg Glu Trp Lys Val Lys Phe Pro Glu Leu Leu Cys Val Trp
35 40 45

Val Ser Ser Ile Arg His
50

<210> 355
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>

<221> source
<223> /note="p.M1I"

<400> 355
Ile Ile Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu
1 5 10 15

Ser Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys
20 25

<210> 356
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R145Q"

<400> 356
Gln Glu Ala Glu Lys Glu Asp Lys Met Leu Ala Leu Ser Leu Glu Asp
1 5 10 15

Glu His Leu Leu Tyr Gly Asp Ile Ile Gln Gln Gln Asp Phe Leu Asp
20 25 30

Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile Met Ala Phe Arg Trp Val
35 40 45

Thr Glu Phe Cys
50

<210> 357
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R125L"

<400> 357
Ala Glu Leu Thr Arg Met Ala Asn Thr Leu Leu His Val Pro Asn Leu

1 5 10 15

His Trp Leu Val Val Glu Asp Ala Pro Leu Leu Arg Thr Pro Leu Thr
20 25 30

Ala Arg Leu Leu Arg Asp Thr Gly Leu Asn Tyr Thr His Leu His Val
35 40 45

Glu Thr Pro Arg
50

<210> 358
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F30fs"

<400> 358
Gly Arg Arg Val Lys Lys Trp Gln Leu Ile Ile Gln Leu Phe Ala Thr
1 5 10 15

Cys Phe Leu Ala Ser Leu Met Phe Phe Gly Asn Gln Ser Ile Ile Thr
20 25 30

Leu

<210> 359
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G88fs"

<400> 359
Pro Val Arg Ile Lys Glu Gln Val Val Gly Leu Leu Ala Trp Asn Asn
1 5 10 15

Cys Ser Cys Glu Ser Ser Gly Gly Gly Pro Pro Pro Pro Leu Pro Glu
20 25 30

Thr Ser Pro Ser Tyr
35

<210> 360
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R538Q"

<400> 360
Glu Ser Cys Ser Ala Arg Glu Gln Glu Cys Glu Val Lys Leu Pro Phe
1 5 10 15

Asn Ala Gln Arg Ile Ile Ser Leu Ser Gln Gln Asn Asp Phe Gln Ser
20 25 30

Leu Leu Lys Met His Lys Leu Thr Pro Glu Gln Leu Asp Cys Ile His
35 40 45

Asp Ile Arg Arg
50

<210> 361
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G45R"

<400> 361
Arg Leu Arg Ala Leu Arg Pro Gly Arg Glu Pro Arg Gln Ser Glu Pro
1 5 10 15

Pro Ala Gln Arg Gly Pro Pro Pro Ser Arg Arg Arg Pro Pro Ala Arg
20 25 30

Ser Thr Ala Ser Gly His Asp Arg Pro Thr Arg Gly Ala Ala Ala Gly
35 40 45

Ala Arg Arg Pro
50

<210> 362
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A231G"

<400> 362
Glu Glu Cys Gly Arg Ala Ala Gly Arg Ala Cys Gly Phe Ala Gln Pro
1 5 10 15

Gly Cys Ser Cys Pro Gly Glu Ala Gly Gly Gly Gly Ser Thr Thr Thr
20 25 30

Thr Ser Pro Gly Pro Pro Ala Ala His Thr Leu Ser Asn Ala Leu Val
35 40 45

Pro Gly Gly Pro
50

<210> 363
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V396M"

<400> 363

Ser Ser Ala Ser Gly Trp Phe Pro Glu Ala Tyr Val Lys Ala Leu Glu
1 5 10 15

Glu Gly Pro Val Asn Pro Met Thr Pro Met Met Thr Pro Met Thr Ser
20 25 30

Met Thr Ser Met Ser Pro Met Thr Pro Met Asn Pro Gly Asn Glu Leu
35 40 45

Pro Ser Arg Ser
50

<210> 364
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N78S"

<400> 364
Ile Glu Glu Arg Arg Ser Arg Arg Lys Val Ser Thr Leu Val Asp Asp
1 5 10 15

Thr Ser Val Ile Asp Asp Asp Ile Val Ser Ser Asn Met Phe Phe Ala
20 25 30

His Gln Leu Ile Pro Asn Ser Cys Ala Thr His Ala Leu Leu Ser Val
35 40 45

Leu Leu Asn Cys
50

<210> 365
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.R227C"

<400> 365
Trp Thr Asp Lys Ala Arg Arg Val Ile Met Glu Arg Ile Gly Leu Ala
1 5 10 15

Thr Ala Gly Glu Pro Tyr His Asp Ile Cys Cys Phe Asn Leu Met Ala
20 25 30

Val Val Pro Asp Arg Arg Ile Lys Tyr Glu Ala Arg Leu His Val Leu
35 40 45

Lys Val Asn Arg
50

<210> 366
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R68P"

<400> 366
Ser Leu Tyr Ser Val Cys Pro Ser Leu Val Val Arg Pro Lys Pro Leu
1 5 10 15

His Ser Cys Thr Gly Ser Pro Ser Leu Pro Pro Ala Tyr Pro Leu Leu
20 25 30

Ser Val Ile Thr Arg Gln Pro Thr Val Ile Ser His Leu Val Pro Ala
35 40 45

Thr Pro Gly Ile
50

<210> 367
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M38fs"

<400> 367
Ser Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile
1 5 10 15

Gln Asp Arg Ala Gly Arg Met Gly Gly Gly Gly Thr Arg Ala Gly Pro
20 25 30

Gly Pro Gly Ala Ser Gly Cys Val His Gln Glu Ala Glu Arg Val Ser
35 40 45

Gln Ala His Arg Gly Arg Thr Gly Gln
50 55

<210> 368
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.F176V"

<400> 368
Arg Leu Thr Gly Ala Ser Asp Lys Pro Gly Glu Val Ser Lys Leu Gly
1 5 10 15

Lys Arg Met Gly Phe Leu Tyr Leu Thr Val Val Tyr Gly His Thr Trp
20 25 30

Gln Val Gln Asp Lys Ile Asp Ala Asn Asn Val Ala Tyr Thr Thr Gly
35 40 45

Lys Leu Ser Phe
50

<210> 369
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F268fs"

<400> 369
Ala Leu Asp Ile Cys Ile Val Ser Phe Asn Gln Ser Ala Ser Ser Val
1 5 10 15

Phe Val Leu Gly Glu Arg Asn Phe Phe Ala Leu Arg Ile Met Asp Lys
20 25 30

Phe Asp Ser
35

<210> 370
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L133R"

<400> 370
Ser Ser Lys Ser Arg Asn Ala Pro Arg Ser Ser Cys Gly Asn Cys Gly
1 5 10 15

Ala Arg Ala Pro Glu His Pro Pro Val Arg Arg Arg Val Glu Ser Leu
20 25 30

Asn Leu Pro Leu Leu Asn Gly Leu Arg Glu Glu Gly Pro Gly Val Phe
35 40 45

Ser Arg Ser Val
50

<210> 371
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.T214M"

<400> 371
Asp Leu His Cys Asn Lys Arg Ile Leu Val Val Val Leu Gln Glu Lys
1 5 10 15

Ile Ala Ala Phe Asp Ser Cys Thr Phe Met Met Lys Lys Phe Phe Val
20 25 30

Thr Ser Cys Tyr Pro Cys Pro Gly Pro Asn Met Asn Pro Ile Ala Leu
35 40 45

Gly Ser Arg Trp
50

<210> 372
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.H37fs"

<400> 372
Arg Gly Leu Ser Gln Ala Ala Leu Leu Leu Leu Arg Gln Pro Gly Ala
1 5 10 15

Arg Gly Leu Ala Arg Ser His Pro Pro Gly Ser Ser Ser Ser Phe His
20 25 30

Leu Trp Met Thr Ser Pro Ser Ser Gln Gly Pro Arg Arg Ser Leu
35 40 45

<210> 373
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G129fs"

<400> 373
Leu Cys Cys Phe Trp Pro Val Gly Ile Ala Ala Phe Cys Leu Ala Gln
1 5 10 15

Lys Val Ser Leu Cys Val Gly Leu Gly Ile Lys Glu Lys Asn Ala Pro
20 25 30

Gln Lys Gln Arg Ala Ile Tyr Leu Arg Arg Glu Gly Gly Arg
35 40 45

<210> 374
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E579K"

<400> 374
Ser Met Gln His Phe Ser Glu Ala Phe His Gln Val Leu Gly Glu Lys
1 5 10 15

His Lys Arg Gly His Leu Ala Glu Ala Lys Lys Gly His Arg Asp Thr
20 25 30

Cys Asp Glu Asp Ser Val Ala Gly Glu Ser Asp Arg Ile Asp Asp Gly
35 40 45

Thr Val Asn Gly
50

<210> 375
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N172S"

<400> 375
Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val
1 5 10 15

Asn Arg Glu Met Ser Pro Leu Val Asp Ser Ser Ile Ala Leu Trp Met
20 25 30

Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly
35 40 45

Gly Trp Asp Ala
50

<210> 376
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H20Q"

<400> 376
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15

Lys Tyr Ile Gln Gln Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp
20 25 30

Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala
35 40 45

<210> 377
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G33R"

<400> 377
Gly Tyr Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu
1 5 10 15

Ser Gln Arg Gly Tyr Glu Trp Asp Ala Arg Arg Asp Val Gly Ala Ala
20 25 30

Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly
35 40 45

His Thr Pro His
50

<210> 378
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R91Q"

<400> 378
Pro Pro Ala Ser Pro Gly Pro Phe Ala Thr Arg Ser Pro Leu Phe Ile
1 5 10 15

Phe Met Arg Arg Ser Ser Leu Leu Ser Gln Gln Ser Ser Ser Gly Tyr
20 25 30

Phe Ser Phe Asp Thr Asp Arg Ser Pro Ala Pro Met Ser Cys Asp Lys
35 40 45

Ser Thr Gln Thr
50

<210> 379
<211> 101
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.L187fs"

<400> 379
Tyr Ala Arg Arg Val Phe Leu Asn Asn Tyr Gln Ala Ala Glu Asp His
1 5 10 15

Pro Arg Met Val Ile Leu Arg Leu Leu Thr Leu His Cys Pro Pro Gly
20 25 30

Val Glu Asn Ala Leu Thr Gly Ser Leu Arg Ser Arg Asp Thr Met Gln
35 40 45

Thr Phe Cys Leu Phe Lys Pro Thr Arg Pro Ser Thr Ala Val Ser Trp
50 55 60

Cys His Tyr Tyr Ala Ala Ser Gly Ser Leu Val Glu Gly Ala Gly Asp
65 70 75 80

Val Ser Glu Asp Thr Glu Leu Asp Gly Thr Thr Phe Leu Phe Ile Thr
85 90 95

Thr Gln Gln Asn Phe
100

<210> 380
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.T52M"

<400> 380
Lys Val Arg Lys Trp Glu Lys Lys Trp Val Thr Val Gly Asp Thr Ser
1 5 10 15

Leu Arg Ile Tyr Lys Trp Val Pro Val Met Met Glu Pro Lys Val Asp
20 25 30

Asp Lys Asn Lys Asn Lys Lys Lys Gly Lys Asp Glu Lys Cys Gly Ser

35 40 45

Glu Val Thr Thr
50

<210> 381
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G980C"

<400> 381
Pro Gln Thr Pro Ser Gln Met Val Pro Leu Pro Ser Ala Asn Pro Pro
1 5 10 15

Gly Pro Leu Lys Ser Pro Gln Val Leu Cys Cys Ser Ser Leu Ser Val
20 25 30

Arg Ser Pro Thr Gly Ser Pro Ser Arg Leu Lys Ser Pro Ser Met Ala
35 40 45

Val Pro Ser Pro
50

<210> 382
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1127fs"

<400> 382
Tyr His Asn Ala Ile Lys Thr Ile Ala Thr Ser Asp Asp Glu Leu Leu
1 5 10 15

Pro Asp Arg Pro Leu Leu Pro Pro Pro Thr Thr Thr Ala Gly Leu Arg
20 25 30

Ala Arg Asp Gln Gln Gln Pro Ala Gln Pro Asp Ala Pro Glu Leu Ser
35 40 45

Arg Cys Pro Glu Pro Tyr Gly His Glu Pro Ala Arg Pro Ala Ala Pro
50 55 60

Val Pro
65

<210> 383
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R37fs"

<400> 383
Arg Ser Lys Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg Ser
1 5 10 15

His Ser Arg Lys Lys Arg Tyr Ser Ser Thr Gly Leu Val Pro Glu His
20 25 30

Ile Gln Gly Leu Val Val Glu Ile Val Cys Ile Leu Glu Ile Ile Val
35 40 45

Ala Ile Thr Glu Ile Ile Glu Glu
50 55

<210> 384
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N1459S"

<400> 384
Leu Pro Cys Ser Ser Ser Pro Gln Glu Thr Thr Gln Ser Arg Pro Met
1 5 10 15

Pro Pro Glu Ala Arg Arg Leu Ile Val Ser Ser Lys Asn Ala Gly Glu
20 25 30

Thr Leu Leu Gln Arg Ala Ala Arg Leu Gly Tyr Glu Glu Val Val Leu
35 40 45

Tyr Cys Leu Glu
50

<210> 385
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P536Q"

<400> 385
Arg Ile Leu Phe Ser Lys Glu Ile Leu Ile Ser Ser Ser Val Asp Ile
1 5 10 15

His Leu Lys Asp Ser Gln Ser Leu Asp Gln Gln Asn Lys Met Ala Ala
20 25 30

Leu Arg Glu Tyr Leu Ala Thr Thr Phe Pro Thr Cys Asp Leu His Glu
35 40 45

His Gly Lys Asp
50

<210> 386
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.E630K"

<400> 386
Asn Asp Gln Arg Gly Arg Asp Gly Gly Glu Gly Cys Ser Trp Met Phe
1 5 10 15

Gln Pro Met Asn Asn Ser Lys Met Arg Lys Lys Lys Arg Asn Leu Gln
20 25 30

Pro Asn Ser Asn Ala Ile Pro Glu Gly Met Arg Glu Pro Ser Thr Asp
35 40 45

Asn Pro Glu Glu
50

<210> 387
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D265fs"

<400> 387
Phe Gln Pro Pro Pro Glu Tyr Gln Leu Thr Ala Ala Glu Leu Lys Gln
1 5 10 15

Ile Val Asp Gln Ser Leu Ser Gly Gly Thr Trp Pro Ala Ala Cys Trp
20 25 30

Cys Ser Ser Ser Pro Ser Ser Ser Ala Thr Trp Thr Ser Pro Gly Ala
35 40 45

Ala Val Pro Val Ala Leu Arg Pro Ser Ala Ser Trp Ser Arg Cys Thr
50 55 60

Cys Ser Ser Ser Ala Thr Met Trp Arg Ser Thr Thr Pro Arg
65 70 75

<210> 388
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R198C"

<400> 388
Leu Glu Asp Ala Val Val Pro Arg Ala Leu Tyr Glu Glu Leu Leu Arg
1 5 10 15

Asn Tyr Gln Gln Gln Gln Glu Glu Met Cys Cys His Leu Gln Gln Glu
20 25 30

Leu Glu Arg Thr Arg Arg Gln Leu Val Gln Gln Ala Lys Lys Leu Lys
35 40 45

Glu Tyr Gly Ala
50

<210> 389
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P383L"

<400> 389
Ser Phe Leu Gly Ser Thr Val Gln Met Gly Lys Gln Met Pro Lys Asn
1 5 10 15

Glu Trp Lys Met Glu Asp Ile Lys Ile Leu Leu Leu Pro Gln Pro Gln
20 25 30

Phe Gln Cys Ala Lys Ser Asp Pro Gly Gly
35 40

<210> 390
<211> 82
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P444fs"

<400> 390
Ser Ser Met Phe Leu Pro Arg Asp Asp Leu Ser Pro Ala Arg Asp Leu
1 5 10 15

Leu Asp Val Pro Ser Arg Asn Pro Pro Gln Gly Leu Thr His Leu Glu
20 25 30

Glu Ile Leu Leu Pro Arg Arg Lys Pro His Ala Ala Leu Gln His Gly
35 40 45

Arg Ala Val His His Gln Gly Asp Gln Pro Asp Lys His Phe Thr Glu
50 55 60

Pro Asp Pro Thr Val Gln Cys Glu Asn Phe Pro His Gln Asn Ala Thr
65 70 75 80

Gly Thr

<210> 391
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L62Q"

<400> 391
Ser Thr Pro Pro Gly Met Asp Leu Ser Leu Ala Pro Pro Pro Arg Glu
1 5 10 15

Arg Pro Ala Ser Ser Ser Ser Ser Pro Gln Gln Gly Cys Phe Glu Pro
20 25 30

Ala Asp Pro Glu Gly Ala Gly Leu Leu Leu Pro Pro Pro Gly Gly Gly
35 40 45

Gly Gly Gly Ser
    50

<210> 392
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R162H"

<400> 392
Ser Glu Asn Glu Arg Leu Ala Ser Val Ala Gln Glu Leu Lys Glu Ile
1   5   10   15

Asn Gln Asn Val Glu Ile Gln Arg Gly His His Leu Arg Asp Asp Ile
            20   25   30

Lys Glu Tyr Lys Phe Arg Glu Ala Arg Leu Leu Gln Asp Tyr Ser Glu
        35   40   45

Leu Glu Glu Glu
    50

<210> 393
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V414L"

<400> 393
Ser Cys Phe Gly Ser Gly Ser Cys Pro His Phe Leu Ala Ala Ala Thr
1   5   10   15

Lys Arg Gly Lys Ile Cys Ile Trp Asp Leu Leu Ser Lys Leu Met Lys
            20   25   30

Val His Leu Lys Phe Glu Ile Asn Ala Tyr Asp Pro Ala Ile Val Gln
35 40 45

Gln Leu Ile Leu
50

<210> 394
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A225M"

<400> 394
Val Phe Ile Pro Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala Glu
1 5 10 15

Ala Val Asp Arg Cys Pro Met Cys Ser Met Met Val Ile Asp Phe Lys
20 25 30

Gln Arg Val Phe Met Ser
35

<210> 395
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H660Q"

<400> 395
Ala Ser Arg Asn Leu Lys His Glu Arg Phe Gln Ser Leu Ser Phe Pro
1 5 10 15

His Thr Lys Glu Met Met Lys Ile Phe Gln Gln Lys Lys Phe Gly Leu
20 25 30

His Asn Phe Arg Thr Asn Gln Leu Glu Ala Ile Asn Ala Ala Leu Leu

35 40 45

Gly Glu Asp Cys
50

<210> 396
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S44L"

<400> 396
Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro Ser Ser
1 5 10 15

Ala Phe Leu Asn Leu Ile Gly Phe Val Leu Leu Arg Arg Glu Leu Gly
20 25 30

Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser Ser
35 40 45

Gln Glu Val Glu
50

<210> 397
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H487Q"

<400> 397
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His His His His His
20 25 30

His His Leu Leu Gln Asp Ala Tyr Met Gln Gln Tyr Gln His Ala Thr
        35   40   45

Gln Gln Gln Gln
    50

<210> 398
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R344W"

<400> 398
Lys Pro Tyr Lys Thr Leu Gln Ala Gln Ala Pro Glu Lys Ser Lys Asn
1   5   10   15

Lys Lys Lys Gln Arg Lys Gly Pro His Trp Trp Lys Ser Gln Thr Leu
            20   25   30

Gln Phe Asp Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile
        35   40   45

Glu Pro Arg Asn
    50

<210> 399
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Q118L"

<400> 399
Pro Arg Pro Leu His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg
1   5   10   15

Gln Gln Glu Glu Gln Gln Gln Gln Leu Leu Leu Pro Arg Gly Glu
20 25 30

Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu
35 40 45

Tyr Asn Ala Leu
50

<210> 400
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.RIAL444del"

<400> 400
Lys Ser Val Glu Leu Val Leu Gly Glu Ser Arg Val Ser Leu Gln Gln
1 5 10 15

His Leu Thr Val Arg Trp Asn Gly Ser Pro Cys Arg Ala Pro His Phe
20 25 30

His Ile Asp Leu Asp Gly Tyr Leu Leu Lys Val Thr Thr Lys Ala Gly
35 40 45

Leu Glu Ile Ser Trp Asp Gly Asp Ser Phe Val Glu Val Met
50 55 60

<210> 401
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R241Q"

<400> 401

Pro Pro Gly Gln Cys Cys Pro Lys Cys Leu Gly Gln Arg Lys Val Phe
1 5 10 15

Asp Leu Pro Phe Gly Ser Cys Leu Phe Gln Gln Ser Asp Val Tyr Asp
20 25 30

Asn Gly Ser Ser Phe Leu Tyr Asp Asn Cys Thr Ala Cys Thr Cys Arg
35 40 45

Asp Ser Thr Val
50

<210> 402
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G455V"

<400> 402
Lys Ala Ile Phe Gly Asp Glu Asp Glu Ser Gly Asp Ser Asp Asp Glu
1 5 10 15

Glu Asp Asp Glu Met Ser Glu Asp Asp Val Val Leu Glu Asn Gly Ser
20 25 30

Ser Asp Glu Glu Ala Glu Glu Glu Glu Asn Ala Glu Met Thr Asp Gln
35 40 45

Tyr Met Ala Val
50

<210> 403
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.E878D"

<400> 403
Gly Glu Met Gln Lys Gln Ala Gln Leu Asn Arg Ala Glu Phe Glu Asp
1 5 10 15

Gln Asp Asp Glu Ala Arg Val Gln Tyr Asp Asp Gly Phe Arg Pro Gly
20 25 30

Met Tyr Val Arg Ile Glu Ile Glu Asn Val Pro Cys Glu Phe Val Gln
35 40 45

Asn Phe Asp Pro
50

<210> 404
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y937N"

<400> 404
Met Glu Lys Ala Asp Gln Ser Leu Ala Ser Leu Pro Ser Gly Leu Pro
1 5 10 15

Ile Thr Cys His Leu Cys Gln Lys Thr Asn Asn Ser Asn Lys Gly Thr
20 25 30

Phe Arg Ala His Tyr Lys Thr Val His Leu Arg Gln Leu His Lys Cys
35 40 45

Lys Val Pro Gly
50

<210> 405
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R512W"

<400> 405
Asn Arg His Ser Ala Asn Pro Asn Pro Arg Leu His Met Pro Met Leu
1   5   10   15

Arg Asn Asn Arg Asp Lys Asp Leu Ile Trp Trp Ala Thr Ser Gly Ala
            20   25   30

Ala Thr Pro Val Ile Ala Ser Thr Lys Ser Asn Leu Ala Leu Thr Ser
        35   40   45

Pro Gly Arg Pro
    50

<210> 406
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S575R"

<400> 406
Leu Gln Asn Pro Leu Pro Ser Gln Leu Val Phe Ser Gly Leu Lys Thr
1   5   10   15

Val Gln Pro Val Pro Pro Phe Tyr Arg Arg Arg Leu Leu Thr Pro Gly
            20   25   30

Glu Met Val Ser Pro Pro Thr Ser Leu Pro Thr Ser Pro Ile Ile Pro
        35   40   45

Thr Ser Gly Thr
    50

<210> 407
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M255I"

<400> 407
Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala
1 5 10 15

Thr Thr Ala Glu Thr Leu Asp Val Gln Ile Ile Lys Gly Glu Phe Tyr
20 25 30

Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu
35 40 45

Phe Pro Ala Ala
50

<210> 408
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P403fs"

<400> 408
Asn Ile Asp Asp Leu Ile Arg Asp Gln Gly Phe Arg Gly Asp Gly Gly
1 5 10 15

Ser Thr Thr Gly Leu Ser Ala Thr Pro Leu Pro His Tyr Leu Ala His
20 25 30

<210> 409
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

<221> source
<223> /note="p.G466V"

<400> 409
Leu Gly Arg Arg Asp Ser Ser Asp Asp Trp Glu Ile Pro Asp Gly Gln
1 5 10 15

Ile Thr Val Gly Gln Arg Ile Gly Ser Val Val Ser Phe Gly Thr Val
20 25 30

Tyr Lys Gly Lys Trp His Gly Asp Val Ala Val Lys Met Leu Asn Val
35 40 45

Thr Ala Pro Thr
50

<210> 410
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G469A"

<400> 410
Arg Asp Ser Ser Asp Asp Trp Glu Ile Pro Asp Gly Gln Ile Thr Val
1 5 10 15

Gly Gln Arg Ile Gly Ser Gly Ser Phe Ala Ala Thr Val Tyr Lys Gly
20 25 30

Lys Trp His Gly Asp Val Ala Val Lys Met Leu Asn Val Thr Ala Pro
35 40 45

Thr Pro Gln Gln
50

<210> 411
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G469V"

<400> 411
Arg Asp Ser Ser Asp Asp Trp Glu Ile Pro Asp Gly Gln Ile Thr Val
1 5 10 15

Gly Gln Arg Ile Gly Ser Gly Ser Phe Val Val Thr Val Tyr Lys Gly
20 25 30

Lys Trp His Gly Asp Val Ala Val Lys Met Leu Asn Val Thr Ala Pro
35 40 45

Thr Pro Gln Gln
50

<210> 412
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V600K"

<400> 412
Arg Asp Leu Lys Ser Asn Asn Ile Phe Leu His Glu Asp Leu Thr Val
1 5 10 15

Lys Ile Gly Asp Phe Gly Leu Ala Thr Lys Lys Lys Ser Arg Trp Ser
20 25 30

Gly Ser His Gln Phe Glu Gln Leu Ser Gly Ser Ile Leu Trp Met Ala
35 40 45

Pro Glu Val Ile Arg
50

<210> 413
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V600E"

<400> 413
Arg Asp Leu Lys Ser Asn Asn Ile Phe Leu His Glu Asp Leu Thr Val
1 5 10 15

Lys Ile Gly Asp Phe Gly Leu Ala Thr Glu Glu Lys Ser Arg Trp Ser
20 25 30

Gly Ser His Gln Phe Glu Gln Leu Ser Gly Ser Ile Leu Trp Met Ala
35 40 45

Pro Glu Val Ile
50

<210> 414
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K601E"

<400> 414
Asp Leu Lys Ser Asn Asn Ile Phe Leu His Glu Asp Leu Thr Val Lys
1 5 10 15

Ile Gly Asp Phe Gly Leu Ala Thr Val Glu Glu Ser Arg Trp Ser Gly
20 25 30

Ser His Gln Phe Glu Gln Leu Ser Gly Ser Ile Leu Trp Met Ala Pro
35 40 45

Glu Val Ile Arg
50

<210> 415
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K601N"

<400> 415
Asp Leu Lys Ser Asn Asn Ile Phe Leu His Glu Asp Leu Thr Val Lys
1 5 10 15

Ile Gly Asp Phe Gly Leu Ala Thr Val Asn Asn Ser Arg Trp Ser Gly
20 25 30

Ser His Gln Phe Glu Gln Leu Ser Gly Ser Ile Leu Trp Met Ala Pro
35 40 45

Glu Val Ile Arg
50

<210> 416
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P24fs"

<400> 416
Met Ser Thr Ala Thr Thr Val Ala Pro Ala Gly Ile Pro Ala Thr Pro
1 5 10 15

Gly Pro Val Asn Pro Pro Pro Pro Gly Gly Leu Gln Pro Gln Gln Ala
20 25 30

Arg Pro Gln Asp Gln Pro Ala Ala Val His Ala Glu Cys Gly Gly Glu
35 40 45

Asp Ala Leu Glu Thr Pro Val Arg Leu Ala Leu Leu Pro Ala Arg Gly
50 55 60

Arg Asn Gln Ile Glu Pro Ala Gly Leu Ser
65 70

<210> 417
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G330W"

<400> 417
His Ala Ala Asp Glu Ala Arg Asp Arg Ile Asn Arg Phe Leu Pro Gly
1 5 10 15

Gly Lys Met Gly Tyr Leu Lys Arg Asn Trp Trp Asp Gly Ser Leu Leu
20 25 30

Tyr Ser Val Val Asn Thr Ala Glu Pro Asp Ala Asp Glu Glu Glu Thr
35 40 45

His Pro Val Asp
50

<210> 418
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V469L"

<400> 418
Asp Gly Glu Leu Asp Leu Ser Gly Ile Asp Asp Leu Glu Ile Asp Arg
1 5 10 15

Tyr Ile Leu Asn Glu Ser Glu Ala Arg Leu Leu Lys Ala Glu Leu Trp
20 25 30

Met Arg Glu Asn Ala Glu Tyr Leu Arg Glu Gln Arg Glu Lys Glu Ala

35 40 45

Arg Ile Ala Lys
50

<210> 419
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K70Q"

<400> 419
Ser Arg Leu Ala Thr Leu Asn Glu Lys Leu Thr Ala Leu Glu Arg Arg
1 5 10 15

Ile Glu Tyr Ile Glu Ala Arg Val Thr Gln Gln Gly Glu Thr Leu Thr
20 25 30

<210> 420
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G107fs"

<400> 420
Leu Ser Gln Leu Arg Leu Arg Leu Glu Glu Val Gly Ala Glu Arg Ala
1 5 10 15

Pro Glu Tyr Thr Glu Pro Leu Gly Gly Cys Ser Gly Ala Ser Arg Phe
20 25 30

Ala Phe Arg Trp Gln Gly Ser Thr Arg Ala Ser Val Trp Met
35 40 45

<210> 421
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R66C"

<400> 421
His Leu Tyr His Tyr Asp His Asp Asn Pro Pro Pro Pro Gln Gln Thr
1 5 10 15

Pro Leu Arg Lys His Lys Lys Lys Gly Cys Cys Gln Ser Arg Pro Ala
20 25 30

Asn Lys Gln Ser Pro Ser Pro Ser Glu Val Ser Gln Ser Pro Gly Arg
35 40 45

Glu Val Met Ser
50

<210> 422
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K1319R"

<400> 422
Thr Ser Ser Gly Arg Arg Arg Val His Asp Gly Lys Lys Ser Ile Arg
1 5 10 15

Ala Thr Asn Tyr Val Glu Ser Asn Trp Arg Arg Lys Gln Cys Lys Glu
20 25 30

Leu Val Asn Leu Ile Phe Gln Cys Glu Asp Ser Glu Pro Phe Arg Gln
35 40 45

Pro Val Asp Leu
50

<210> 423
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R787C"

<400> 423
Thr Val Glu Lys Lys Lys Lys Pro Ser Tyr Thr Thr Gln Arg Asn Asp
1 5 10 15

Tyr Glu Pro Ser Cys Gly Arg Ser Leu Cys Cys Arg Thr Gln Arg Lys
20 25 30

Arg Gln His Thr Tyr Gln Thr Arg Ser Asn Ile Glu His Asn Ser Gln
35 40 45

Ala Ser Cys Gln
50

<210> 424
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H160N"

<400> 424
Val Asn Tyr Val Lys Pro Pro Asn Val Val Asn Ile Thr Ser Ala Arg
1 5 10 15

Gln Leu Thr Gly Cys Ser Arg Phe Gly Asn Asn Ile Phe Pro Ser Ser
20 25 30

Ala Tyr Gln His Ile Lys Met His Lys Arg Ile Leu Gly His Leu Ser
35 40 45

Ser Val Tyr Cys
    50

<210> 425
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G36A"

<400> 425
Leu Leu Gln Leu Leu Leu Gln Leu Leu Leu Leu Leu Leu Leu Ala
1   5   10   15

Ala Gly Gly Ala Arg Ala Arg Trp Arg Ala Ala Glu Gly Thr Ser Ala
            20   25   30

His Leu Arg Asp Ile Phe Leu Gly Arg Cys Ala Glu Tyr Arg Ala Leu
        35   40   45

Leu Ser Pro Glu
    50

<210> 426
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.T451fs"

<400> 426
Leu Ser Asp Leu Val Ser Arg Ala Met His His Leu Gln Pro Leu Asn
1   5   10   15

Ala Lys His His Gly Asn Gly Thr Pro Cys Thr Thr Ser Arg Gly His
            20   25   30

Cys Thr Gly Ser Pro Arg Pro Cys Thr Pro Phe Ala Ile Ser Cys Thr

35 40 45

Ala His Lys Trp Asn Gly Lys Thr Pro Thr Trp Ser Leu Pro Lys Ser
50 55 60

Thr Ser Arg Trp Lys Gly Pro Ser Ser Cys Cys Arg Arg
65 70 75

<210> 427
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A561V"

<400> 427
Leu Leu Pro Gly Val Asp Cys Glu Pro Arg Gln Leu Arg Ala Asp Asp
1 5 10 15

Cys Phe Cys Ala Ser Arg Lys Leu Asp Val Val Val Ala Ile Glu Ala
20 25 30

Lys Phe Lys Gln Asp Leu Gly Phe Arg Met Leu Asn Cys Gly Arg Thr
35 40 45

Asp Leu Val Lys
50

<210> 428
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G265A"

<400> 428
Cys Met Glu Ser Leu Phe Arg Asp Ile Tyr Ser Arg Val Val Ala Ser
1 5 10 15

Gly Val Pro Arg Ser Cys Ser Gly Pro Ala Ala Ser Gly Ser Gly Ser
20 25 30

Gly Pro Gly Pro Ser Ser Gly Pro Gly Ala Ala Pro Ala Ala Asp Lys
35 40 45

Glu Arg Glu Ala
50

<210> 429
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S436L"

<400> 429
His Pro Tyr Gly Ser Lys Trp Val His Arg Gln Ala Leu His Phe Leu
1 5 10 15

Cys Glu Glu Phe Ser Gln Val Met Thr Leu Leu Asp Val Phe Tyr Glu
20 25 30

Leu Ser Lys Asp His Leu Leu Thr Ala Ile Gln Ser Asp Tyr Leu Gln
35 40 45

Ala Ser Glu Gln
50

<210> 430
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L31F"

<400> 430
Thr Arg Ala Ala Thr Met Ile Gly Glu Ile Ala Ala Ala Val Ser Phe
1 5 10 15

Ile Ser Lys Phe Leu Arg Thr Lys Gly Phe Phe Thr Ser Glu Arg Gln
20 25 30

Leu Gln Thr Phe Ser Gln Ser Leu Gln Glu Leu Leu Ala Glu His Tyr
35 40 45

Lys His His Trp
50

<210> 431
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q86K"

<400> 431
Lys Tyr Cys Ala Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly
1 5 10 15

Thr Thr Cys Val Lys Leu Glu Asp Arg Lys Lys Thr Ser Trp Lys Glu
20 25 30

Glu Lys Asn Ile Ser Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro
35 40 45

Asn Asp Asn Gly
50

<210> 432
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.L15F"

<400> 432
Met Glu Pro Ala Ala Ala Leu His Phe Ser Leu Pro Ala Ser Phe Phe
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Leu Leu Ser Leu Cys Ala Leu Val Ser
20 25 30

Ala Gln Phe Thr Val Val Gly Pro Ala
35 40

<210> 433
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E153K"

<400> 433
Phe Gln Asp Gly Asp Phe Tyr Glu Lys Ala Leu Val Glu Leu Lys Val
1 5 10 15

Ala Ala Leu Gly Ser Asn Leu His Val Lys Lys Val Lys Gly Tyr Glu
20 25 30

Asp Gly Gly Ile His Leu Glu Cys Arg Ser Thr Gly Trp Tyr Pro Gln
35 40 45

Pro Gln Ile Gln
50

<210> 434
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.I416M"

<400> 434
Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser Ile Ala
1 5 10 15

Val Trp Asp Met Ala Ser Pro Thr Asp Met Met Thr Leu Arg Arg Val
20 25 30

Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp Lys
35 40 45

Tyr Ile Val Ser
50

<210> 435
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G260W"

<400> 435
Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly Trp Gly Gln
1 5 10 15

Tyr Leu Phe Lys Asn Lys Pro Pro Asp Trp Trp Asn Ala Pro Pro Asn
20 25 30

Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile Gln Asp Ile Glu Thr
35 40 45

Ile Glu Ser Asn
50

<210> 436
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F996L"

<400> 436
Val Phe Trp Asp Gly Ser Phe Trp Lys Leu Ser Gln Asn Ile Ser Glu
1 5 10 15

Leu Lys Asp Gly Glu Leu Trp Asn Lys Leu Leu Phe Val Arg Ile Leu
20 25 30

Asn Ala Asn Asp Glu Ala Thr Val Ser Val Leu Gly Glu Leu Ala Ala
35 40 45

Glu Met Asn Gly
50

<210> 437
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1416fs"

<400> 437
Cys Leu Glu Asp Met Pro Gly Leu Val Gly Gly Ser Ser Arg Arg Arg
1 5 10 15

Gly Gly Gly Ser Pro Glu Lys Pro Pro Lys Pro Gln Ala Ala Ser Arg
20 25 30

Ser Pro Arg Thr Leu Gln Pro Thr Ser Gln Gln Gln Trp Ala Pro Gly
35 40 45

Leu Trp Thr Thr Gly Pro His Thr Gly Glu Gly Trp Pro Pro Arg Asn
50 55 60

<210> 438
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V1627I"

<400> 438
Val Leu Arg Pro Ser Thr Ala Glu Leu Val Pro Ala Arg Ser Pro Ser
1 5 10 15

Glu Thr Leu Ala Tyr Gln His Leu Pro Ile Ile Arg Ile Phe Val Ala
20 25 30

Leu Phe Asp Tyr Asp Pro Val Ser Met Ser Pro Asn Pro Asp Ala Gly
35 40 45

Glu Glu Glu Leu
50

<210> 439
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A85S"

<400> 439
Gly Arg Arg Arg Arg Ser Cys Ser Pro Ala Pro Thr Trp Pro Pro Leu
1 5 10 15

Cys Cys Tyr Pro Gln Ser Arg Pro Thr Ser Ser Ser Ala Ala Gly Pro
20 25 30

Gly Ala Cys Met Arg Ala Ser Gly Arg Pro His Gly Asn Thr Thr Ala
35 40 45

Ser Thr Ala Pro
50

<210> 440
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R1111C"

<400> 440
Lys Gln Thr Ala Ser Gln Val Glu Gln Pro Ile Ile Thr Gln Gly Ser
1 5 10 15

Ser Val Thr Lys Ile Thr Phe Glu Gly Cys Cys Gln Pro Pro Thr Val
20 25 30

Thr Lys Ile Thr Gly Gly Ser Ser Val Pro Lys Leu Thr Ser Pro Val
35 40 45

Thr Ser Ile Ser
50

<210> 441
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V135L"

<400> 441
Pro Gly Ser Pro Asn Ser Glu Pro Val Gly Trp Ile Ala Val Tyr Gly
1 5 10 15

Gln Gly Tyr Ser Pro Asn Ser Gly Asp Leu Leu Gln Gly Leu Gln Ala
20 25 30

Ala Trp Glu Ala Leu Gln Thr Ser Gly Arg Pro Ile Thr Pro Gly Thr
35 40 45

Leu Arg Gln Leu
50

<210> 442

<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S261fs"

<400> 442
Gln Leu Leu Gln Gln His Gly Ala Glu Leu Pro Thr His Pro Ser Lys
1 5 10 15

Lys Arg Lys His Ser Glu Ser Pro Pro Gln His Pro Gln Cys Pro Asp
20 25 30

Ala Glu Trp Asn Asp Gln Thr Gly Ala Trp Asp Arg Asp Ser Pro Ala
35 40 45

Ser Ala Pro His Ser Ser Pro Ile Ala Thr Leu Ala Ser Pro Gly Ser
50 55 60

Ala Leu Pro Gly Pro Trp Phe Leu Ala Ser Gln His Cys Pro Cys Pro
65 70 75 80

Asp Thr Ala Leu Ala Pro Ala Arg Cys Pro Leu Pro Arg Pro Pro Ala
85 90 95

Gly Gln

<210> 443
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D60V"

<400> 443
Leu Pro Ile Thr His Thr Arg Gln Val Pro Ser Lys Pro Ile Asp His
1 5 10 15

Ser Thr Ile Thr Ser Trp Val Ser Pro Val Val Phe Asp Thr Ala Ala
20 25 30

Gly Ser Leu Phe Pro Ala Tyr Gln Lys His Gln Asn Arg Ala Arg His
35 40 45

Ser Ser Arg Lys
50

<210> 444
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R335Q"

<400> 444
Lys Leu His Arg Leu Gln Thr Ala Leu Ser Leu Tyr Ser Thr Ser Leu
1 5 10 15

Cys Gly Leu Val Leu Leu Val Asp Asn Gln Gln Ile Asn Ser Tyr Ser
20 25 30

Gly Ile Lys Arg Asp Phe Ala Thr Val Cys Gln Glu Cys Thr Asp Phe
35 40 45

His Phe Pro Arg
50

<210> 445
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E28Q"

<400> 445
Ala Pro Ser Gly Thr Val Ser Asp Ser Glu Ser Ser Asn Ser Ser Ser
1 5 10 15

Asp Ala Glu Glu Leu Glu Arg Cys Arg Gln Gln Ala Ala Met Pro Ala
20 25 30

Trp Gly Leu Glu Gln Arg Pro His Val Ala Gly Lys Pro Arg Ala Gly
35 40 45

Ala Ala Asn Ser
50

<210> 446
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K143T"

<400> 446
Val Phe Tyr Asn Gly Glu Asn Ser Pro Val His Lys Glu Lys Arg Glu
1 5 10 15

Ala Ala Lys Lys Lys Gln Glu Arg Lys Thr Thr Arg Ala Lys Glu Thr
20 25 30

Leu Glu Lys Lys Lys Leu Leu Lys Glu Leu Trp Glu Ser Ser Lys Lys
35 40 45

Val His
50

<210> 447
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R67fs"

<400> 447
Gln Pro Gly Ala Phe Gln Leu Ser Gly Asp Gln Leu Val Val Ala Arg
1 5 10 15

Pro Gly Glu Pro Ala Ala Ala Arg Gly Ala Ser Thr Ser Ser Val Thr
20 25 30

Ala Ser Cys Ala Ser Thr Gly Ser Ser Thr Ala Ser Ala Ala Thr Ser
35 40 45

Arg Gly Met Trp Asn
50

<210> 448
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E295K"

<400> 448
Phe Ser Leu Ala Lys Ser Glu Ile Gly Ser Ser Met Ser Glu Ile Leu
1 5 10 15

Leu Ser Gln Val Thr Asn Met Arg Thr Lys Lys Leu Ser Phe Asn Ile
20 25 30

Gln Ala Leu Ala Val Cys Ala Asn Ile Cys Leu Ala Thr Lys Asp Arg
35 40 45

Gln Asn Pro Ser
50

<210> 449
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R90fs"

<400> 449
Ser Ser Asp Glu Ser Asp Thr Asn Lys Lys Leu Lys Gln Thr Ser Arg
1 5 10 15

Lys Lys Lys Lys Glu Lys Lys Lys Lys Gly Ser Ile Ser Ile Ile Arg
20 25 30

Lys Gln Arg Gly Ser Met Gly Arg Arg Val Ala Ala Gly Leu Arg Gln
35 40 45

Thr Pro Ile Leu Lys Arg Thr Asn Leu Pro Glu Ala Leu Glu Ala Val
50 55 60

Lys Arg Asn Leu Arg Asn Arg Ile Lys Glu Ile Met Leu Gln Leu Ile
65 70 75 80

Leu Asp Ile Ala Leu Phe Gly Leu Arg Thr Phe Arg Leu
85 90

<210> 450
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D115N"

<400> 450
Arg Lys His Gln His His Lys Lys Thr Lys Arg Lys His Gly Pro Ser
1 5 10 15

Ser Ser Ser Arg Ser Glu Thr Asp Thr Asn Asn Ser Glu Lys Asp Lys
20 25 30

Pro Ser Arg Gly Val Gly Gly Ser Lys Lys Glu Ser Glu Glu Pro Asn
35 40 45

Gln Gly Asn Asn
50

<210> 451
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R100I"

<400> 451
Ala Ser Arg Asp Met Tyr Phe Asp Ile Pro Leu Glu His Arg Glu Thr
1 5 10 15

Ser Ile Ile Lys Arg His Pro Pro Gln Ile Ile Leu Gln Lys Leu Glu
20 25 30

Pro Ile Asp Leu Pro Arg Val Ile Thr Ser Gly Arg Leu Leu Ser Gln
35 40 45

Arg Glu Ala Arg
50

<210> 452
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R279I"

<400> 452
Gly Glu Cys Val Pro Gly Phe Thr Val Pro Asn Leu Leu Pro Lys Trp
1 5 10 15

Ala Pro Asp His Cys Ser Glu Val Glu Ile Ile Met Asp Ser Gly Leu
20 25 30

Asp Lys Phe Ser Asp Ser Thr Phe Leu Leu Pro Ser Arg Pro Ala Gln
35 40 45

Arg Gly Tyr His
50

<210> 453
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R6W"

<400> 453
Met Ala Glu Gly Ser Trp Trp Ile Pro Gln Ala Arg Ala Leu Leu Gln
1 5 10 15

Gln Cys Leu His Ala Arg Leu Gln Ile Arg Pro Ala Asp Gly Asp Val
20 25 30

<210> 454
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F230L"

<400> 454
Asp Ser Ala Ala Leu Leu Cys Gln Ala Leu Ser Thr Asn Tyr Gln Ile
1 5 10 15

Lys Lys Leu Asp Leu Ser His Asn Gln Leu Leu Ser Asp Val Gly Gly
20 25 30

Glu His Leu Gly Gln Met Leu Ala Ile Asn Val Gly Leu Thr Ser Leu
35 40 45

Asp Leu Ser Trp
50

<210> 455
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G90V"

<400> 455
Cys Cys Gly Glu Cys Ser Thr Cys Phe Cys Thr Glu Glu Lys Ser Glu
1 5 10 15

Cys Gln Arg His Glu Glu Thr Ser Pro Val Val Ser Cys Asn His Gln
20 25 30

Ile Met Ser Ala Ser Thr Ile Ser Ala Phe Cys Ala Thr Pro Arg Phe
35 40 45

Lys Gln Leu Phe
50

<210> 456
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.P313fs"

<400> 456
Gly Leu Gln Pro Ala Gly Pro Leu Gly Gln Ser His Leu Ala His His
1 5 10 15

Ser Met Ala Pro Tyr Pro Phe Pro Pro Thr Gln Ile
20 25

<210> 457
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V488I"

<400> 457
Leu Ala Leu Pro Ala Asp Leu Val Pro Ile Leu Gly Asp Gln Ser Asn
1 5 10 15

Glu Lys Gly Gly Ser Tyr Asn Ser Val Ile Ile Gly Ala Ala Pro Leu
20 25 30

Thr Ser Asp Pro Pro Thr Pro Pro Ser Ser Thr Pro Ser Phe Lys Pro
35 40 45

Pro Val Thr Arg
50

<210> 458
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V753F"

<400> 458
Pro Gly Ser Gly Asn Thr Gln Pro Ser Gly Asn Thr Ala Ser Val Gln
1 5 10 15

Gly Ser Thr Ser Leu Pro Ala Gln Ser Phe Phe Arg Ala Pro Ala Thr
20 25 30

Ala Ser Asn His Pro Leu Asn Pro Gly Ala Thr Pro Gln Pro Lys Phe
35 40 45

Gly Ala Pro Asp
50

<210> 459
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G906W"

<400> 459
Arg Arg Pro Thr Thr Thr Ser Ser His Pro Leu Asn Thr Gly Ser Ile
1 5 10 15

Ser His Ser Thr Leu Gly Ala Thr Asp Trp Trp Gln Gln Lys Ser Asp
20 25 30

Ser Ser Phe Ile Leu Gly Asn Pro Ala Thr Pro Ala Pro Val Ile Gly
35 40 45

Leu Thr Ser Pro
50

<210> 460
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S24F"

<400> 460
Met Ala Ala Pro Glu Ala Pro Pro Leu Asp Arg Val Phe Arg Thr Thr
1 5 10 15

Trp Leu Ser Thr Glu Cys Asp Phe Phe His Pro Leu Pro Pro Ser Tyr
20 25 30

Arg Lys Phe Leu Phe Glu Thr Gln Ala Ala Asp Leu Ala Gly Gly Thr
35 40 45

Thr Val
50

<210> 461
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D340N"

<400> 461
Gly Ser Lys Lys Ala Pro Ala Lys Ser Val Lys Glu Arg Ile Ala Asp
1 5 10 15

Ser Gln Glu His Ile Ser Thr Ser Ile Asn Asn Phe Asn Ile Ile Lys
20 25 30

Ile Leu Asn Asn Pro Arg Ala Tyr Thr Leu Pro Ile Ser Lys Glu Glu
35 40 45

Ser Arg Leu Ser
50

<210> 462
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G98fs"

<400> 462
Arg Lys Lys Asn Gln Ala Leu Leu Arg Arg Tyr Gln Glu Ile Gln Glu
1 5 10 15

Asp Arg Arg Gln Ala Glu Gln Gly Gly Trp Leu
20 25

<210> 463
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G65S"

<400> 463
Arg Ala Cys Pro Val Ala Cys Pro Val Gly Cys Pro Ile Ala Cys Pro
1 5 10 15

Val Ser Cys Pro Val Ala Cys Pro Val Ser Ser Cys Pro Val Gly Ser
20 25 30

Met Ala Thr Ala Pro Gln Gly Leu Ser Pro Gln Glu Trp Glu Ala Asp
35 40 45

Arg Glu Thr Gly
50

<210> 464
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D118A"

<400> 464
Arg Ala Ser Asn Glu Thr Leu Val Ser Cys Ser Ser Ser Gly Ser Asp
1 5 10 15

Gln Gln Arg Thr Ile Arg Glu Pro Glu Ala Ala Trp Gly Pro Tyr Arg
20 25 30

Arg His Arg Asn Pro Ser Thr Ala Asp Ala Tyr Asn Ser His Leu Lys
35 40 45

Glu

<210> 465

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L244I"

<400> 465
Ser Asp Thr Ser Val Ile Gln Phe Tyr Pro Ser Lys Phe Val Leu Ile
1 5 10 15

Thr Asp Ile Leu Asp Thr Phe Gly Lys Ile Ile Val Tyr Glu Arg Ile
20 25 30

Phe Ser Met Cys Val Asp Ser Arg Ser Val Leu Pro Asp His Phe Ser
35 40 45

Pro Glu Asn Ala
50

<210> 466
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S21del"

<400> 466
Met Gly Leu Lys Met Ser Cys Leu Lys Gly Phe Gln Met Cys Val Ser
1 5 10 15

Ser Ser Ser Ser His Asp Glu Ala Pro Val Leu Asn Asp Lys His Leu
20 25 30

Asp Val Pro Asp Ile Ile Ile Thr Pro Pro Thr Pro Thr Gly Met Met
35 40 45

<210> 467
<211> 30

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R151I"

<400> 467
Ala Asn Leu Ser Asp Glu Lys Ala Phe Val Phe Ser Val Ala Leu Ala
1 5 10 15

Glu Ile Asn Arg Lys Ile Ile Asn Gln Ile Ile Leu Ile Leu
20 25 30

<210> 468
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L63V"

<400> 468
Leu Cys Leu Arg Ala Leu Ala Phe Cys Ala Leu Ala Lys Pro Arg Ala
1 5 10 15

Ser Ser Leu Gly Pro Gly Pro Gly Glu Val Val Ala Ala Arg Ser Pro
20 25 30

Val Leu Arg Gly Pro Gln Ala Pro Leu Arg Pro Gly Gly Trp Ala Pro
35 40 45

Asp Gly Leu Lys
50

<210> 469
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G12R"

<400> 469
Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Arg Arg Ala Ser Leu
1 5 10 15

Trp Ala Ala Leu Leu Leu Gly Ala Val Ala Leu Arg Pro Ala Glu Ala
20 25 30

Val Ser Glu Pro Thr Thr
35

<210> 470
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R262C"

<400> 470
Pro His Leu Ala Asn Gly His Val Val Pro Ile Lys Pro Gln Val Lys
1 5 10 15

Gly Val Val Arg Glu Glu Asn Lys Val Cys Cys Ala Val Pro Thr Trp
20 25 30

Ala Ser Val Gln Val Val Asp Asp Pro Gly Ser Leu Ala Ser Val Glu
35 40 45

Ser Pro Gly Thr
50

<210> 471
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.P50fs"

<400> 471
Tyr Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu
1 5 10 15

Gln Lys Ala Gly Glu Val Val Pro Pro Pro Cys Thr Ser Ser Ala Ser
20 25 30

Thr Cys Val Ser Arg Gln Ala Cys Arg Tyr Pro Ser Ser Gln Pro Leu
35 40 45

Gln Arg Phe Thr Phe Pro Ser Val Thr Pro Gly Met Gln Ala Ser
50 55 60

<210> 472
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T225I"

<400> 472
Glu Ser Asp Ile Phe Ser Ile Arg Glu Val Ser Phe Gln Ser Thr Gly
1 5 10 15

Glu Ser Glu Trp Lys Asp Thr Asn Tyr Ile Ile Leu Asn Thr Asp Ser
20 25 30

Leu Asp Trp Ala Leu Tyr Asp His Leu Met Asp Phe Leu Ala Asp Arg
35 40 45

Gly Val Asp Asn
50

<210> 473
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G194fs"

<400> 473
Cys Val Trp His Ile Gln Val Ala Thr Asp His Ala Ile Gln Leu Lys
1 5 10 15

Ile Glu Ala Leu Ser Ile Glu Ser Val Gly Leu Leu Pro Phe
20 25 30

<210> 474
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P308fs"

<400> 474
Asn Cys Ala Asp Gly Ser Asp Glu Thr Asn Cys Ser Ala Lys Phe Ser
1 5 10 15

Gly Ser Val Glu Gln Ser His Pro Pro Pro Arg Leu Leu Ala Pro
20 25 30

<210> 475
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P216fs"

<400> 475
Ala Glu Cys Ser Ser Glu Leu Tyr Thr Glu Ala Ser Gly Tyr Ile Ser
1 5 10 15

Ser Leu Glu Tyr Pro Arg Ser Tyr Pro Leu Thr Cys Ala Ala Thr Thr
20 25 30

Ala Ser Gly Trp Ser Gly Ala Ser Pro Cys Thr Ser Ser Ser Trp Ser
35 40 45

Leu Leu Ile Leu Met Thr Thr Ser Lys Tyr Thr Ala Pro Met Thr Ser
50 55 60

Tyr Arg Ser Met Pro Thr Gly Arg Thr Leu Ala Ser Ser Val Gly Ser
65 70 75 80

Lys Gly Pro Pro Thr Ser Thr Pro Ala Ala Met Leu Trp Ile Cys Cys
85 90 95

Ser Ser Gln Met Ser Arg Gly Thr Ala Gly Ala Gly Ser Cys Ala Thr
100 105 110

Pro Pro Arg Ser Ser Ser Ala Pro Ser Pro Arg Pro
115 120

<210> 476
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L351fs"

<400> 476
Pro Asp Tyr Arg Gln Asn Glu Ser His Asn Phe Ser Gly Asp Ile Ala
1 5 10 15

Leu Leu Glu Leu Gln His Ser Ile Pro Trp Ala Pro Thr Ser Ser Arg
20 25 30

Ser Val Cys Pro Ile Met Arg Pro Ser Thr Ala Ala Ala Cys Trp Ala
35 40 45

Thr Ser Val Gly Leu Ala Trp Arg Trp Ala Gly
50 55

<210> 477
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R538C"

<400> 477
Pro Pro Gly Tyr Phe Pro Ala Gly Arg Tyr Val Val Val Ala Glu Ser
1 5 10 15

Pro Leu Pro Pro Gly Glu Trp Glu Leu Cys Cys Arg Ala Ala Pro Gly
20 25 30

Pro Ala Tyr Glu Glu Glu Gly Thr Pro Leu Arg Tyr Gln Arg Leu Val
35 40 45

Pro Ser Arg Ser
50

<210> 478
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S123G"

<400> 478
Trp Trp His Leu Arg Ala Leu Gly Pro Asp Ala Thr Ser Ser Cys Thr
1 5 10 15

Lys Thr Pro Ser Ala Leu Glu Pro Leu Gly Gly Ser Ser Thr Leu Gln
20 25 30

Asp Ser Leu Glu Lys Val Pro Arg Ala Pro Thr Leu Pro Asp Thr Leu
35 40 45

Gln Gly Ser Leu
    50

<210> 479
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.S688Y"

<400> 479
Glu Ser Phe Glu Asn Val Leu Lys Glu Gly Thr Glu Lys Gly Thr Gln
1   5   10   15

Glu Ile Ala Glu Gly Leu Ser Glu Lys Tyr Tyr Gly Lys His Val Ser
            20   25   30

Ala Glu Glu Lys Glu Lys Asp Lys Ser Lys Leu Trp Glu Glu Ser Thr
        35   40   45

Ala Gln Val Lys
    50

<210> 480
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G1454S"

<400> 480
Ala Gly Val Gly Thr Pro Gly Ala Leu Glu Arg Lys Thr Ser Gly Leu
1   5   10   15

Gly Gln Glu Gln Glu Glu Gly Ser Glu Ser Ser Gln Glu Ala Ala Thr
            20   25   30

Gly Ser Gly Asp Gly Arg Gln Glu Thr Gly Ala Ala Glu Lys Phe Arg

35 40 45

Leu Gly Leu Ser
50

<210> 481
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D254N"

<400> 481
Pro Gly Leu Arg Asp Ile Leu Asn Thr Trp Glu Lys Asp Leu Arg Thr
1 5 10 15

Arg Phe Arg Thr Gln Asn Asp Phe Ala Asn Asn Leu Ser Ile Ser Ser
20 25 30

Glu Ile Val Thr Leu Pro Ala Val Ala Leu
35 40

<210> 482
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R541L"

<400> 482
Leu Ser Pro Gln Lys Ile Asp Gln Ala Leu Arg Arg Phe Arg Ser Gly
1 5 10 15

Glu Asn Met Leu Leu Glu Pro Ala Leu Leu Leu Tyr Leu Lys Glu Leu
20 25 30

<210> 483
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E382D"

<400> 483
Leu Lys Leu Pro Leu Arg Phe Gln Arg Leu Gly His Leu Val Ala Leu
1 5 10 15

Met Ala Leu Leu Cys Gly Asp Pro Gln Asp Asp Lys Val Ala Glu Glu
20 25 30

Ala Ala Glu Gly Ile His Ser Leu Leu His Ile Thr Leu Arg Leu Lys
35 40 45

Tyr Ile Thr His
50

<210> 484
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P46fs"

<400> 484
Lys Ala Gly Arg Arg Ala Ala Cys Arg Ser Ser Val Ser Arg Arg Pro
1 5 10 15

Leu His Ser Met Pro Leu Tyr Pro Pro Thr Thr Ser Ser Thr Pro Arg
20 25 30

Phe Cys Cys Val Thr Thr Trp Arg Lys Arg Ser Ser Ser Trp Ala Thr
35 40 45

Leu Pro Gly
50

<210> 485
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1088Q"

<400> 485
Leu Glu Val Gln Met Ala Gln Pro Asn Tyr Gly Leu Glu Leu Val Thr
1 5 10 15

Gly Ser Ala Lys Asn Gly Thr Tyr Phe Gln Gln Ile His Ile Asn Lys
20 25 30

Tyr Lys Met Val Glu Thr Ile Thr Cys Leu Ser Arg Glu Pro Phe Pro
35 40 45

Ala Ser Asn Tyr
50

<210> 486
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P28L"

<400> 486
Ala Ser Ala Thr Ala Ala Trp His Cys Pro Pro Leu Cys Leu Pro Pro
1 5 10 15

Leu Pro Ala Ser Ala Pro Thr Ser Pro Leu Leu Asn Pro Ala Thr Arg
20 25 30

Pro Ala Pro Gly Pro Gly Arg Arg Ala Arg Cys Pro Gln Ser Ala His
35 40 45

Pro Ala Pro Thr
50

<210> 487
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P32fs"

<400> 487
Arg Pro Leu Gly Val Phe Glu Cys Glu Leu Cys Thr Leu Thr Ala Pro
1 5 10 15

Tyr Ser Tyr Val Gly Gln Lys Pro Pro Gln His Pro Val Asp Gly Pro
20 25 30

Pro Gly Gly Lys Leu Cys His Glu Gly Ser Leu His Leu Arg Gln Gly
35 40 45

Gln Ile Pro Gly Pro Arg Leu Val Leu Gln Phe Val Gln Gln Ala Gly
50 55 60

Val Cys Gly Pro Gly Met Gln Phe Ile Leu Leu Gln Glu Ile Leu Pro
65 70 75 80

Pro Leu Cys Pro Gly Glu His Gln Cys Phe Ser Ser Gly Asn Ser Ala
85 90 95

Arg Leu Gly Glu Lys Glu Ser Ser Ile Lys Glu Asp Pro Gln Pro Ala
100 105 110

Arg Phe Ser Asp Val Ser Ala Thr Gly Ala Arg Ser Ser Gly Gly Thr
115 120 125

Leu His Arg Ala Pro Gly Pro Ala Cys Ala Arg Asp Ala Ala Glu Leu
130 135 140

Gly Ala Ala Met Pro Gly Leu Val Ser Gly Pro Leu Gly Ala Ala Leu
145 150 155 160

Gln Pro Arg Gly Ala Gly Val Gln Leu Gly Ala Ala Thr Gly Pro Gly

165 170 175

Ser Cys Ser Lys Arg Val Val Gln Arg Gln Met Pro Asp Lys Thr Gln
180 185 190

Pro Gly Thr Arg Pro Gly Pro Pro Thr Cys Pro Ser Gly Pro Arg Pro
195 200 205

Glu

<210> 488
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K19E"

<400> 488
Met Gly Asn Ile Leu Thr Cys Cys Ile Asn Ser His Cys Gly Trp Pro
1 5 10 15

Arg Gly Glu Glu Asp Ala Pro Cys Tyr Glu Ser Asp Thr Asp Ile Tyr
20 25 30

Glu Thr Val Ala Ala Ala Thr Ser Glu Ser Thr Thr Val
35 40 45

<210> 489
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N456K"

<400> 489
Ile Met Leu Glu Glu Glu Pro Ser Ile Thr Ser Gly Glu Ser Gln Thr
1 5 10 15

Thr Tyr Ser Thr Phe Ser Ala Pro Leu Lys Lys Lys Ala Asn Arg Lys
20 25 30

Lys Leu Ile Glu Ser Leu Ser Pro Asp Phe Cys His Gln Asn Lys Gly
35 40 45

Leu Leu Leu Thr
50

<210> 490
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P272H"

<400> 490
Val Glu Tyr Pro Ile Cys Leu Val Cys Leu Arg Pro Arg Ser Pro Ser
1 5 10 15

Cys Pro Leu Pro Arg Tyr Arg Thr Gly His His Arg Leu Leu Ala Phe
20 25 30

Pro Gln Leu Leu Pro Cys Val Gln Gly Gln Glu Ser Gly Pro Leu Arg
35 40 45

Ile Gly Ile Gly
50

<210> 491
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.1225_1226insS"

<400> 491
Gly Arg Pro Gln Pro Pro Thr Leu Asp Pro Thr Ser Thr Ser Tyr Glu
1 5 10 15

Ser Gln Leu Gly Gln Asn Ser Ser Ser Ser Ser Glu Glu Ser Pro Lys
20 25 30

Lys Asp Thr Glu Pro Gly Ser Ser Pro Cys Ser Pro Glu Leu Gln Gly
35 40 45

Gly Thr Arg Arg Ala Ser
50

<210> 492
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T315P"

<400> 492
Leu Glu Leu Arg Ser Glu Gly Val Pro Cys Ile Ala Ser Gly Val Leu
1 5 10 15

Val Ser Tyr Pro Ser Val Gly Gly Ala Pro Pro Arg Pro Ser Ala Ser
20 25 30

Cys Gln Gln Gln Arg Ala Gly His Ser Asp Val Arg Leu Ser Ala His
35 40 45

His His Arg Met
50

<210> 493
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P890fs"

<400> 493
Leu Leu His Asn Pro Ala Phe Cys Ser Leu Ala Thr Thr Lys Arg Arg
1 5 10 15

His Gln Gln Thr Val Thr Ile Pro Pro Ser Pro Arg Cys Pro Phe His
20 25 30

Met Ser Ser Cys Arg
35

<210> 494
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R552Q"

<400> 494
Arg Thr Cys His Ala Leu Gln Glu Asp Glu Lys Leu Val Lys Lys Ala
1 5 10 15

Glu Lys Gln Val Thr Leu Ala Leu Gln Gln Gln Gln Arg Asn Leu His
20 25 30

Glu His Lys Val Ser Leu Val Glu Asn His Leu Ala Gly Leu Glu Gly
35 40 45

Arg Ala Leu Ala
50

<210> 495
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.R740L"

<400> 495
Ile Ile Ser Ser Gln Asn Tyr Thr Ser Thr Gly Gln Leu Gln Trp Leu
1 5 10 15

Leu Asn Thr Leu Tyr Asn His Gln Gln Leu Leu Gly Arg Gly Ser Pro
20 25 30

Cys Ile Gln Cys Arg Tyr Asp Ser Tyr Arg Leu Leu Gln Tyr Asp Leu
35 40 45

Asp Ser Pro Leu
50

<210> 496
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R217C"

<400> 496
Ser Trp Leu Asp Asn Asn Gly Lys Ser Ala Val Lys Lys Leu Lys Asn
1 5 10 15

Ser Leu Pro Leu Arg Lys Glu Leu Asp Cys Cys Leu Lys Asp Glu Leu
20 25 30

Ser His Gln Leu Gln Leu Ser Asp Ile Arg Trp Gln Arg Ser Trp Gly
35 40 45

Ile Ala His Arg
50

<210> 497
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D227E"

<400> 497
Ala Glu Arg Arg Thr Ser Glu Gln Ile Thr His Arg Leu Ser Lys Leu
1   5   10   15

Ser Glu Arg Arg Pro Ser Val Gln Ile Glu Glu Ser Gly Ser Ser Val
            20   25   30

Pro Ser Asp Gln Ser Pro Ser Val Gln Ile Asp Ser Gly Ser Ser Val
        35   40   45

Pro Ser Asp Gln
    50

<210> 498
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R333W"

<400> 498
Leu Ala Leu Ala Gln Glu Phe Gln Met Lys Thr Val Thr Val Ser Leu
1   5   10   15

Glu Asp His Thr Phe Ala Asp Val Val Trp Trp Leu Val Ser Asn Ala
            20   25   30

Ser Met Leu Val Ser Met His Gly Ala Gln Leu Val Thr Thr Leu Phe
        35   40   45

Leu Pro Arg Gly
    50

<210> 499
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R185Q"

<400> 499
Ser Asn Met Pro Leu Asn Asn Ser Ser Gln Glu Val Thr Lys Asp Leu
1 5 10 15

Leu Asp Met Ile Asp His Thr Ser Ile Gln Gln Thr Ile Glu Glu Leu
20 25 30

Ala Gly Lys Ile Glu Phe Glu Asn Glu Leu Asn His Met Cys Gly His
35 40 45

Cys Gln Asp Ser
50

<210> 500
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S6L"

<400> 500
Met Ser Ala Ala Ala Leu Leu Pro Ala Ser Glu Arg Gly Trp Lys Ser
1 5 10 15

Glu Lys Leu Asp Glu Ala Gln Ala Leu Ala Arg Ser Cys Ala Ala Arg
20 25 30

<210> 501
<211> 52
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<220>
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<223> /note="p.E800Q"

<400> 501
Ser Lys Asp Thr Glu Ala His Ile Ser Glu Pro Glu Asp Leu Gly Lys
1 5 10 15

Ile Arg Ser Pro Pro Pro Asp His Val Gln Gln Val Glu Thr Ala Arg
20 25 30

Glu Gly Lys Gln Tyr Trp Asn Pro Arg Asn Ser Ser Glu Leu Ser Gly
35 40 45

Leu Val Asn Thr
50

<210> 502
<211> 30
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<400> 502
Met Glu Val Asn Asn Ile Asn Gly Glu Ser Arg Ser Thr Leu Thr Thr
1 5 10 15

Leu Pro Phe Pro Gly Ala Glu Ala Asn Ser Pro Gly Lys Ala
20 25 30

<210> 503
<211> 52
<212> PRT
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<220>
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<223> /note="p.R114Q"

<400> 503
Leu Phe Phe Trp Ser Phe Asn Gly Leu Leu Leu Val Val Asp Thr Thr

240

1 5 10 15

Gly Lys Pro Asn Phe Ile Ser Arg Tyr Gln Gln Ile Gln Val Gly Lys
20 25 30

Asn Glu Pro Val Asp Pro Val Lys Leu Arg Gln Ser Ile Arg Thr Val
35 40 45

Leu Phe Asn Gln
50

<210> 504
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.Q245R"

<400> 504
Pro Arg Ala Ala Gly Ala Pro Arg Pro Arg Leu Leu Leu Arg Thr Gly
1 5 10 15

Ser Leu Asp Glu Ser Leu Gly Pro Leu Arg Arg Ala Ala Ala Gly Phe
20 25 30

Val Gln Thr Ala Leu Ala Arg Lys Leu Ser Pro Glu Ala Pro Ala Pro
35 40 45

Ser Ser Ala Thr
50

<210> 505
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<220>
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<220>
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<400> 505
Arg Thr Gly Ala Ile Asn Glu Cys Val Thr Phe Ile Phe Asn Arg Tyr
1 5 10 15

Ala Lys Lys Leu Gln Val Ser Arg His Thr Thr Lys Phe Gly Tyr Gly
20 25 30

Val Leu Val Thr Arg Val Ala Ser Thr Ala Ala Gly Gly Ile Ala Leu
35 40 45

Lys Lys Ser Gly
50

<210> 506
<211> 34
<212> PRT
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<220>
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<220>
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<400> 506
Gly Met Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu
1 5 10 15

Lys Asn Glu Pro Gln Arg Pro Pro Pro Ala Val Ser Ser Pro Tyr Ser
20 25 30

Cys Val

<210> 507
<211> 52
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<220>
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<223> /note="p.R687S"

<400> 507
Gly Met Ser Leu Glu Gly Pro Ser Ala Phe Leu Cys Gly Ser Ser Leu
1 5 10 15

Lys Trp Ser Pro Glu Met Lys Asn Ala Ser Ser Cys Val Gln Lys Glu
20 25 30

Asn Pro Leu Thr Gln Ala Val Pro Lys Cys Gln Arg Trp Glu Lys Leu
35 40 45

Gln Asn Ser Arg
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<210> 508
<211> 43
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 508
Gly Ser Ser Ser Glu Glu Glu Asp Ser Gly Lys Gln Ala Leu Ala Pro
1 5 10 15

Gly Leu Ser Pro Ser Gln Arg Pro Gly Val Pro Ala Leu Pro Val Ala
20 25 30

Gly Ala Leu Arg Arg Arg Arg Lys Arg Met Cys
35 40

<210> 509
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<223> /note="p.L179fs"

<400> 509

Arg Ala Arg Glu Leu Thr Val Gln Lys Ala Glu Ala Leu Met Arg Glu
1 5 10 15

Leu Asp Glu Glu Gly Ser Asp Pro Pro Cys Arg Gly Gly Pro Ser Ala
20 25 30

Ser Asp Arg Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg
35 40 45

Gly Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu
50 55 60

Leu Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys
65 70 75 80

Gly Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu
85 90 95

Pro Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr
100 105 110

Ala Val Thr Val Met Ala Gly Ser Val Pro Ser Ala Gln Ser Val Asp
115 120 125

Ala Leu Glu Ser Pro Gly Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro
130 135 140

Arg Asn Leu Leu Trp Arg Glu Met Ser Ile Phe Leu Pro Gly Ile Phe
145 150 155 160

<210> 510
<211> 52
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.E30K"

<400> 510
Ser Lys Glu Leu Gln Gly Ala Thr His Arg Tyr Ala Pro Cys Asp Trp
1 5 10 15

Tyr Tyr His Val Pro Val Lys Arg Ser Lys Lys Lys Ala Val Asp Ala

20 25 30

Pro Pro Ala Ser Gln Ile Pro Gly Leu Ser Asn Leu Gly Asp Ser His
35 40 45

Ser Glu Asn Leu
50

<210> 511
<211> 52
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G140W"

<400> 511
His Gln His Ile Leu Thr Gln His Gly Tyr Thr Val Val Ile Ala Glu
1 5 10 15

Glu Arg Leu Asn Ala Gly Leu Gly Pro Trp Trp Leu Leu Glu Gln Gly
20 25 30

Asp Leu Gly Ser Trp Asp Leu Leu Ile Cys Leu Ser Ser Lys Lys Ala
35 40 45

Glu Gly Thr Pro
50

<210> 512
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R238L"

<400> 512
Pro Ser Val Cys Leu Asp Gln Gly Met Gln Leu Lys Pro Ser Thr Ser
1 5 10 15

Ser His Leu Leu Lys Thr Val Lys Pro Leu Leu Val Trp Lys Pro Gly
20 25 30

Asp Trp Ser Arg Glu Gln Leu Asn Glu Thr Thr Val Leu Ala Pro His
35 40 45

Glu Thr Ile Phe
50

<210> 513
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A10T"

<400> 513
Met Trp Thr Glu Glu Ala Gly Ala Thr Thr Thr Glu Ala Gln Glu Ser
1 5 10 15

Gly Ile Arg Asn Lys Ser Ser Ser Ser Ser Gln Ile Pro Val Val Gly
20 25 30

Val Val Thr Glu
35

<210> 514
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P342fs"

<400> 514
Gly Tyr Glu Thr His Leu Glu Thr Thr Gly His Lys Lys Met Pro Gln
1 5 10 15

Ala Phe Glu Pro Pro Met Pro Pro Pro Ala Asn Pro Gln Leu Leu Cys
20 25 30

Gln Asn Pro Glu Lys Leu Ala Leu Lys Glu Asp Leu Leu Tyr Leu Arg
35 40 45

Thr Ser Gly Glu Pro Trp Asp Thr Glu Arg Asn Leu Arg Pro Leu Ser
50 55 60

Leu Gln Cys Gln Ser Leu Ala Leu Pro
65 70

<210> 515
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R136W"

<400> 515
Ile Thr Asn His Arg Glu Lys Lys Leu Gln Gln Ser Thr Lys Tyr Trp
1 5 10 15

Cys Leu Asn Gln Ser Ala Glu Ser Leu Trp Trp Ile Cys Ala Met Arg
20 25 30

Gly Gly Glu Asn Arg Pro Pro Ala Arg Val Gln Ser Ser Ser Glu Glu
35 40 45

Leu Glu Leu Arg
50

<210> 516
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.R145fs"

<400> 516
Asn Gly Asp Gly Glu Ile Thr Leu Val Glu Leu Gln Gln Ala Met Gln
1 5 10 15

Arg Leu Leu Gly Glu Arg Leu Thr Pro Gly Arg Ser Leu Arg Leu Ser
20 25 30

Gly Arg Leu Met Leu Met Glu Thr Ala Gln Leu Thr Leu Lys Ser Leu
35 40 45

<210> 517
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S720Y"

<400> 517
Ser Leu Met Asp Lys Ala Phe Asp Pro Thr Arg Arg Gln Trp Tyr Leu
1 5 10 15

His Ala Val Ala Asn Pro Gly Leu Ile Tyr Tyr Leu Thr Gly Pro Tyr
20 25 30

Leu Asp Val Gly Gly Ala Gly Tyr Val Val Thr Ile Ser His Thr Ile
35 40 45

His Ser Ser Ser
50

<210> 518
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T665M"

<400> 518
Asn Phe Asp Glu Gly Thr Pro Pro Thr Asn Phe Asp Thr Phe Pro Ala
1 5 10 15

Ala Ile Met Thr Val Phe Gln Ile Leu Met Met Gly Glu Asp Trp Asn
20 25 30

Glu Val Met Tyr Asp Gly Ile Lys Ser Gln Gly Gly Val Gln Gly Gly
35 40 45

Met Val Phe Ser
50

<210> 519
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.S772Y"

<400> 519
Glu Val Ser Pro Leu Ser Ala Ala Asn Met Ser Ile Ala Val Lys Glu
1 5 10 15

Gln Gln Lys Asn Gln Lys Pro Ala Lys Tyr Tyr Val Trp Glu Gln Arg
20 25 30

Thr Ser Glu Met Arg Lys Gln Asn Leu Leu Ala Ser Arg Glu Ala Leu
35 40 45

Tyr Asn Glu Met
50

<210> 520
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S710L"

<400> 520
Arg Arg Ser Thr Phe Asp Asn Phe Pro Gln Ser Leu Leu Thr Val Phe
1 5 10 15

Gln Ile Leu Thr Gly Glu Asp Trp Asn Leu Leu Val Met Tyr Asp Gly
20 25 30

Ile Met Ala Tyr Gly Gly Pro Ser Phe Pro Gly Met Leu Val Cys Ile
35 40 45

Tyr Phe Ile Ile
50

<210> 521
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<220>
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<223> /note="p.R1073L"

<400> 521
Ala Lys Ser Asn Pro Glu Glu Cys Arg Gly Leu Phe Ile Leu Tyr Lys
1 5 10 15

Asp Gly Asp Val Asp Ser Pro Val Val Leu Leu Glu Arg Ile Trp Gln
20 25 30

Asn Ser Asp Phe Asn Phe Asp Asn Val Leu Ser Ala Met Met Ala Leu
35 40 45

Phe Thr Val Ser
50

<210> 522
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A352E"

<400> 522
Ala Lys Gly Ile Thr Asp Tyr Lys Lys Gly Phe Ser Phe Ala Phe Glu
1 5 10 15

Gln Leu Leu Asn Tyr Asn Val Ser Arg Glu Glu Asn Cys Asn Lys Ile
20 25 30

Ile Met Leu Phe Thr Asp Gly Gly Glu Glu Arg Ala Gln Glu Ile Phe
35 40 45

Asn Lys Tyr Asn
50

<210> 523
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.A332T"

<400> 523
Cys Leu Asn Gly Thr Leu Val Gln Ala Asp Arg Thr Asn Lys Glu His
1 5 10 15

Phe Arg Glu His Leu Asp Lys Leu Phe Thr Thr Lys Gly Ile Gly Met
20 25 30

Leu Asp Ile Ala Leu Asn Glu Ala Phe Asn Ile Leu Ser Asp Phe Asn
35 40 45

His Thr Gly Gln
50

<210> 524
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.R608H"

<400> 524
Ala Ser His Arg Asp His Asn His Arg Asp Glu Thr His Gly Ser Ser
1 5 10 15

Asp His Arg His Arg Glu Ser Arg His His His Ser Arg Asp Val Asp
20 25 30

Arg Glu Gln Asp His Asn Glu Cys Asn Lys Gln Arg Ser Arg His Lys
35 40 45

Ser Lys Asp Arg
50

<210> 525
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V134I"

<400> 525
Ile Leu Ser Val Thr Leu Leu Phe Phe Gly Gly Leu Cys Val Ala Ala
1 5 10 15

Ser Glu Phe His Arg Ser Arg His Asn Ile Ile Ile Leu Ser Ala Gly
20 25 30

Ile Phe Phe Val Ser Ala Gly Leu Ser Asn Ile Ile Gly Ile Ile Val
35 40 45

Tyr Ile Ser Ala
50

<210> 526

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A138V"

<400> 526
Thr Leu Leu Phe Phe Gly Gly Leu Cys Val Ala Ala Ser Glu Phe His
1 5 10 15

Arg Ser Arg His Asn Val Ile Leu Ser Val Val Gly Ile Phe Phe Val
20 25 30

Ser Ala Gly Leu Ser Asn Ile Ile Gly Ile Ile Val Tyr Ile Ser Ala
35 40 45

Asn Ala Gly Asp
50

<210> 527
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R232W"

<400> 527
Leu Arg Ala Lys Ser His Ser Glu Phe Leu Lys Lys Ser Thr Phe Ala
1 5 10 15

Arg Leu Pro Pro Tyr Arg Tyr Arg Phe Trp Trp Arg Arg Ser Ser Ser
20 25 30

Arg Ser Thr Glu Pro Arg Ser Arg Asp Leu Ser Pro Ile Ser Lys Gly
35 40 45

Phe His Thr Ile
50

<210> 528
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G121R"

<400> 528
Met Ile Arg Ser Ala Thr Pro Phe Pro Leu Val Ser Leu Phe Phe Met
1 5 10 15

Phe Ile Gly Phe Ile Leu Asn Asn Ile Arg Arg His Ile Arg Pro His
20 25 30

Arg Thr Ile Leu Ala Phe Val Ser Gly Ile Phe Phe Ile Leu Ser Gly
35 40 45

Leu Ser Leu Val
50

<210> 529
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V146G"

<400> 529
Leu Arg Val Val Arg Ala Ser Ser Ile Phe Pro Ile Leu Ser Ala Ile
1 5 10 15

Leu Leu Leu Leu Gly Gly Val Cys Val Gly Gly Ala Ser Arg Val Tyr
20 25 30

Lys Ser Lys Arg Asn Ile Ile Leu Gly Ala Gly Ile Leu Phe Val Ala
35 40 45

Ala Gly Leu Ser
    50

<210> 530
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.S190L"

<400> 530
Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg Trp Phe
1   5   10   15

Lys Gly Asn Thr Glu Leu Lys Gly Lys Leu Leu Glu Val Glu Glu Trp
            20   25   30

Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His Lys
        35   40   45

Glu Asp Asp Gly
    50

<210> 531
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R959S"

<400> 531
Asp Ala Ala Leu Glu Val Gln Pro Pro Asp Thr Trp Asp Ser Phe Pro
1   5   10   15

Leu Phe Gln Leu Leu Asn Asp Phe Leu Ser Ser Thr Asp Tyr Asn Leu
            20   25   30

Cys Asn Gly Lys Phe His Lys His Leu Gln Asp Leu Phe Ala Pro Leu
35 40 45

Val Val Arg Tyr
50

<210> 532
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A1073T"

<400> 532
Pro Ser Trp Met Ala Ala Ile Tyr Asp Ala Asp Asn Gly Ser Gly Thr
1 5 10 15

Ser Glu Asp Leu Phe Trp Lys Leu Asp Thr Thr Leu Gln Thr Phe Ile
20 25 30

Arg Asp Leu His Trp Pro Glu Glu Glu Phe Gly Lys His Leu Glu Gln
35 40 45

Arg Leu Lys Leu
50

<210> 533
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K60N"

<400> 533
Tyr Ile Glu Gly Lys Glu Leu Glu Asn Phe Phe Gln Glu Leu Glu Lys
1 5 10 15

Ala Arg Lys Gly Ser Gly Met Met Ser Asn Asn Ser Asp Asn Phe Gly

20 25 30

Glu Lys Met Lys Glu Phe Met Gln Lys Tyr Asp Lys Asn Ser Asp Gly
35 40 45

Lys Ile Glu Met
50

<210> 534
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R258C"

<400> 534
Lys Glu Met Asn Ile Gln Gln Leu Thr Asn Tyr Arg Lys Ser Val Met
1 5 10 15

Ser Leu Ala Glu Ala Gly Lys Leu Tyr Cys Cys Lys Asp Leu Glu Ile
20 25 30

Val Leu Cys Ser Glu Pro Pro Met
35 40

<210> 535
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R81T"

<400> 535
Asp Tyr Val Gln Met Lys Ala Ser Glu Leu Lys Gln Glu Gln Glu Thr
1 5 10 15

Gln Gly Ser Ser Ser Ala Ala Gln Lys Thr Thr Ala Cys Asn Thr Ala
20 25 30

Thr Cys Val Thr His Arg Leu Ala Gly Leu Leu Ser Arg Ser Gly Gly
35 40 45

Met Val Lys Ser
50

<210> 536
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E340K"

<400> 536
Glu Arg Met Arg Glu Glu Glu Lys Arg Ala Ala Glu Glu Arg Gln Arg
1 5 10 15

Ile Lys Glu Glu Glu Lys Arg Ala Ala Lys Lys Glu Arg Gln Arg Ile
20 25 30

Lys Glu Glu Glu Lys Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu
35 40 45

Glu Glu Lys Arg
50

<210> 537
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V231I"

<400> 537
Leu Asn Glu Thr Ser Gly Asn Cys Gln Thr Glu Phe Glu Gly Val His
1 5 10 15

Ser Gln Lys Gln Asn Arg Gln Thr Cys Ile Ile Arg Lys Ser Leu Ile
20 25 30

Cys Ala Phe Ala Met Ala Phe Ile Ile Ser Val Met Leu Ile Ala Ala
35 40 45

Asn Gln Ile Leu
50

<210> 538
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G131V"

<400> 538
Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile Leu
1 5 10 15

Glu Ala Val Leu His Cys His Gln Met Val Val Val Val His Arg Asp
20 25 30

Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala
35 40 45

Val Lys Leu Ala
50

<210> 539
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T466fs"

<400> 539

Arg His Arg Ser Asn Ser Leu Thr Arg Val Asp Gly Gln Pro Arg Gly
1 5 10 15

Ala Ala Ile Ala Trp Pro Glu Lys Lys Asn Gln Ala Cys Val Pro Ala
20 25 30

Asn Thr Phe Cys Ser Thr Ser Arg Cys Glu Leu
35 40

<210> 540
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T466fs"

<400> 540
Arg His Arg Ser Asn Ser Leu Thr Arg Val Asp Gly Gln Pro Arg Gly
1 5 10 15

Ala Ala Ile Ala Trp Pro Glu Lys Lys Pro Gly Leu Arg Pro Ser Gln
20 25 30

His Leu Leu Leu Tyr Ile Thr Leu Arg Val Val Lys Trp Ile Pro Ala
35 40 45

Leu Ala Thr Ala Ser Ala Trp Pro Ala Pro Ser Ala Lys Thr Val Trp
50 55 60

His Pro Thr Leu Leu Ile
65 70

<210> 541
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.K131R"

<400> 541
Arg Ile Ala Val Ile Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu
1 5 10 15

Glu Asn Thr Trp Phe Ser Tyr Leu Lys Arg Arg Gly Tyr Leu Thr Leu
20 25 30

Ser Asp Ser Gly Asp Lys Val Ala Val Glu Trp Asp Lys Asp His Gly
35 40 45

Val Leu Glu Ser
50

<210> 542
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.LV303del"

<400> 542
Leu His Thr Ser Ser Glu Leu Gln Ser Pro Ser Ser Tyr Phe Ala Ser
1 5 10 15

Arg Pro Trp Val Arg Ala Lys Gly Leu Leu Gly Phe Pro Val Leu Thr
20 25 30

Leu His Pro Pro Leu Pro Ser Gly Cys Ser
35 40

<210> 543
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E13K"

<400> 543
Met Glu Val Gln Val Ser Gln Ala Ser Leu Gly Phe Lys Lys Leu Thr
1 5 10 15

Ser Val Glu Lys Ser Leu Arg Glu Trp Ser Arg Leu Ser Arg Glu Val
20 25 30

Ile Ala Trp Leu Cys Pro Ser
35

<210> 544
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R423Q"

<400> 544
Ile Glu Lys Asp Lys Tyr Arg Lys Gln Ile Arg Glu Leu Glu Glu Lys
1 5 10 15

Asn Asp Glu Met Arg Ile Glu Met Val Gln Gln Arg Glu Ala Cys Ile
20 25 30

Val Asn Leu Glu Ser Lys Leu Arg Arg Leu Ser Lys Asp Ser Asn Asn
35 40 45

Leu Asp Gln Ser
50

<210> 545
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 545
Leu Asp Asp Asp Ser His Glu Arg Tyr Ser Phe Gly Pro Ser Ser Ile
1 5 10 15

His Ser Ser Ser Ser Ser His Gln Ser Lys Lys Gly Leu Asp Ala Tyr
20 25 30

Asp Leu Glu Gln Val Asn Leu Met Phe Arg Lys Phe Ser Leu Glu Arg
35 40 45

Pro Phe Arg Pro
50

<210> 546
<211> 52
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<400> 546
Ser Lys Ile Asn Arg Ala Gly Arg Leu Leu Asp Ile Leu His Thr Lys
1 5 10 15

Gly Gln Arg Gly Tyr Val Val Phe Leu Asp Asp Ser Leu Glu Phe Tyr
20 25 30

Tyr Pro Glu Leu Tyr Lys Leu Val Thr Gly Lys Glu Pro Thr Arg Arg
35 40 45

Phe Ser Thr Ile
50

<210> 547
<211> 52
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<400> 547
Ala Asn Ile Glu Ala Val Ala Ala Lys Asn Lys His Cys Leu Leu Glu
1 5 10 15

Ala Gly Ile Gly Cys Thr Arg Asp Leu Met Met Lys Ser Asn Ile Tyr
20 25 30

Pro Ile Val Leu Phe Ile Arg Val Cys Glu Lys Asn Ile Lys Arg Phe
35 40 45

Arg Lys Leu Leu
50

<210> 548
<211> 52
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<220>
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<400> 548
Leu Gln Asn His Thr Asp Phe Lys Asp Lys Ile Val Leu Asp Val Gly
1 5 10 15

Cys Gly Ser Gly Ile Leu Ser Phe Phe Val Val Ala Gln Ala Gly Ala
20 25 30

Arg Lys Ile Tyr Ala Val Glu Ala Ser Thr Met Ala Gln His Ala Glu
35 40 45

Val Leu Val Lys
50

<210> 549
<211> 52
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<220>
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<223> /note="p.R54Q"

<400> 549
Glu Arg Arg Leu Lys Glu Glu Glu Glu Ala Arg Leu Lys Tyr Glu Lys
1 5 10 15

Glu Glu Met Glu Arg Leu Glu Ile Gln Gln Gln Ile Glu Lys Glu Lys
            20 25 30

Trp His Arg Leu Glu Ala Lys Asp Leu Glu Arg Arg Asn Glu Glu Leu
        35 40 45

Glu Glu Leu Tyr
    50

<210> 550
<211> 52
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<400> 550
Met Asn Leu Pro His Pro Gly Leu His Pro His Gln Thr Pro Ala Pro
1 5 10 15

Leu Pro Asn Pro Gly Leu Tyr Pro Pro Leu Leu Val Ser Met Ser Pro
            20 25 30

Gly Gln Pro Pro Pro Gln Gln Leu Leu Ala Pro Thr Tyr Phe Ser Ala
        35 40 45

Pro Gly Val Met
    50

<210> 551
<211> 52
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<223> /note="p.P645L"

<400> 551
Thr Tyr Phe Ser Ala Pro Gly Val Met Asn Phe Gly Asn Pro Ser Tyr
1 5 10 15

Pro Tyr Ala Pro Gly Ala Leu Pro Pro Leu Leu Pro Pro Pro His Leu
20 25 30

Tyr Pro Asn Thr Gln Ala Pro Ser Gln Val Tyr Gly Gly Val Thr Tyr
35 40 45

Tyr Asn Pro Ala
50

<210> 552
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.S658L"

<400> 552
Pro Ser Tyr Pro Tyr Ala Pro Gly Ala Leu Pro Pro Pro Pro Pro Pro
1 5 10 15

His Leu Tyr Pro Asn Thr Gln Ala Pro Leu Leu Gln Val Tyr Gly Gly
20 25 30

Val Thr Tyr Tyr Asn Pro Ala Gln Gln Gln Val Gln Pro Lys Pro Ser
35 40 45

Pro Pro Arg Arg
50

<210> 553
<211> 52
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<223> /note="p.S232F"

<400> 553
Arg Gln Arg Lys Leu Trp Lys Asp Glu Gly Arg Trp Glu His Asp Lys
1 5 10 15

Phe Arg Glu Asp Glu Gln Ala Pro Lys Phe Phe Arg Gln Glu Leu Ile
20 25 30

Ala Leu Tyr Gly Tyr Asp Ile Arg Ser Ala His Asn Pro Asp Asp Ile
35 40 45

Lys Pro Arg Arg
50

<210> 554
<211> 45
<212> PRT
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<223> /note="p.F781fs"

<400> 554
Asp Leu Ala Gln Ile Ile Ile Pro Lys Asp Asn Ser Ser Leu Leu Lys
1 5 10 15

Arg Leu Ala Cys Ile Ala Ala Phe Phe Val Asp Ser Ser Ser Tyr His
20 25 30

Pro Phe Lys Ile Asn Gln Asn Ile Arg Phe Gln Lys Phe
35 40 45

<210> 555
<211> 31
<212> PRT
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polypeptide"

<220>
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<223> /note="p.R5W"

<400> 555
Met Ser Asn Pro Trp Trp Ser Leu Glu Glu Glu Lys Tyr Asp Met Ser
1 5 10 15

Gly Ala Arg Leu Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu
20 25 30

<210> 556
<211> 42
<212> PRT
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polypeptide"

<220>
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<223> /note="p.R23fs"

<400> 556
Met Ala Ala Val Pro Arg Val Glu Gly Val Phe Ile Phe Leu Ile Glu
1 5 10 15

Asp Ser Gly Lys Lys Lys Gly Val Arg Ile Leu Lys Leu Cys Ser Lys
20 25 30

Val Ser Phe Arg Val Asp Trp Ile Thr Ser
35 40

<210> 557
<211> 97
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polypeptide"

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<223> /note="p.R471fs"

<400> 557
Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met
1 5 10 15

Pro Gln Pro Thr Phe Thr Leu Arg Lys Asn Leu Ser Ser Leu Leu Ile
20 25 30

Asp Gly Ala Ile Leu Phe Val Leu Phe Cys Phe Val Phe Leu Arg Gln
35 40 45

Asn Leu Ala Leu Ser Pro Arg Leu Glu Cys Ser Gly Val Ile Ser Ala
50 55 60

His Arg Lys Leu Arg Leu Pro Gly Ser Gly His Ser Pro Ala Ser Ala
65 70 75 80

Ser Arg Val Ala Gly Thr Thr Gly Ala Arg His His Thr Trp Leu Ile
85 90 95

Phe

<210> 558
<211> 52
<212> PRT
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<220>
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<220>
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<400> 558
Asp Asp Ala Leu Asp Lys Leu Ser Asp Ser Leu Gly Gln Arg Gln Pro
1 5 10 15

Asp Pro Asp Glu Asn Lys Pro Met Glu Glu Glu Lys Val Lys Glu Lys
20 25 30

Ala Lys Ala Glu His Arg Asp Lys Leu Gly Glu Arg Asp Asp Thr Ile
35 40 45

Pro Pro Glu Tyr
50

<210> 559
<211> 52
<212> PRT
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polypeptide"

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<223> /note="p.T425M"

<400> 559
Met Ile Val Glu Glu Val Arg Ala Ile Arg Phe Asn Gln Glu Gln Glu
1 5 10 15

Ser Glu Val Leu Asn Arg Arg Ser Ser Met Met Ser Gly Ser Leu Glu
20 25 30

Thr Thr Ser Ser Lys Asp Ile Arg Gln Met Ser Gln Gln Gln Asp Leu
35 40 45

Leu Ser Ala Leu
50

<210> 560
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.E152K"

<400> 560
Phe Asp Glu Glu Arg Ala Gln Gln Glu Asp Ala Leu Ala Gln Gln Ala
1 5 10 15

Phe Glu Glu Ala Arg Arg Arg Thr Arg Lys Lys Phe Glu Asp Arg Asp
20 25 30

Arg Ser His Arg Glu Glu Met Glu Val Arg Val Ser Gln Leu Leu Ala
35 40 45

Val Thr Gly Lys
50

<210> 561
<211> 76
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 561
Pro Ile Lys Ile Tyr Gly Arg Met Ile Pro Cys Lys His Val Phe Cys
1 5 10 15

Tyr Asp Cys Ala Ile Leu His Glu Lys Arg Glu Ile Arg Cys Val Gln
20 25 30

Ala Val Val Ile Leu Cys Ser Glu Leu Ser Ser Val His Glu Val Leu
35 40 45

Ser Ser Cys Val Ala Leu Phe Lys Gly Ala Arg Glu His Ile Cys Leu
50 55 60

Arg Glu Thr Tyr Arg Leu Ile Ser Thr Ile Ala Ile
65 70 75

<210> 562
<211> 59
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 562
Glu Cys Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro
1 5 10 15

Gly Gly Ala Ala Leu Gly Glu Ala Pro Leu Gly Glu Trp His Leu Leu
20 25 30

Arg Ser Glu Ala Thr Thr Met Ser Gln Gln Gly Lys Pro Ala Met Ala
35 40 45

Pro Val Gly Pro Ser Thr Ser Thr Arg Ser Trp
50 55

<210> 563
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<223> /note="p.E102fs"

<400> 563
Glu Ser Gly Glu Gly Ser Ala Leu Glu Lys Ser Leu Ala Val Ser Gln
1 5 10 15

Gly Gly Glu Leu Tyr Glu Glu Trp Leu Gly Thr
20 25

<210> 564
<211> 52
<212> PRT
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<220>
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<220>
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<400> 564
Glu Ser Gln Glu Asp Glu Lys Leu Leu Gln Ala Thr Glu Lys Phe Gln
1 5 10 15

Ala Glu Cys Ala Leu Lys Phe Pro Asn Cys Cys Gln Cys Leu Thr Thr
20 25 30

Val Ile Asp Ile Ser Gly Lys Thr Val Phe Ile Thr Arg Tyr Leu Lys

35 40 45

Pro Leu Asn Pro
50

<210> 565
<211> 29
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<220>
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<400> 565
Leu Glu Arg Asp Pro Thr Pro Cys Glu Leu Thr Tyr Lys Val Pro Thr
1 5 10 15

Arg His Ser Met Ser Gln Ile Pro Pro Ser Ser Pro Leu
20 25

<210> 566
<211> 52
<212> PRT
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<223> /note="p.R417L"

<400> 566
Gly Ile Lys Gly Gly Ile Arg Arg Trp Asn Tyr Phe Phe Pro Glu Glu
1 5 10 15

Leu Leu Val Tyr Asp Ile Cys Lys Tyr Leu Leu Trp Cys Glu Asn Ile
20 25 30

Gly Arg Ala His Lys Ser Asn Asn Ile Met Ile Leu Val Asp Leu Lys
35 40 45

Asn Glu Val Trp
50

<210> 567
<211> 34
<212> PRT
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<220>
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<400> 567
Met Glu Val Lys Gly Gln Leu Val Val Ser Ser Pro Thr Phe Asn Ala
1 5 10 15

Pro Ala Ala Leu Phe Gly Glu Ala Ala Pro Gln Val Lys Ser Glu Arg
20 25 30

Leu Arg

<210> 568
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W397L"

<400> 568
Ile Glu Gln Ala Gln Lys Leu Thr Ala Thr Gln Ser His Leu Glu Asn
1 5 10 15

Arg Lys Gln Gln Leu Gln Gln Glu Gln Leu Leu Tyr Leu Glu Ser Leu
20 25 30

Ile Gln Ala Arg Gln Arg Leu Gln Gly Ser His Asn Gln Cys Leu Asn
35 40 45

Arg Gln Asp Val
50

<210> 569
<211> 52
<212> PRT
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polypeptide"

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<223> /note="p.R838C"

<400> 569
Asn Ile Tyr Val Asp Ala Leu Leu Lys Glu Phe Glu Gln Phe Asn Arg
1 5 10 15

Arg Leu Asn Glu Val Ser Lys Arg Val Cys Cys Ile Pro Leu Pro Val
20 25 30

Ser Asn Ile Leu Trp Glu His Cys Ile Arg Leu Ala Asn Arg Thr Ile
35 40 45

Val Glu Gly Tyr
50

<210> 570
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E313K"

<400> 570
Ala Glu Lys Ala Lys Pro Asp Ala Leu His Gly Leu Arg Val His Ser
1 5 10 15

Trp Val Leu Val Leu Ser Gly Lys Arg Lys Lys Val Pro Glu Asn Phe
20 25 30

Phe Ile Asp Pro Phe Thr Gly His Ser Tyr Ser Thr Gln Asp Glu His
35 40 45

Phe Leu Gly Ile
    50

<210> 571
<211> 52
<212> PRT
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<220>
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<223> /note="p.S1264L"

<400> 571
Asn Thr Thr Ser Ile Lys Thr Gln Met Glu Leu Thr Ile Lys Asp Leu
1   5   10   15

Glu Ser Glu Ile Ser Arg Ile Lys Thr Leu Leu Gln Ala Asp Phe Asn
            20   25   30

Lys Thr Glu Leu Glu Arg Tyr Lys Glu Leu Tyr Leu Glu Glu Val Lys
        35   40   45

Val Arg Glu Ser
    50

<210> 572
<211> 39
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.K420fs"

<400> 572
Lys Glu Glu Glu Lys Glu Lys Leu Trp Lys Lys Lys Glu Leu Leu Gln
1   5   10   15

Arg Ala Glu Lys Lys Lys Lys Ile Lys Asn Thr Gly Pro Arg Lys Asn
            20   25   30

Arg Ser Gly Lys Lys Trp Lys

35

<210> 573
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P488H"

<400> 573
Ile Leu Pro Lys Tyr Gln Asp Gln Asn Phe Leu Pro Lys Asp Gln Asn
1 5 10 15

Phe Leu Ser Arg Asp Gln His Val Leu His His Lys Asp Gln Asp Ile
20 25 30

Leu Pro Lys Tyr Gln Asp Gln Asn Phe Leu Pro Lys Asp Gln Asn Phe
35 40 45

Leu Ser Arg Asp
50

<210> 574
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E153Q"

<400> 574
Gly Tyr Lys Lys Glu Ile Ser Lys Leu Tyr Gln Asp Met Gln Arg Lys
1 5 10 15

Val Glu Leu Asn Glu Glu Lys His Lys Gln Gln Leu Ile Glu Lys Lys
20 25 30

Glu Met Glu Ile Ser Glu Leu Asn Ala Lys Leu Arg Ser Gln Glu Lys
35 40 45

Glu Lys Gln Asn
    50

<210> 575
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.P200fs"

<400> 575
Gln Trp Asp Gly Ala Ala Leu Arg Leu His Ala Arg His Lys Glu Gln
1   5   10   15

Gln Arg Gln Phe Gly Leu Thr Pro Pro Trp Ile Phe Glu Ala Thr Ser
            20   25   30

Pro

<210> 576
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="p.P200fs"

<400> 576
Gln Gln Trp Asp Gly Ala Ala Leu Arg Leu His Ala Arg His Lys Glu
1   5   10   15

Gln Gln Arg Gln Phe Gly Leu Thr Pro Leu Asp Leu
            20   25

<210> 577
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A332S"

<400> 577
Lys Glu Leu Ser Asp Ile Trp Ser Ala Val His Val Leu Gln Asn Ser
1 5 10 15

Ile Asp Ser Leu Thr Leu Cys Ser Gly Ser Ser Cys Pro Lys Ala Ser
20 25 30

Ser Leu Arg Gly His Lys Gly His Gln Cys Leu Ser Pro Pro Leu Pro
35 40 45

Ser Trp Asp Ser
50

<210> 578
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D5020Y"

<400> 578
Gly Tyr Thr Leu Ser Asn Ser Lys Gly Pro Val Gln Pro Thr Ala Gln
1 5 10 15

Gly Glu Glu Lys Gly Gly Leu Arg Ile Tyr Tyr Met Glu Asp Lys Met
20 25 30

Leu Pro Lys Cys Thr Asp Leu Lys Ala Lys Gln Leu Leu Leu Ser Asp
35 40 45

Ile Leu Asn Thr
50

<210> 579
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K162R"

<400> 579
Leu Asp Asp Cys Ile Phe Asn Met Val Leu Leu Lys Val Pro Ser Ser
1 5 10 15

Leu Ser Ala Glu Glu Leu Glu Ala Ile Arg Arg Leu Ile Arg Phe Gly
20 25 30

Lys Lys Lys Asn Thr His Ser Leu Phe Val Phe Ile Ile Pro Glu Asn
35 40 45

Phe Lys Gly Cys
50

<210> 580
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R207L"

<400> 580
Lys Leu Arg Met Glu Gln Glu Glu Glu Leu Lys Asp Met Ser Lys Ile
1 5 10 15

Ile Leu Asn Ala Lys Cys His Ala Ile Leu Leu Asp Ala Gln Ile Leu
20 25 30

Glu Lys Gln Gln Ile Gln Lys Glu Leu Asp Thr Glu Glu Lys Arg Leu
35 40 45

Asp Gln Met Met

50

<210> 581
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R279L"

<400> 581
Arg Ile Arg Gly Arg Arg Gln Ile Val Glu Gln Met Glu Lys Asn Gln
1 5 10 15

Glu Glu Arg Ser Leu Leu Ala Glu Gln Leu Leu Glu Gln Glu Lys Glu
20 25 30

Gln Met Leu Glu Tyr Met Glu Gln Leu Gln Glu Glu Asp Leu Lys Asp
35 40 45

Met Glu Arg Arg
50

<210> 582
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R209I"

<400> 582
Ala Gln Asn Asp Leu Val Phe Glu Ala Val Gln Asp Lys Gly Asn Met
1 5 10 15

Glu Gln Ala Ile Leu Glu Met Lys Lys Ile Ile Phe Glu Ala Arg Gln
20 25 30

Gly Glu Phe Ile Glu Met Lys Ser Asn Leu Lys His Leu Glu Val Leu
35 40 45

Val Ala Gln Gln
    50

<210> 583
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R58C"

<400> 583
Phe Val Val His Thr Val Gln Phe Leu Asn Arg Phe Ser Thr Val Cys
1   5   10   15

Glu Glu Lys Leu Ala Asp Leu Ser Leu Cys Cys Ile Gln Gln Ile Glu
            20   25   30

Thr Thr Leu Asn Ile Leu Asp Ala Lys Leu Ser Ser Ile Pro Gly Leu
        35   40   45

Asp Asp Val Thr
    50

<210> 584
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R230H"

<400> 584
Gly Gln Lys Trp Glu His Phe Ile Thr Ala Pro Lys Thr Lys Lys Phe
1   5   10   15

Lys Ile Pro Thr Met Arg Val Thr Asn His His Lys Pro Ser Arg Arg
            20   25   30

Gly Ser Thr Leu Ser Leu Ser Arg Ala Ser Gly Gly Ser Ser Pro Gln
35 40 45

Ser Ser Met Ile
50

<210> 585
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N440T"

<400> 585
Ile Glu Gln Leu Glu Arg Glu Gly Asn Glu Glu Glu Ile Gln Arg Glu
1 5 10 15

Asn Tyr Gln Asp Asn Ile Ser Ser Met Thr Thr Ile Ser Ile Gln Asn
20 25 30

Thr Trp Lys His Leu His Ala Asp Arg Ile Gly Arg Gly Ser Lys Ala
35 40 45

Glu Asp Glu Asp
50

<210> 586
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R259I"

<400> 586
Asn Arg Glu Arg Lys Cys Lys Leu Lys Asp Gln Ser Asp Lys Glu Glu
1 5 10 15

Gly Thr Arg Asp Ile Ser Ser Pro Lys Ile Ile Leu Arg Asp Arg Gln
20 25 30

Ala Leu Phe Pro Ala Lys Val Thr Asn Val Ser Leu Leu Glu Lys Phe
35 40 45

Glu Arg Ser Glu
50

<210> 587
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.K677fs"

<400> 587
Ile Thr Cys Glu Lys Ile Glu Ala Leu Glu Gln Glu Asn Ser Glu Leu
1 5 10 15

Glu Arg Glu Asn Arg Lys Leu Lys Lys Asn Ile Gly
20 25

<210> 588
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P1851fs"

<400> 588
Gln Lys Leu Gly Ala Pro Glu Ala Leu Gly Gly Arg Glu Thr Gly Ser
1 5 10 15

His Thr Leu Gln Ser Pro Ala Pro Pro Gln Leu Pro
20 25

<210> 589

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L271M"

<400> 589
Gln Lys Lys Ser Ala Lys Glu Arg Lys Pro Ser Thr Thr Ser Ser Gly
1 5 10 15

Lys Tyr Glu Asp Ser Asp Gly Cys Tyr Met Met Gln Lys Thr Arg Pro
20 25 30

Pro Arg Lys Leu Glu Leu Arg Gln Leu Ser Thr Gly Ser Ser Ser Arg
35 40 45

Ala Asn Arg Ile
50

<210> 590
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V236M"

<400> 590
Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu Leu Leu
1 5 10 15

Phe Phe Ile Pro Gly Val Val Met Ala Met Met Ala Tyr Gly Leu Ile
20 25 30

Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp Ser
35 40 45

Asp Ser Gln Ser
50

<210> 591
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

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<223> /note="p.A932T"

<400> 591
Glu Thr Leu Leu Lys Lys Pro Leu Ala Leu Lys Met Ser Thr Ile Asn
1 5 10 15

Glu Ala Val Leu Phe Glu Asp Met Ile Thr Thr Leu Asn Glu Lys Pro
20 25 30

Thr Thr Gly Lys Glu Leu Ser Phe Lys Glu Pro Leu Ala Leu Gln Glu
35 40 45

Ser Pro Thr Tyr
50

<210> 592
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.S185I"

<400> 592
Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His
1 5 10 15

Tyr Thr Cys Ser Ser His Phe Pro Tyr Ile Ile Gln Tyr Gln Phe Trp
20 25 30

Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro
35 40 45

Leu Leu Val Met
50

<210> 593
<211> 52
<212> PRT
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<220>
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<223> /note="p.E214D"

<400> 593
Ile Phe Gly Gly Ile Ser Phe Phe Pro Leu Asp Lys Met Thr Tyr Leu
1 5 10 15

Lys Ile Gln Ser Phe Ile Asn Arg Met Asp Asp Glu Ser Leu Asn Ile
20 25 30

Val Lys Tyr Thr Ala Phe Leu Tyr Asn Asp Gln Leu Ile Trp Ser Gly
35 40 45

Leu Glu Gln Asp
50

<210> 594
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.R594Q"

<400> 594
Ser Asp Leu Lys Val Pro Leu Thr Val Thr Trp Gln Phe Gln Pro Ala
1 5 10 15

Ser Ser His Ile Phe His Gln Leu Ile Gln Gln Ile Thr His Asn Gly
20 25 30

Thr Ile Glu Trp Gly Asn Phe Leu Ser Arg Phe Gln Lys Lys Thr Lys
35 40 45

Val Ser Gln Ser
50

<210> 595
<211> 52
<212> PRT
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<220>
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<223> /note="p.D283Y"

<400> 595
Pro Asp Glu Thr Trp Met Phe Ile Thr Lys Lys Gln Thr Asp Gln Thr
1 5 10 15

Thr Leu Arg Ile Gln Pro Ala Val Lys Tyr Tyr Phe Gln Val Asn Ile
20 25 30

Thr Ala Asp Ser Leu Phe Ala Glu Gly Lys Pro Leu Glu Leu Val Cys
35 40 45

Leu Val Val Ser
50

<210> 596
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.L470Q"

<400> 596
Ala Tyr Phe Leu Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe
1 5 10 15

Lys Ser Pro Ser Lys Thr Tyr Ile Gln Gln Gln Lys Thr Arg Asp Glu

20 25 30

Asn Ile Lys Val Gly Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys
35 40 45

Arg Leu Lys Glu
50

<210> 597
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.V721M"

<400> 597
Ser Asp Met Glu Leu Arg Leu Val Gly Gly Ser Ser Arg Cys Ala Gly
1 5 10 15

Lys Val Glu Val Asn Val Gln Gly Ala Met Met Gly Ile Leu Cys Ala
20 25 30

Asn Gly Trp Gly Met Asn Ile Ala Glu Val Val Cys Arg Gln Leu Glu
35 40 45

Cys Gly Ser Ala
50

<210> 598
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N228T"

<400> 598
Ser Leu Asn Phe Asn Gly Asn Asn Val Lys Gly Ile Glu Leu Gly Ala
1 5 10 15

Phe Asp Ser Thr Ile Phe Gln Ser Leu Thr Thr Phe Gly Gly Thr Pro
20 25 30

Asn Leu Ser Val Ile Phe Asn Gly Leu Gln Asn Ser Thr Thr Gln Ser
35 40 45

Leu Trp Leu Gly
50

<210> 599
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.W41L"

<400> 599
Gly Asn Ser Glu His Ala Phe Gln Gly Pro Thr Ser Phe His Val Ile
1 5 10 15

Gln Thr Ser Ser Phe Thr Asn Ser Thr Leu Leu Ala Gln Thr Gln Gly
20 25 30

Ser Gly Trp Leu Asp Asp Leu Gln Ile His Gly Trp Asp Ser Asp Ser
35 40 45

Gly Thr Ala Ile
50

<210> 600
<211> 52
<212> PRT
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<220>
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<223> /note="p.R89C"

<400> 600
Thr Ile Ile Phe Leu His Asn Trp Ser Lys Gly Asn Phe Ser Asn Glu
1 5 10 15

Glu Leu Ser Asp Leu Glu Leu Leu Phe Cys Cys Phe Tyr Leu Phe Gly
20 25 30

Leu Thr Arg Glu Ile Gln Asp His Ala Ser Gln Asp Tyr Ser Lys Tyr
35 40 45

Pro Phe Glu Val
50

<210> 601
<211> 67
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L25fs"

<400> 601
Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Ser Pro Ser Ala Ala Ser Arg
20 25 30

Ser Arg Pro Ser Pro Ile Ala Ala Gly Arg Ala Pro Thr Ala Trp Arg
35 40 45

Gly Trp Gly Ser Cys Arg Arg Thr Ala Gly Ala Thr Thr Arg Thr Pro
50 55 60

Ser Ala Leu
65

<210> 602
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.F85V"

<400> 602
Gly Asp Leu Gln Thr His Gly Trp Asp Thr Val Leu Gly Thr Ile Arg
1 5 10 15

Phe Leu Lys Pro Trp Ser His Gly Asn Val Val Ser Lys Gln Glu Leu
20 25 30

Lys Asn Leu Gln Ser Leu Phe Gln Leu Tyr Phe His Ser Phe Ile Gln
35 40 45

Ile Val Gln Ala
50

<210> 603
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A283T"

<400> 603
Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn Ser
1 5 10 15

Gln Arg Asn Trp His Asp Ser Ile Thr Thr Thr Cys Lys Glu Val Gly
20 25 30

Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
35 40 45

Leu Gln Ser Ser
50

<210> 604
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.Q164fs"

<400> 604
Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser
1 5 10 15

Pro Arg Gly Lys Asn Ile Gln Gly Gly Arg Pro Ser Pro Cys Leu Ser
20 25 30

Trp Ser Ser Arg Ile Val Ala Pro Gly His Ala Leu Ser Cys Arg Thr
35 40 45

Arg Arg Arg Trp Ser Ser Lys
50 55

<210> 605
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E156K"

<400> 605
Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
1 5 10 15

Gln Asn Leu Lys Trp Ser Thr Ala Val Lys Lys Phe Cys Lys Lys Lys
20 25 30

Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro
35 40 45

Gly Gly Ile Leu
50

<210> 606
<211> 36

<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P174fs"

<400> 606
Ala Ser Ala Leu Pro Ala Pro Pro Thr Gly Ser Ala Leu Pro Asp Pro
1 5 10 15

Gln Thr Ala Ser Ala Leu Pro Asp Pro Gln Gln Pro Leu Pro Ser Leu
20 25 30

Arg Pro Trp Arg
35

<210> 607
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.Y197H"

<400> 607
Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser
1 5 10 15

Lys Ala Gly Met Glu Glu Asp His Thr His His Glu Gly Leu Asp Ile
20 25 30

Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu
35 40 45

Val Lys Trp Ser
50

<210> 608
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.Y197D"

<400> 608
Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser
1 5 10 15

Lys Ala Gly Met Glu Glu Asp His Thr Asp Asp Glu Gly Leu Asp Ile
20 25 30

Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu
35 40 45

Val Lys Trp Ser
50

<210> 609
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D280fs"

<400> 609
Pro Leu Cys Val Ser Pro Lys Tyr Gly Cys Asn Phe Asn Asn Gly Gly
1 5 10 15

Cys His Gln Asp Cys Phe Glu Gly Gly Met Ala Pro Ser Ser Ala Ala
20 25 30

Ala Asp Gln Asp Ser Gly Cys Trp Met Thr Trp
35 40

<210> 610
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L646fs"

<400> 610
Gly Glu Arg Lys Gln Phe Ala Val Val Leu Leu Ser Leu Arg Leu Leu
1 5 10 15

Ala Lys Phe Leu Gly Phe Val Ala Phe Pro Ala Ile Pro Gly Ala
20 25 30

<210> 611
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.N123fs"

<400> 611
Ala Tyr Ala Val Ile Tyr Leu Lys Lys Thr Pro Glu Glu Ala Tyr Arg
1 5 10 15

Ala Leu Leu Ser Gly Ser Asn Pro Pro Ile Phe His Ser Gly Met Leu
20 25 30

Pro Leu Glu Ile Ala Leu Thr Ile Ser Pro Phe Ser Thr Val Cys Arg
35 40 45

Glu Ser Glu Arg Asp Tyr Asn Met Asp Phe Leu Thr Leu Arg His Leu
50 55 60

Met Trp Met Asn Met Asn Ile Met Ser Glu Leu Lys Met Val Thr Ser
65 70 75 80

Thr Gly Leu Phe Gln Glu Asn Phe
85

<210> 612

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R375C"

<400> 612
Gly Ser Val Ile Gly Pro Gln Gln Gln Phe Leu Val Met Lys Gln Thr
1 5 10 15

Asn Leu Trp Leu Glu Gly Asp Tyr Phe Cys Cys Gln Lys Leu Lys Gly
20 25 30

Gln Glu Asn Gly Gln His Arg Ala Ala Phe Ser Lys Leu Leu Ser Gly
35 40 45

Val Asp Asp Ile
50

<210> 613
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K322fs"

<400> 613
Glu Asn Leu Asn Arg Pro Arg Leu Lys Gln Val Glu Lys Phe Lys Asp
1 5 10 15

Asn Thr Ile Pro Asp Lys Val Lys Lys Ser Ile Phe Leu Ala Lys Glu
20 25 30

Ser Ser Gly Arg Ala Tyr Val
35

<210> 614
<211> 33

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L460fs"

<400> 614
Ile Thr Lys Leu Asp Ser Ser Ile Ile Ser Glu Gly Lys Ile Ser Thr
1 5 10 15

Ile Thr Pro Gln Ile Gln Ala Phe Asn His Lys Lys Gln Gln Gln Lys
20 25 30

Val

<210> 615
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D555E"

<400> 615
Glu Val Arg Arg Ile Glu Asn Tyr Arg Val Glu Gly Met Glu Ile Tyr
1 5 10 15

Ser Thr Thr Leu Trp His Leu Gln Lys Glu Glu Val Ala Leu Ser Val
20 25 30

Leu Ser Lys Asp Leu Thr Asp Met Asp Lys Asn Ser Pro Glu Ala Trp
35 40 45

Cys Ala Ala Gly
50

<210> 616
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.N571I"

<400> 616
Ser Thr Thr Leu Trp His Leu Gln Lys Asp Val Ala Leu Ser Val Leu
1 5 10 15

Ser Lys Asp Leu Thr Asp Met Asp Lys Ile Ile Ser Pro Glu Ala Trp
20 25 30

Cys Ala Ala Gly Asn Cys Phe Ser Leu Gln Arg Glu His Asp Ile Ala
35 40 45

Ile Lys Phe Phe
50

<210> 617
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I91fs"

<400> 617
Cys Thr Thr Pro Gln Cys Lys Tyr Leu Leu Ala Lys Cys Cys Val Asp
1 5 10 15

Leu Ser Lys Leu Ala Glu Gly Glu Gln Ser Tyr Leu Val Glu Cys Leu
20 25 30

Ile Ser Arg Lys Ala Met Met Ile Leu Leu Leu Ser Leu Val Ile Gln
35 40 45

Leu Ala Leu Leu Phe His Cys Trp Asp Met Tyr Ile Ala Arg Gln Ile
50 55 60

Gly Leu Pro Lys Asp Gln Asn Val Thr Lys Arg Ala Leu Val
65 70 75

<210> 618
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P242S"

<400> 618
Leu Glu Ser Ser Asn Ser Lys Tyr Ser Leu Asn Thr Asp Ser Ser Val
1 5 10 15

Ser Tyr Ile Asp Ser Ala Val Ile Ser Ser Ser Asp Thr Val Pro Leu
20 25 30

Gly Thr Gly Thr Ser Ile Leu Ser Lys Gln Val Gln Asn Lys Pro Lys
35 40 45

Thr Gly Arg Ser
50

<210> 619
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P675T"

<400> 619
Glu Gln Ser Glu His Tyr Ser Lys Gln Leu Glu Asn Glu Leu Glu Gly
1 5 10 15

Leu Lys Gln Lys Gln Ile Ser Tyr Ser Thr Thr Gly Val Cys Ser Ile
20 25 30

Glu His Gln Gln Glu Ile Thr Lys Leu Lys Thr Asp Leu Glu Lys Lys

35 40 45

Ser Ile Phe Tyr
50

<210> 620
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P405fs"

<400> 620
Gly Pro Cys Leu Arg Asn Arg Tyr Gly Glu Asp Val Arg Ser Ala Leu
1 5 10 15

Leu Asp Pro Asp Trp Val Cys Pro Pro Val Val Gly Ser Ala Ile Ala
20 25 30

Ala Thr Val Gly Ser Val Thr Ala Ala Val Pro Gln Glu Ser Ser Phe
35 40 45

Ile Trp Pro Ser Phe Met Val Met Thr Met Leu Arg Asn Ile Trp Arg
50 55 60

Ala Tyr Lys Arg Ser Trp
65 70

<210> 621
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E243K"

<400> 621
Glu Pro Leu Asp Arg Glu Arg Ile Ala Thr Tyr Thr Leu Phe Ser His
1 5 10 15

Ala Val Ser Ser Asn Gly Asn Ala Val Lys Lys Asp Pro Met Glu Ile
20 25 30

Leu Ile Thr Val Thr Asp Gln Asn Asp Asn Lys Pro Glu Phe Thr Gln
35 40 45

Glu Val Phe Lys
50

<210> 622
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D254Y"

<400> 622
Thr Leu Phe Ser His Ala Val Ser Ser Asn Gly Asn Ala Val Glu Asp
1 5 10 15

Pro Met Glu Ile Leu Ile Thr Val Thr Tyr Tyr Gln Asn Asp Asn Lys
20 25 30

Pro Glu Phe Thr Gln Glu Val Phe Lys Gly Ser Val Met Glu Gly Ala
35 40 45

Leu Pro Gly Thr
50

<210> 623
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E349K"

<400> 623
Asp Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Pro Leu Asp Tyr Glu
1 5 10 15

Ser Arg Arg Leu Tyr Thr Leu Lys Val Lys Lys Ala Glu Asn Thr His
20 25 30

Val Asp Pro Arg Phe Tyr Tyr Leu Gly Pro Phe Lys Asp Thr Thr Ile
35 40 45

Val Lys Ile Ser
50

<210> 624
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R472C"

<400> 624
Leu Asp Arg Glu Leu Ser Gln Trp His Asn Leu Thr Val Ile Ala Ala
1 5 10 15

Glu Ile Asn Asn Pro Lys Glu Thr Thr Cys Cys Val Ala Val Phe Val
20 25 30

Arg Ile Leu Asp Val Asn Asp Asn Ala Pro Gln Phe Ala Val Phe Tyr
35 40 45

Asp Thr Phe Val
50

<210> 625
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.S577R"

<400> 625
Asn Gly Phe Asn Arg His Glu Ile Ser Thr Tyr Leu Leu Pro Val Val
1 5 10 15

Ile Ser Asp Asn Asp Tyr Pro Ile Gln Arg Arg Ser Thr Gly Thr Leu
20 25 30

Thr Ile Arg Val Cys Ala Cys Asp Ser Gln Gly Asn Met Gln Ser Cys
35 40 45

Ser Ala Glu Ala
50

<210> 626
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R128S"

<400> 626
Ile Ile Asp Glu Lys Thr Gly Asp Ile His Ala Thr Arg Arg Ile Asp
1 5 10 15

Arg Glu Glu Lys Ala Phe Tyr Thr Leu Ser Ser Ala Gln Ala Ile Asn
20 25 30

Arg Arg Thr Leu Arg Pro Val Glu Pro Glu Ser Glu Phe Val Ile Lys
35 40 45

Ile His Asp Ile
50

<210> 627
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K357T"

<400> 627
Lys Lys Pro Val Asp Phe Glu Thr Lys Arg Ala Tyr Ser Leu Lys Val
1 5 10 15

Glu Ala Ala Asn Val His Ile Asp Pro Thr Thr Phe Ile Ser Asn Gly
20 25 30

Pro Phe Lys Asp Thr Val Thr Val Lys Ile Ser Val Glu Asp Ala Asp
35 40 45

Glu Pro Pro Met
50

<210> 628
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D674N"

<400> 628
Ser Lys Glu Asp Ile Arg Asp Asn Val Ile His Tyr Asp Asp Glu Gly
1 5 10 15

Gly Gly Glu Glu Asp Thr Gln Ala Phe Asn Asn Ile Gly Ala Leu Arg
20 25 30

Asn Pro Lys Val Ile Glu Glu Asn Lys Ile Arg Arg Asp Ile Lys Pro
35 40 45

Asp Ser Leu Cys
50

<210> 629
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P706T"

<400> 629
Pro Lys Val Ile Glu Glu Asn Lys Ile Arg Arg Asp Ile Lys Pro Asp
1 5 10 15

Ser Leu Cys Leu Pro Arg Gln Arg Pro Thr Thr Met Glu Asp Asn Thr
20 25 30

Asp Ile Arg Asp Phe Ile His Gln Arg Leu Gln Glu Asn Asp Val Asp
35 40 45

Pro Thr Ala Pro
50

<210> 630
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A721S"

<400> 630
Lys Leu Thr Pro Arg His Gln Thr Ser Ser Thr Leu Glu Ser Ile Asp
1 5 10 15

Val Gln Glu Phe Ile Lys Gln Arg Leu Ser Ser Glu Ala Asp Leu Asp
20 25 30

Pro Ser Val Pro Pro Tyr Asp Ser Leu Gln Thr Tyr Ala Tyr Glu Gly
35 40 45

Gln Arg Ser Glu
50

<210> 631
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A195T"

<400> 631
Glu Met Ser Asp Met Gly Thr Ser Val Leu Gln Val Thr Ala Thr Asp
1 5 10 15

Ala Asp Asp Pro Thr Tyr Gly Asn Ser Thr Thr Arg Val Val Tyr Ser
20 25 30

Ile Leu Gln Gly Gln Pro Tyr Phe Ser Val Asp Pro Lys Thr Gly Val
35 40 45

Ile Arg Thr Ala
50

<210> 632
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D547Y"

<400> 632
Gln Asp Pro Asp Arg Tyr Met Gln Gln Asn Ile Arg Tyr Thr Lys Leu
1 5 10 15

Ser Asp Pro Ala Asn Trp Leu Lys Ile Tyr Tyr Pro Val Asn Gly Gln
20 25 30

Ile Thr Thr Ile Ala Val Leu Asp Arg Glu Ser Pro Asn Val Lys Asn
35 40 45

Asn Ile Tyr Asn
50

<210> 633
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P433H"

<400> 633
Ile Gln Ile Ile Ser Ala Lys Asp Pro Asp Val Thr Asn Asn Ser Ile
1 5 10 15

Arg Tyr Ser Ile Asp Arg Ser Ser Asp His His Gly Arg Phe Phe Tyr
20 25 30

Val Asp Ile Thr Thr Gly Ala Leu Met Thr Ala Arg Pro Leu Asp Arg
35 40 45

Glu Glu Phe Ser
50

<210> 634
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A134V"

<400> 634
Ile Asp Asp Thr Thr Gly Asp Ile His Ala Ile Gln Arg Leu Asp Arg
1 5 10 15

Glu Glu Arg Ala Gln Tyr Thr Leu Arg Val Val Gln Ala Leu Asp Arg
20 25 30

Arg Thr Gly Arg Pro Met Glu Pro Glu Ser Glu Phe Ile Ile Lys Ile
35 40 45

Gln Asp Ile Asn

50

<210> 635
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V403I"

<400> 635
Glu Gly Leu Asn Ser Met Phe Glu Val Tyr Leu Val Gly Asn Asn Ser
1 5 10 15

His His Phe Ile Ile Ser Pro Thr Ser Ile Ile Gln Gly Lys Ala Asp
20 25 30

Ile Arg Ile Arg Val Ala Ile Pro Leu Asp Tyr Glu Thr Val Asp Arg
35 40 45

Tyr Asp Phe Asp
50

<210> 636
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F1132Y"

<400> 636
Ala Ser Val Pro Glu Asp Ile Pro Glu Gly His Ser Ile Leu Gln Leu
1 5 10 15

Lys Ala Thr Asp Ala Asp Glu Gly Glu Tyr Tyr Gly Arg Val Trp Tyr
20 25 30

Arg Ile Leu His Gly Asn His Gly Asn Asn Phe Arg Ile His Val Ser
35 40 45

Asn Gly Leu Leu
    50

<210> 637
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.F177L"

<400> 637
Phe Ile Val Asn Ala Thr Asp Pro Asp Leu Gly Ala Gly Gly Ser Val
1   5   10   15

Leu Tyr Ser Phe Gln Pro Pro Ser Gln Leu Leu Phe Ala Ile Asp Ser
            20   25   30

Ala Arg Gly Ile Val Thr Val Ile Arg Glu Leu Asp Tyr Glu Thr Thr
        35   40   45

Gln Ala Tyr Gln
    50

<210> 638
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Q237K"

<400> 638
Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn Met Asp Arg Glu
1   5   10   15

Asn Arg Glu Gln Tyr Gln Val Val Ile Lys Lys Ala Lys Asp Met Gly
            20   25   30

Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn Ile Thr Leu
35 40 45

Thr Asp Val Asn
50

<210> 639
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q225K"

<400> 639
Pro Tyr Phe Ser Val Glu Pro Lys Thr Gly Val Ile Lys Thr Ala Leu
1 5 10 15

Pro Asn Met Asp Arg Glu Ala Lys Asp Lys Lys Tyr Leu Leu Val Ile
20 25 30

Gln Ala Lys Asp Met Val Gly Gln Asn Gly Gly Leu Ser Gly Thr Thr
35 40 45

Ser Val Thr Val
50

<210> 640
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F523L"

<400> 640
Glu Asn Ala Lys Pro Gly Gln Leu Ile Gln Thr Val Ser Val Met Asp
1 5 10 15

Lys Asp Asp Pro Pro Arg Gly His Lys Leu Leu Phe Phe Glu Pro Val
20 25 30

Pro Glu Phe Thr Leu Asn Pro Asn Phe Thr Ile Val Asp Asn Lys Asp
35 40 45

Asn Thr Ala Gly
50

<210> 641
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R218G"

<400> 641
Gln Ala Gly Ala Thr Leu Asp Tyr Glu Arg Ser Arg Thr His Tyr Ile
1 5 10 15

Thr Val Val Ala Lys Asp Gly Gly Gly Gly Gly Leu His Gly Ala Asp
20 25 30

Val Val Phe Ser Ala Thr Thr Thr Val Thr Val Asn Val Glu Asp Val
35 40 45

Gln Asp Met Ala
50

<210> 642
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E79del"

<400> 642
Ser Pro Tyr Arg Arg Glu Asp Ser Met Glu Asp Arg Gly Glu Glu Asp

1 5 10 15

Asp Ser Leu Ala Ile Lys Pro Pro Gln Met Ser Arg Lys Glu Lys Val
20 25 30

His His Arg Lys Asp Glu Lys Arg Lys Glu Lys Cys Arg His His Ser
35 40 45

His Ser Ala Glu Gly
50

<210> 643
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R880S"

<400> 643
Asp Phe Gly Leu Ala Arg Leu Tyr Ser Ser Glu Glu Ser Arg Pro Tyr
1 5 10 15

Thr Asn Lys Val Ile Thr Leu Trp Tyr Ser Ser Pro Pro Glu Leu Leu
20 25 30

Leu Gly Glu Glu Arg Tyr Thr Pro Ala Ile Asp Val Trp Ser Cys Gly
35 40 45

Cys Ile Leu Gly
50

<210> 644
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R108C"

<400> 644
Gly Ser Asp Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu
1 5 10 15

Val Gln Ser Pro Val Arg Val Arg Met Cys Cys Asn His Pro Pro Arg
20 25 30

Lys Ile Ser Thr Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp
35 40 45

Ile Arg Leu Pro
50

<210> 645
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H1592Q"

<400> 645
Leu Asp Glu Glu His Arg Arg Leu Arg Glu Ala Ser Gly Glu Gly Trp
1 5 10 15

Lys Gly Gln Asp Pro Phe Arg Asp Leu Gln Gln Ser Leu Leu Met Glu
20 25 30

Ile Gln Ala Leu Arg Leu Gln Leu Glu Arg Ser Ile Glu Thr Ser Ser
35 40 45

Thr Leu Gln Ser
50

<210> 646
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P409L"

<400> 646
Tyr Lys Phe Pro Ser Leu Phe Ile Asn Gln Phe Tyr Pro Arg Pro Gly
1 5 10 15

Thr Pro Ala Ala Lys Met Glu Gln Val Leu Leu Ala Gln Val Lys Lys
20 25 30

Gln Arg Thr Lys Asp Leu Ser Arg Val Phe His Ser Tyr Ser Pro Tyr
35 40 45

Asp His Lys Ile Gly
50

<210> 647
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H83Y"

<400> 647
Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala
1 5 10 15

Asp Pro Ala Thr Leu Thr Arg Pro Val Tyr Tyr Asp Ala Ala Arg Glu
20 25 30

Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg Leu
35 40 45

Asp Val Arg Asp
50

<210> 648
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.D108Y"

<400> 648
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
1 5 10 15

Arg Ala Gly Ala Arg Leu Asp Val Arg Tyr Tyr Ala Trp Gly Arg Leu
20 25 30

Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr
35 40 45

Leu Arg Ala Ala
50

<210> 649
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V31A"

<400> 649
Asp Val Asp Phe Leu Glu Asp Val Pro Leu Leu Glu Asp Ile Pro Leu
1 5 10 15

Leu Glu Asp Val Pro Leu Leu Glu Asp Ala Ala Pro Leu Leu Glu Asp
20 25 30

Thr Ser Arg Leu Glu Asp Ile Asn Leu Met Glu Asp Met Ala Leu Leu
35 40 45

Glu Asp Val Asp
50

<210> 650
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A60G"

<400> 650
Val Ser Ala Pro Asp Gly Pro Ser Asp Pro Ser Ile Ser Val Ser Ser
1 5 10 15

Glu Gln Ser Gly Ala Gln Gln Pro Pro Gly Gly Leu Gln Val Glu Arg
20 25 30

Ile Val Asp Lys Arg Lys Asn Lys Lys Gly Lys Thr Glu Tyr Leu Val
35 40 45

Arg Trp Lys Gly
50

<210> 651
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L640I"

<400> 651
Cys His Ser Ala Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn
1 5 10 15

Gly Ile Pro Gln Gln His Thr Gln Val Ile Ile Phe Ile Ala Lys Ile
20 25 30

Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala
35 40 45

Thr Gly Arg Asn
50

<210> 652
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A309P"

<400> 652
Tyr Leu Asn Pro Met Ala Ala Phe Ala Ala Ala Gln Met Gln Gln Met
1 5 10 15

Ala Ala Leu Asn Met Asn Gly Leu Ala Pro Pro Ala Pro Met Thr Pro
20 25 30

Thr Ser Gly Gly Ser Thr Pro Pro Gly Ile Thr Ala Pro Ala Val Pro
35 40 45

Ser Ile Pro Ser
50

<210> 653
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G614fs"

<400> 653
Ala Val Asp Ala Asp Ser Gly Glu Asn Ala Arg Leu His Tyr Arg Leu
1 5 10 15

Val Asp Thr Ala Ser Thr Phe Leu Gly Ala Ala Ala Leu Gly Leu Arg
20 25 30

Ile Leu Pro Pro Pro Leu Thr Ser Pro Ser Arg Ser Thr Thr Ala Pro
35 40 45

Val Gly Ser Gln Cys Val Pro Ser Trp Thr Ala Arg Arg Trp Ser Thr
50 55 60

Thr Ala Ser Gly Trp Arg Arg Trp Thr Thr Ala Arg Pro Pro
65 70 75

<210> 654
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.16_17insP"

<400> 654
Met Arg Ser Pro Ala Thr Gly Val Pro Leu Pro Thr Pro Pro Pro Pro
1 5 10 15

Pro Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu
20 25 30

Gly Asp Gln Val Gly Pro Cys Arg Ser Leu Gly Ser Arg
35 40 45

<210> 655
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L17P"

<400> 655
Met Arg Ser Pro Ala Thr Gly Val Pro Leu Pro Thr Pro Pro Pro Pro
1 5 10 15

Pro Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Leu Leu Gly
20 25 30

Asp Gln Val Gly Pro Cys Arg Ser Leu Gly Ser
35 40

<210> 656
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E21K"

<400> 656
Met Ser Leu Asp Phe Gly Ser Val Ala Leu Pro Val Gln Asn Glu Asp
1 5 10 15

Glu Glu Tyr Asp Lys Lys Glu Asp Tyr Glu Arg Glu Lys Glu Leu Gln
20 25 30

Gln Leu Leu Thr Asp Leu Pro His Asp Met Leu Asp Asp Asp Leu
35 40 45

<210> 657
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S2058L"

<400> 657
Thr Glu Val Tyr Asp Leu Pro Gln Arg Pro Asn Asp Val Gln Leu Phe
1 5 10 15

Tyr Gly Ser Met Cys Lys Ile Ile Leu Leu Leu Val Ile Gly Glu Phe
20 25 30

Arg Asp Cys Ile Ser Ser Arg Glu Phe Leu Gln Pro Ser Ser Lys Ala
35 40 45

Ser Leu Glu Ser
50

<210> 658

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S253L"

<400> 658
Val Asn Val Asn Pro Glu Ile Thr Ala Leu Gln Thr Met Leu Ala Glu
1 5 10 15

Cys Gln Glu Asn Leu Lys Lys Leu Thr Leu Leu Ile Glu Lys Arg Leu
20 25 30

Asp Cys Leu Glu Gln Lys Met Lys Gly Lys Val Met Val Asp Glu Asn
35 40 45

Thr Trp Thr Asn
50

<210> 659
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A85fs"

<400> 659
Arg Ala Arg Met Ala Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn
1 5 10 15

Thr Thr Glu Met Leu Gln Glu Trp Leu Gly Ala Met Thr Met Leu Leu
20 25 30

Trp Ser Gly Gly Leu Arg Ala Ser Pro Gly Ser Thr Gln Met Lys Arg
35 40 45

Val Pro Ser Thr Gly Pro Lys Lys Gly Thr Ser Phe
50 55 60

<210> 660
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E95D"

<400> 660
Phe Val Ala Ser Pro Leu Ala Lys Ser Phe Gly Ile Lys Glu Thr Val
1 5 10 15

Arg Lys Val Thr Pro Asn Thr Val Leu Asp Asp Asn Phe Phe Lys His
20 25 30

Ser Thr Arg Gln Pro Leu Gln Thr Asp Ile Tyr Gly Leu Ala Lys Lys
35 40 45

Cys Asn Leu Thr
50

<210> 661
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.K63fs"

<400> 661
Thr Asp Lys Asp Glu Ala Ile Asp Tyr His Glu Leu Lys Val Ala Met
1 5 10 15

Arg Ala Leu Gly Phe Asp Val Lys Lys Leu Met Tyr
20 25

<210> 662
<211> 53
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R314M"

<400> 662
Ile Asn Val Ser Val Ala Ile Ile Thr Phe Ala Ser Glu Pro Lys Val
1 5 10 15

Leu Met Ser Val Leu Asn Asp Asn Ser Met Met Asp Met Thr Glu Val
20 25 30

Ile Ser Ser Leu Glu Asn Ala Asn Tyr Lys Asp His Glu Asn Gly Thr
35 40 45

Gly Thr Asn Thr Tyr
50

<210> 663
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P129fs"

<400> 663
Ala Arg Lys Lys Lys Glu Asp Glu Leu Trp Ala Ser Phe Leu Asn Asp
1 5 10 15

Val Gly Pro Lys Ser Lys Val Pro Pro Lys Tyr Thr Ser
20 25

<210> 664
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R441H"

<400> 664
Leu Cys Lys Glu Asn Tyr Leu Leu Pro Glu Ala Lys Glu Ile Val Cys
1 5 10 15

Lys Asp Gly Arg Trp Gln Ser Leu Pro His His Cys Val Glu Ser Thr
20 25 30

Ala Tyr Cys Gly Pro Pro Pro Ser Ile Asn Asn Gly Asp Thr Thr Ser
35 40 45

Phe Pro Leu Ser
50

<210> 665
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K37fs"

<400> 665
Cys Phe His Leu Arg Phe Cys Lys Val Thr Tyr Thr Ser Gln Glu Asp
1 5 10 15

Leu Val Glu Lys Lys Cys Leu Ala Lys Asn Ile Leu Thr Ser Pro Ala
20 25 30

Ile Lys Ser Ser Ala Ser His Gly Arg Asp Ala Leu Arg Ala Pro Val
35 40 45

Phe Val Asn Tyr Arg Ile Ser Ala Gln Arg Met Ala Leu Gln Cys Val
50 55 60

Gln Leu Thr Gly Glu Ala Ser Gln His Thr Val Asn Lys Arg Val Trp
65 70 75 80

Asn Val Phe Ile Gln Gly Gln Ser Phe

85

<210> 666
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T18A"

<400> 666
Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15

Gly Ala Ala Trp Ala Ser Arg Glu Met Leu Arg Pro Arg Cys Arg Pro
20 25 30

Ile Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys
35 40

<210> 667
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T79M"

<400> 667
Pro Cys Leu Gly Gly Met Ala Ser Gly Pro Cys Gly Glu Gln Phe Lys
1 5 10 15

Ser Ala Phe Ser Cys Phe His Tyr Ser Met Met Glu Glu Ile Lys Gly
20 25 30

Ser Asp Cys Val Asp Gln Phe Arg Ala Met Gln Glu Cys Met Gln Lys
35 40 45

Tyr Pro Asp Leu
50

<210> 668
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P597fs"

<400> 668
Trp Arg Trp Gly Glu Pro Pro Val Ala Val Pro Ala Pro Gln Gln Ala
1 5 10 15

Asp Gly Asn Pro Asp Val Pro Pro Pro Val Leu Phe Lys Ala Asp Gln
20 25 30

Ser Glu Ser Ser Leu Ser Ser Gly
35 40

<210> 669
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R975H"

<400> 669
Leu Gly Pro His Met Leu Arg Arg Leu Lys Ala Asp Val Phe Lys Asn
1 5 10 15

Met Pro Ser Lys Thr Glu Leu Ile Val His His Val Glu Leu Ser Pro
20 25 30

Met Gln Lys Lys Tyr Tyr Lys Tyr Ile Leu Thr Arg Asn Phe Glu Ala
35 40 45

Leu Asn Ala Arg
50

<210> 670
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A801T"

<400> 670
Tyr Val Val Thr Tyr Thr Gly Asp Lys Glu Ser Arg Ser Val Ile Arg
1 5 10 15

Glu Asn Glu Phe Ser Phe Glu Asp Asn Thr Thr Ile Arg Ser Gly Lys
20 25 30

Lys Val Phe Arg Met Lys Lys Glu Val Gln Ile Lys Phe His Val Leu
35 40 45

Leu Thr Ser Tyr
50

<210> 671
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E40A"

<400> 671
Ala Arg Gly Ala Leu Gly Gln Gln Gln Ser Leu Gly Ala Arg Ala Leu
1 5 10 15

Ala Ser Ala Gly Ser Glu Ser Arg Asp Ala Ala Tyr Ser Tyr Val Val
20 25 30

Val Gly Ala Gly Ser Ala Gly Cys Val Leu Ala Gly Arg Leu Thr Glu
35 40 45

Asp Pro Ala Glu
    50

<210> 672
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.K373E"

<400> 672
Leu Lys Pro Glu Asn Val Leu Leu Ser Ser Gln Glu Glu Asp Cys Leu
1   5   10   15

Ile Lys Ile Thr Asp Phe Gly His Ser Glu Glu Ile Leu Gly Glu Thr
            20   25   30

Ser Leu Met Arg Thr Leu Cys Gly Thr Pro Thr Tyr Leu Ala Pro Glu
        35   40   45

Val Leu Val Ser Val
    50

<210> 673
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.K373E"

<400> 673
Leu Lys Pro Glu Asn Val Leu Leu Ser Ser Gln Glu Glu Asp Cys Leu
1   5   10   15

Ile Lys Ile Thr Asp Phe Gly His Ser Glu Glu Ile Leu Gly Glu Thr
            20   25   30

Ser Leu Met Arg Thr Leu Cys Gly Thr Pro Thr Tyr Leu Ala Pro Glu

35 40 45

Val Leu Val Ser
50

<210> 674
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P284fs"

<400> 674
Leu Ile Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser
1 5 10 15

Ser Ser Asp Thr Arg Val Gly Ala Pro Ser His Arg Val Trp His Ser
20 25 30

Arg Pro Leu His Gln Gly Arg Arg Asp Ala Gly Leu Leu
35 40 45

<210> 675
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K264N"

<400> 675
Cys Gly Leu Asn Val His Lys Gln Cys Ser Lys Met Val Pro Asn Asp
1 5 10 15

Cys Lys Pro Asp Leu Lys His Val Lys Asn Asn Val Tyr Ser Cys Asp
20 25 30

Leu Thr Thr Leu Val Lys Ala His Thr Thr Lys Arg Pro Met Val Val
35 40 45

Asp Met Cys Ile
50

<210> 676
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I43M"

<400> 676
Ala Glu Glu Tyr Gln Pro Pro Ile Trp Lys Ser Tyr Leu Tyr Gln Leu
1 5 10 15

Gln Gln Glu Ala Pro Arg Pro Lys Arg Met Met Ile Cys Pro Arg Glu
20 25 30

Val Glu Asn Arg Pro Lys Tyr Tyr Gly Arg Glu Phe His Gly Ile Ile
35 40 45

Ser Arg Glu Gln
50

<210> 677
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L23del"

<400> 677
Met Gly Ser Gly Pro Leu Ser Leu Pro Leu Ala Leu Ser Pro Pro Arg
1 5 10 15

Leu Leu Leu Leu Leu Leu Ser Leu Leu Pro Val Ala Arg Ala Ser Glu
20 25 30

Ala Glu His Arg Leu Phe Glu Arg Leu Phe Glu Asp Tyr Asn Glu Ile
35 40 45

Ile Arg
50

<210> 678
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S396R"

<400> 678
Leu Ile Glu Ser Met His Lys Met Ala Ser Ala Pro Arg Phe Trp Pro
1 5 10 15

Glu Pro Glu Gly Glu Pro Pro Ala Thr Arg Arg Gly Thr Gln Ser Leu
20 25 30

His Pro Pro Ser Pro Ser Phe Cys Val Pro Leu Asp Val Pro Ala Glu
35 40 45

Pro Gly Pro Ser
50

<210> 679
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P361Q"

<400> 679
Trp Ala Arg Val Val Ile Leu Lys Tyr Met Ser Arg Val Leu Phe Val
1 5 10 15

Tyr Asp Val Gly Glu Ser Cys Leu Ser Gln Gln His His Ser Arg Glu
20 25 30

Arg Asp His Leu Thr Lys Val Tyr Ser Lys Leu Pro Glu Ser Asn Leu
35 40 45

Lys Ala Ala Arg
50

<210> 680
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R507fs"

<400> 680
Pro Glu Gly Asn Lys Gly Phe Gly Arg Lys Val Phe Ser Pro Val Ile
1 5 10 15

Arg Ser Ser Phe Thr His Cys Arg Pro His Trp Thr Leu Ser Pro Gln
20 25 30

Gly Pro Arg Ile Leu Leu
35

<210> 681
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A1114fs"

<400> 681
Ile Thr Ala Phe Tyr Ser Gly Ser Pro Ala Pro Thr Ser Ser Ala Pro
1 5 10 15

Leu Ala Gln Pro Ser Gln Ala Pro Pro Lys Pro Gly Leu His Cys Gly

20 25 30

His Gln His Asn Pro Thr Cys Ser His His Ser Ala Gln Gly Pro Ala
35 40 45

Ser Pro Cys His Cys His Pro Ser Pro Asp
50 55

<210> 682
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A1114fs"

<400> 682
Val Ile Thr Ala Phe Tyr Ser Gly Ser Pro Ala Pro Thr Ser Ser Ala
1 5 10 15

Pro Leu Ala Gln Pro Ser Gln Ala Pro Gln Ala Trp Ser Thr Leu Trp
20 25 30

Pro Pro Ala Gln Pro His Leu Gln Pro Pro Phe Cys Pro Arg Ala Arg
35 40 45

Gln Pro Leu Pro Leu Pro Pro Gln Pro Arg Leu Ala Leu Ser Pro Ala
50 55 60

Pro Gln Gln Val Pro
65

<210> 683
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.E728K"

<400> 683
Ala Glu Ser Glu Leu Ala Phe Pro Ser Phe Leu Leu Gln Cys Phe Leu
1 5 10 15

Gly Ala Leu Trp Leu Ala Leu Ser Gly Lys Lys Ile Lys Asp Lys Glu
20 25 30

Leu Pro Gln Tyr Leu Ala Leu Thr Pro Arg Lys Lys Arg Pro Tyr Asp
35 40 45

Asn Trp Leu Glu
50

<210> 684
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V553M"

<400> 684
Val Thr Phe Val Asp Pro Ser Gly Glu Phe Met Asp Ala Val Arg Val
1 5 10 15

Leu Pro Phe Asp Pro Arg Gly Ala Gly Met Met Tyr His Glu Val Lys
20 25 30

Ala Met Arg Lys Lys Ala Pro Val Ile Leu His Thr Ser Gln Ser Asn
35 40 45

Thr Ile Pro Leu
50

<210> 685
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S250I"

<400> 685
Thr Gly Thr Leu Val Lys Ser His Leu Ile Ala Asn Ala Asp Val Gln
1 5 10 15

Ser Ile Ala Val Ala Asp Gln Glu Asp Ile Ile Phe Val Val Gly Thr
20 25 30

Ala Glu Gly Thr Val Phe His Phe Gln Leu Val Pro Val Thr Ser Asn
35 40 45

Ser Ser Glu Lys
50

<210> 686
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V668A"

<400> 686
Ser Glu Pro Gln His Gln Gln Arg Leu Gly Glu Ile Gln His Met Ser
1 5 10 15

Gln Ala Cys Leu Leu Ser Leu Leu Pro Ala Ala Pro Arg Asp Val Leu
20 25 30

Glu Thr Glu Asp Glu Glu Pro Pro Pro Arg Arg Trp Cys Asn Thr Cys
35 40 45

Gln Leu Tyr Tyr
50

<210> 687
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.L89P"

<400> 687
Gln Leu Leu Gln Leu Gln Gln Leu Leu Gln Gln Ser Pro Pro Gln Ala
1 5 10 15

Pro Leu Pro Met Ala Val Ser Arg Gly Pro Pro Pro Pro Gln Gln Pro
20 25 30

Gln Gln Pro Leu Leu Asn Leu Gln Gly Thr Asn Ser Ala Ser Leu Leu
35 40 45

Asn Gly Ser Met
50

<210> 688
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.*684K"

<400> 688
Gly Arg Glu Thr Asp Ala Phe Val Cys Arg Pro Asn Ala Ala Leu Cys
1 5 10 15

Arg Val Tyr Tyr Glu Ala Asp Thr Thr Lys Lys Glu Lys
20 25

<210> 689
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.G576A"

<400> 689
Ala Gly Gly Pro Pro Lys Lys Gly Lys Pro Ala Ala Pro Gly Gly Ala
1 5 10 15

Gly Asn Thr Gly Thr Lys Asn Lys Lys Ala Ala Leu Glu Thr Lys Glu
20 25 30

Ile Val Glu Pro Glu Leu Ser Ile Glu Val Cys Glu Glu Lys Ala Ser
35 40 45

Ala Val Leu Pro
50

<210> 690
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.645_645R>RR"

<400> 690
Ile Leu Leu Gly Ser Ile Glu Arg Ser Gln Val Val Ala Leu Leu Gly
1 5 10 15

Ala Gln Leu Ser Pro Ala Arg Arg Arg Arg Arg Arg Gln His Met Gln
20 25 30

Glu Arg Arg Ala Thr Gln Thr Ser Pro Leu Ser Asp Gln Glu Gly Pro
35 40 45

Pro Thr Pro Glu Ala Ser Val
50 55

<210> 691
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P124Q"

<400> 691
Tyr Pro Val Ala Leu Val Ser Phe Ser Ser Gly Phe Ser Gln Ser Ile
1 5 10 15

Thr Pro Ser Ser Gly Gly Ser Gly Ile Gln Gln Glu Leu Lys Thr Met
20 25 30

Leu Ala Gly Val Ile Leu Glu Asp Tyr Leu Asp Ile Lys Asn Phe Gly
35 40 45

Ala Lys Val Val
50

<210> 692
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V210M"

<400> 692
Cys Asp Glu Arg Cys Arg Arg Arg Arg Lys Gly Pro Ser Ala Gly Pro
1 5 10 15

Arg Arg Ser Ser Val Ser Thr Ile Gln Met Met Glu Trp Pro Glu Pro
20 25 30

Asp Leu Ala Pro Ala Ile Lys Tyr Tyr Ser Asp Gly Gln His Arg Pro
35 40 45

Pro Pro Ala Gln
50

<210> 693
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S172A"

<400> 693
Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu Phe Gly
1 5 10 15

Pro Ala Ile Phe Ile Gly Trp Ala Gly Ala Ala Ala Leu Val Ile Leu
20 25 30

Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys Ala
35 40 45

Gly Tyr Arg Val
50

<210> 694
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.W217L"

<400> 694
Met Ser Gln Pro Leu Leu Met Phe Ser Phe Phe Trp Leu Gly Leu Ser
1 5 10 15

Trp Asp Ser Ser Gly Arg Ser Trp Phe Leu Leu Glu Asp Gly Ser Val
20 25 30

Pro Ser Pro Ser Leu Phe Ser Thr Lys Glu Leu Asp Gln Ile Asn Gly
35 40 45

Ser Lys Gly Cys
50

<210> 695
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R423H"

<400> 695
Gly Gln Pro Asp Asn His Gly Phe Gly Asn Cys Val Glu Leu Gln Ala
1 5 10 15

Ser Ala Ala Phe Asn Trp Asn Asn Gln His His Cys Lys Thr Arg Asn
20 25 30

Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg Trp Gly Pro
35 40 45

Gly Ser
50

<210> 696
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.R209H"

<400> 696
Tyr Asn Glu Ser Ser Thr Phe Trp His Pro Arg Glu Pro Ser Asp Pro
1 5 10 15

Asn Glu Arg Cys Val Val Leu Asn Phe His His Lys Ser Pro Lys Arg
20 25 30

Trp Gly Trp Asn Asp Val Asn Cys Leu Gly Pro Gln Arg Ser Val Cys
35 40 45

Glu Met Met Lys
50

<210> 697

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 697
Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Asn Val Thr Phe Trp His
1 5 10 15

Ser Gly Glu Pro Asn Asn Leu Asp Glu Leu Leu Cys Ala Ile Ile Asn
20 25 30

Phe Arg Ser Ser Glu Glu Trp Gly Trp Asn Asp Ile His Cys His Val
35 40 45

Pro Gln Lys Ser
50

<210> 698
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q298E"

<400> 698
Glu Gly Pro Ala Gly Asp Ser Met Asp Ala Glu Gly Pro Ala Gly Arg
1 5 10 15

Ala Arg Arg Val Ser Gly Glu Pro Gln Glu Glu Ser Gly Asp Gly Ser
20 25 30

Leu Ser Pro Gln Ala Glu Ala Ile Glu Val Ala Ala Gly Glu Ser Ala
35 40 45

Gly Arg Ser Pro
50

<210> 699
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 699
Ala Ala Lys Lys His Glu Glu Glu Lys Lys Glu Leu Glu Arg Lys Leu
1 5 10 15

Ser Asp Leu Glu Lys Lys Met Glu Thr Lys Pro Gln Pro Val Ser Gly
20 25 30

Ala Glu Ser Gln Val
35

<210> 700
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R68L"

<400> 700
Cys Lys Pro His His Gln Phe Lys Glu Ser Asp Cys His Tyr Leu Glu
1 5 10 15

Ala Arg Ser Leu Asn Glu Arg Asp Tyr Leu Leu Asp Arg Arg Tyr Val
20 25 30

Asp Glu Tyr Arg Asn Asp Tyr Cys Glu Gly Tyr Val Pro Arg His Tyr
35 40 45

His Arg Asp Ile
50

<210> 701
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G206S"

<400> 701
Ile Ser Trp Trp Ser Ser Gly Thr Gly Gly Ala Gly Leu Leu Gly Ala
1 5 10 15

Leu Ser Tyr Leu Gly Leu Thr Gln Ala Ser Ser Leu Ser Pro Gln Gln
20 25 30

Thr Leu Leu Ser Met Leu Gly Ile Pro Ala Leu Leu Leu Ala Ser Tyr
35 40 45

Phe Leu Leu Leu
50

<210> 702
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T615M"

<400> 702
Leu Glu Gly Glu Asp Leu Gly Glu Leu Asp Lys Ala Met Gln His Ile
1 5 10 15

Ser Tyr Leu Asn Ser Arg Gln Phe Pro Met Met Pro Gly Ile Arg Arg
20 25 30

Leu Lys Ile Thr Ser Thr Ile Lys Cys Phe Asn Glu Ala Thr Cys Ile
35 40 45

Ser Val Pro Pro
    50

<210> 703
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P759L"

<400> 703
Tyr Ser Ile Tyr Gly Val Gly Ser Met Ser Arg Tyr Glu Gln Val Leu
1   5   10   15

His His Ile Arg Tyr Arg Asn Trp Arg Leu Leu Ala Ser Leu Glu Ala
            20   25   30

Arg Arg Phe Arg Ile Lys Cys Ser Glu Leu Asn Gly Arg Tyr Thr Ser
        35   40   45

Asn Glu Phe Asn
    50

<210> 704
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G463R"

<400> 704
Ser Glu Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser
1   5   10   15

Ile Gln Val Val Pro Arg Ile His Glu Arg Arg Asn Ile Ser Lys Gln
            20   25   30

Asp Glu Thr Met Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe

35 40 45

Thr Leu Lys Ile
50

<210> 705
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I81K"

<400> 705
Ile Arg Arg Asn Phe Val Leu Thr Ala Ala His Cys Ala Gly Arg Ser
1 5 10 15

Ile Thr Val Thr Leu Gly Ala His Asn Lys Lys Thr Glu Glu Glu Asp
20 25 30

Thr Trp Gln Lys Leu Glu Val Ile Lys Gln Phe Arg His Pro Lys Tyr
35 40 45

Asn Thr Ser Thr
50

<210> 706
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R110Q"

<400> 706
Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu Ile Glu Asn Val
1 5 10 15

Ala Lys Gln Phe Gly Ala Gln Val His Gln Gln Arg Ser Ser Glu Val
20 25 30

Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu Phe Leu Asn
35 40 45

Tyr His Asn Glu
50

<210> 707
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A230T"

<400> 707
Glu Ile Val Ser Lys Leu Leu Ser Glu Asn Thr Asn Leu Thr Thr Gln
1 5 10 15

Glu His Glu Asn Ile Ile Val Ala Ile Thr Thr Pro Leu Leu Glu Asn
20 25 30

Asn His Pro Pro Pro Asp Leu Cys Glu Phe Phe Cys Lys His Cys Arg
35 40 45

Glu Arg Pro Arg
50

<210> 708
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S26T"

<400> 708
Met Glu Glu Pro Gln Arg Ala Arg Ser His Thr Val Thr Thr Thr Ala
1 5 10 15

Ser Ser Phe Ala Glu Asn Phe Ser Thr Thr Thr Ser Ser Ser Phe Ala
20 25 30

Tyr Asp Arg Glu Phe Leu Arg Thr Leu Pro Gly Phe Leu Ile Val Ala
35 40 45

Glu Ile Val Leu
50

<210> 709
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L396P"

<400> 709
Arg Ser Ile Ile Gly Phe Val Lys Leu Arg Ser Asn Lys Val Lys Arg
1 5 10 15

Ser Gln Lys Leu Val Tyr Met Gly Lys Pro Pro Lys Glu Lys Glu Ser
20 25 30

Phe Gly Glu Ile Ser Val Leu Leu Gln Val Pro Phe Thr Cys Thr Ile
35 40 45

Ile Thr Lys Lys
50

<210> 710
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K510T"

<400> 710

Ala Glu Ile Ala Leu Gln Glu Ala Thr Glu Ser Arg Leu Arg Gly Leu
1 5 10 15

Asp Gln Gln Leu Asp Asp Leu Gln Thr Thr Thr Phe Ala Arg Leu Leu
20 25 30

Ala Glu Leu Glu Ser Ser Ala Leu Lys Ile Ala Tyr Arg Ile Glu Arg
35 40 45

Leu Glu Trp Gln
50

<210> 711
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P249L"

<400> 711
Ser Glu Gly Leu Gly Met Tyr Ile Lys Ser Thr Tyr Asp Gly Leu His
1 5 10 15

Val Ile Thr Gly Thr Thr Glu Asn Ser Leu Leu Ala Asp Arg Cys Lys
20 25 30

Lys Ile His Ala Gly Asp Glu Val Ile Gln Val Asn His Gln Thr Val
35 40 45

Val Gly Trp Gln
50

<210> 712
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.E20K"

<400> 712
Met Ala Asp Lys Arg Lys Leu Gln Gly Glu Ile Asp Arg Cys Leu Lys
1 5 10 15

Lys Val Ser Lys Lys Gly Val Glu Gln Phe Glu Asp Ile Trp Gln Lys
20 25 30

Leu His Asn Ala Ala Asn Ala Asn Gln Lys Glu Lys Tyr Glu
35 40 45

<210> 713
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S248fs"

<400> 713
Gln Glu Ile Leu Ser Cys Asn Ala Asp Ile Val Ser Leu Gln Glu Val
1 5 10 15

Glu Thr Glu Gln Tyr Tyr Ser Phe Phe Trp
20 25

<210> 714
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R102W"

<400> 714
Glu Pro Asp Gly Asp Arg Val Val Tyr Thr Gly Thr Tyr Asp Thr Glu
1 5 10 15

Gly Val Thr Pro Thr Lys Ser Gly Glu Trp Trp Gln Pro Ile Gln Ile
20 25 30

Thr Met Pro Phe Thr Asp Ile Gly Thr Phe Glu Thr Val Trp Gln Val
35 40 45

Lys Phe Tyr Asn
50

<210> 715
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D252Y"

<400> 715
Gln Thr Pro Ser Thr Trp Pro Asp Pro Glu Ser Phe Pro Leu Lys Phe
1 5 10 15

Phe Leu Arg Tyr Arg Pro Leu Ile Leu Tyr Tyr Gln Trp Gln His Val
20 25 30

Glu Leu Ser Asp Gly Thr Ala His Thr Ile Thr Asp Ala Tyr Ala Gly
35 40 45

Lys Glu Tyr Ile
50

<210> 716
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S379F"

<400> 716
Leu Glu Ile Pro Asn Val Gln Leu Asp Asp Ala Gly Ile Tyr Glu Cys
1 5 10 15

Arg Ala Glu Asn Ser Arg Gly Lys Asn Phe Phe Phe Arg Gly Gln Leu
20 25 30

Gln Val Tyr Thr Tyr Pro His Trp Val Glu Lys Leu Asn Asp Thr Gln
35 40 45

Leu Asp Ser Gly
50

<210> 717
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T178N"

<400> 717
Ile Asp Gly Thr Phe Ile Ile Ser Asn Pro Ser Glu Ala Lys Asp Ser
1 5 10 15

Gly His Tyr Gln Cys Leu Ala Thr Asn Asn Asn Val Gly Ser Ile Leu
20 25 30

Ser Arg Glu Ala Thr Leu Gln Phe Ala Tyr Leu Gly Asn Phe Ser Gly
35 40 45

Arg Thr Arg Ser
50

<210> 718
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R807M"

<400> 718

Asn Asn Glu Gly Glu Gly Ser Leu Ser Thr Val Thr Ile Val Tyr Ser
1 5 10 15

Gly Glu Asp Glu Pro Gln Leu Ala Pro Met Met Gly Thr Ser Leu Gln
20 25 30

Ser Phe Ser Ala Ser Glu Met Glu Val Ser Trp Asn Ala Ile Ala Trp
35 40 45

Asn Arg Asn Thr
50

<210> 719
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S1029I"

<400> 719
Glu Pro Gly Thr Trp Met Arg Tyr Asn Leu Gln Ser Ala Leu Arg Ser
1 5 10 15

Ala Ala Arg Glu Phe Ser His Met Leu Ile Ile Arg Pro Val Pro Gly
20 25 30

Tyr Glu Pro Gly Tyr Ile Pro Gly Tyr Asp Thr Pro Gly Tyr Val Pro
35 40 45

Gly Tyr His Gly
50

<210> 720
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.F395L"

<400> 720
Glu Pro Tyr Thr Val Pro Val Phe Phe Asn Ala Thr Ser Tyr Leu Glu
1 5 10 15

Val Pro Gly Arg Leu Asn Gln Asp Leu Leu Leu Ser Val Ser Phe Gln
20 25 30

Phe Arg Thr Trp Asn Pro Asn Gly Leu Leu Val Phe Ser His Phe Ala
35 40 45

Asp Asn Leu Gly
50

<210> 721
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y436S"

<400> 721
Leu Phe Ser Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu Leu Phe Leu
1 5 10 15

Ser Asp Gly Lys Leu Lys Ser Asn Leu Ser Ser Gln Pro Gly Lys Leu
20 25 30

Pro Ser Asp Ile Thr Ala Gly Val Glu Leu Asn Asp Gly Gln Trp His
35 40 45

Ser Val Ser Leu
50

<210> 722
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I12F"

<400> 722
Met Leu Leu Phe Tyr Leu Leu Val Val Leu Ser Phe Phe Asp Ser Thr
1   5   10   15

Lys Ala Ser Ala Leu Thr Asn Pro Asn Val Ala Leu Phe Leu Leu Ala
            20   25   30

Asp Asp Cys Asp Asp Pro
        35

<210> 723
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P185S"

<400> 723
Ser Lys Ile Glu Gly Ile Glu Asn Met Cys Asn Leu Gln Lys Leu Asn
1   5   10   15

Leu Ala Gly Asn Glu Ile Glu His Ile Ser Ser Val Trp Leu Gly Lys
            20   25   30

Lys Leu Lys Ser Leu Arg Val Leu Asn Leu Lys Gly Asn Lys Ile Ser
        35   40   45

Ser Leu Gln Asp
    50

<210> 724
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R920fs"

<400> 724
Pro Lys Thr Glu Lys Pro Pro Ala Arg Lys Lys Ser Gly His Pro Ala
1 5 10 15

Pro Ser Ser Met Arg Ser Arg Gly Gly Ser Leu Glu Met Ser Pro Pro
20 25 30

Thr Leu Ser Pro Leu Cys Ser Leu Ile Val Val Ile Leu Ile Asn Ala
35 40 45

His

<210> 725
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K732N"

<400> 725
Asp Pro Leu Thr Val Lys Asp Pro Ile Cys Ala His Gly Asn Asp Asp
1 5 10 15

Leu Leu Pro Pro Val Asp Arg Ile Asp Asn Asn Asn Ser Thr Ala Ser
20 25 30

Tyr Leu Lys Asn Tyr Pro Leu Tyr Arg Gln Asp Tyr Asn Pro Lys Pro
35 40 45

Lys Pro Ser Asn
50

<210> 726
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.H617R"

<400> 726
Thr Lys Val Val Ser Ser Gln Ser Ser Phe Pro Leu Ala Ala Glu Gln
1 5 10 15

Thr Ile Ile Ser Ala Leu Lys Ala Ile Arg Arg Ala Leu Met Glu Asn
20 25 30

Ala Val Gln Pro Leu Leu Thr Ser Val Gly Asp Ala Ile Glu Ala Ile
35 40 45

Ile Ile Thr Met
50

<210> 727
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R1082I"

<400> 727
Ser Thr Val Gly Ala Leu Asn Lys Ile Gly Thr Asp Gly Thr Gln Val
1 5 10 15

Ala Met Val Gln Phe Thr Asp Asp Pro Ile Ile Thr Glu Phe Lys Leu
20 25 30

Asn Ala Tyr Lys Thr Lys Glu Thr Leu Leu Asp Ala Ile Lys His Ile
35 40 45

Ser Tyr Lys Gly
50

<210> 728
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K708R"

<400> 728
Ala Arg Gly Pro Asn Gly Ser Val Gly Glu Lys Gly Asp Pro Gly Asn
1 5 10 15

Arg Gly Leu Pro Gly Pro Pro Gly Lys Arg Arg Gly Gln Ala Gly Pro
20 25 30

Pro Gly Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro
35 40 45

Gly Pro Gly Cys
50

<210> 729
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G884fs"

<400> 729
Asp Arg Gly Ser Arg Gly Glu Lys Gly Asp Pro Gly Lys Asp Gly Val
1 5 10 15

Gly Gln Pro Gly Leu Pro Gly Pro Pro Asp Pro Arg Asp Leu Trp Ser
20 25 30

Thr Cys Arg Ser Arg Thr Asp Pro Ser
35 40

<210> 730
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P538Q"

<400> 730
Gly Pro Pro Gly Leu Ile Gly Ser Pro Gly Leu Lys Gly Gln Gln Gly
1 5 10 15

Ser Ala Gly Ser Met Gly Pro Arg Gly Gln Gln Pro Gly Asp Val Gly
20 25 30

Leu Pro Gly Glu His Gly Ile Pro Gly Lys Gln Gly Ile Lys Gly Glu
35 40 45

Lys Gly Asp Pro
50

<210> 731
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L550I"

<400> 731
Gly Pro Ala Gly Ala Pro Gly Leu Val Gly Pro Leu Gly Pro Ser Gly
1 5 10 15

Pro Lys Gly Lys Lys Gly Glu Pro Ile Ile Ile Ser Thr Ile Gln Gly
20 25 30

Met Pro Gly Asp Arg Gly Asp Ser Gly Ser Gln Gly Phe Arg Gly Val
35 40 45

Ile Gly Glu Pro
50

<210> 732
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G516W"

<400> 732
Gln Gly Pro Ile Gly Pro Pro Gly Glu Glu Gly Lys Arg Gly Pro Arg
1 5 10 15

Gly Asp Pro Gly Thr Val Gly Pro Pro Trp Trp Pro Val Gly Glu Arg
20 25 30

Gly Ala Pro Gly Asn Arg Gly Phe Pro Gly Ser Asp Gly Leu Pro Gly
35 40 45

Pro Lys Gly Ala
50

<210> 733
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G612W"

<400> 733
Leu Gly Pro Leu Gly Ala Pro Gly Glu Asp Gly Arg Pro Gly Pro Pro
1 5 10 15

Gly Ser Ile Gly Ile Arg Gly Gln Pro Trp Trp Ser Met Gly Leu Pro
20 25 30

Gly Pro Lys Gly Ser Ser Gly Asp Pro Gly Lys Pro Gly Glu Ala Gly
35 40 45

Asn Ala Gly Val
50

<210> 734
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A2378D"

<400> 734
Gly Gln Lys Gly Asp Pro Gly Tyr Pro Gly Pro Ala Gly Pro Lys Gly
1 5 10 15

Asn Arg Gly Asp Ser Ile Asp Gln Cys Asp Asp Leu Ile Gln Ser Ile
20 25 30

Lys Asp Lys Cys Pro Cys Cys Tyr Gly Pro Leu Glu Cys Pro Val Phe
35 40 45

Pro Thr Glu Leu
50

<210> 735
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D2792N"

<400> 735
Tyr Phe Phe Val Val Leu Gly Ile Gly Arg Lys Val Asn Ile Lys Glu
1 5 10 15

Val Tyr Thr Phe Ala Ser Glu Pro Asn Asn Asn Val Phe Phe Lys Leu
20 25 30

Val Asp Lys Ser Thr Glu Leu Asn Glu Glu Pro Leu Met Arg Phe Gly
35 40 45

Arg Leu Leu Pro

50

<210> 736
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T2224M"

<400> 736
Gln Glu Asp Phe Leu Gly Gly Asn Gly Phe Ile Gly Gln Glu Leu Asn
1 5 10 15

Ser Gly Arg Glu Ser Pro Phe Val Lys Met Met Glu Asp Asn Gly Ser
20 25 30

Asp Tyr Leu Val Tyr Leu Pro Ser Gln Met Phe Glu Pro Gln Lys Leu
35 40 45

Met Ile Asn Tyr
50

<210> 737
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P211Q"

<400> 737
Gly Val Glu Arg Ser Ser Ala Thr Leu Phe Val Asp Cys Asn Arg Ile
1 5 10 15

Glu Ser Leu Pro Ile Lys Pro Arg Gly Gln Gln Ile Asp Ile Asp Gly
20 25 30

Phe Ala Val Leu Gly Lys Leu Ala Asp Asn Pro Gln Val Ser Val Pro
35 40 45

Phe Glu Leu Gln
    50

<210> 738
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P283fs"

<400> 738
Arg Ile Thr Pro Ser Gln Thr Thr Asp Glu Arg Gly Pro Pro Gly Glu
1   5   10   15

Gln Gly Pro Pro Gly Pro Pro Gly Pro Leu Glu Phe Gln Ala Ser Met
            20   25   30

Ala Ser Thr Val Thr Glu Val Leu Arg Ala Pro Arg Ala Pro Arg Val
        35   40   45

Leu Gln Val Asn Arg Glu Ser Gln Glu Leu Gln Ala Ser Leu Ala His
    50   55   60

Leu Ala Leu Met Asp
65

<210> 739
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R425C"

<400> 739
Asn Val Ile Pro Val Leu Met Glu Phe Leu Ser Asp Asn Asn Glu Ala
1   5   10   15

Ala Ala Ala Asp Val Leu Glu Phe Val Cys Cys Glu Ala Ile Gln Arg
20 25 30

Phe Asp Asn Leu Arg Met Leu Ile Val Glu Lys Met Leu Glu Val Phe
35 40 45

His Ala Ile Lys
50

<210> 740
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V66L"

<400> 740
Ser Phe Ala Leu Ala Arg Ala Ala Gly Ala Pro His Gly Gly Asp Leu
1 5 10 15

Gln Pro Pro Ala Cys Pro Glu Pro Arg Leu Trp Arg Gln Leu Ser Leu
20 25 30

Ser Ala Ala Ala Val Val Asp Ser Ala Pro Arg Pro Leu Gln Pro Tyr
35 40 45

Leu Arg Leu Met
50

<210> 741
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.*526R"

<400> 741

Leu Thr Gln Arg Glu Val Gln Ala Lys Gln Leu Glu Leu Glu Ile Lys
1 5 10 15

Asn Leu Arg Met Gly Ser Glu Gln Leu Arg Arg Ala Glu Thr Ser Ala
20 25 30

Leu Leu Thr Leu Arg Asp Thr Thr Arg Leu His Gly Glu Val
35 40 45

<210> 742
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L86I"

<400> 742
Pro Ser Lys Ala Ala Glu Arg Val Val Gly Arg Trp Leu Leu Val Cys
1 5 10 15

Ser Gly Thr Val Ala Gly Ala Val Ile Ile Ile Gly Gly Val Thr Arg
20 25 30

Leu Thr Glu Ser Gly Leu Ser Met Val Asp Trp His Leu Ile Lys Glu
35 40 45

Met Lys Pro Pro
50

<210> 743
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S8L"

<400> 743
Met Ala Val Val Gly Val Ser Leu Leu Val Ser Arg Leu Leu Gly Arg

1 5 10 15

Ser Arg Pro Gln Leu Gly Arg Pro Met Ser Ser Gly Ala His Gly Glu
20 25 30

Glu Gly

<210> 744
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P784fs"

<400> 744
Thr Asp Glu Ala Val Pro Ala Phe Gln Pro His Thr Gly Ser Leu Val
1 5 10 15

Ala Val Ala Pro Ser Arg His Pro Pro Glu Gln Arg Arg Glu Lys Gly
20 25 30

Leu Ser Ser Pro Lys His Gly Phe Gly Ile Val Ser Thr Ser Val Thr
35 40 45

His Leu Val Arg Gly His Ser Val
50 55

<210> 745
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P290Q"

<400> 745
Ser Ala His Glu Tyr Ser Ser Ser Pro Asp Asp Ala Ile Phe Gln Ser
1 5 10 15

Leu Ala Arg Ala Tyr Ser Ser Phe Asn Gln Gln Ala Met Ser Asp Pro
20 25 30

Asn Arg Pro Pro Cys Arg Lys Asn Asp Asp Asp Ser Ser Phe Val Asp
35 40 45

Gly Thr Thr Asn
50

<210> 746
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q127H"

<400> 746
Ser Lys Ser Pro Asn Leu Ser Lys His Asp Phe Leu Gly Gln Val Phe
1 5 10 15

Cys Thr Leu Gly Glu Ile Val Gly Ser His His Gly Ser Arg Leu Glu
20 25 30

Lys Pro Ile Val Gly Ile Pro Gly Lys Lys Cys Gly Thr Ile Ile Leu
35 40 45

Thr Ala Glu Glu
50

<210> 747
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T855K"

<400> 747
Thr Pro Arg Leu Pro Met Asn Lys Glu Trp Pro Ser Asn Leu Asp Leu
1 5 10 15

Arg Lys Glu Leu Ser Glu Pro Ser Ser Lys Lys Arg Ile Tyr Ala Ile
20 25 30

Ala Lys Ala Ile Asp Asp Asn Met Ser Leu Asp Glu Ile Glu Lys Leu
35 40 45

Thr Tyr Ile Asp
50

<210> 748
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P219Q"

<400> 748
Asn Pro Pro Leu Gln Arg Ser Ser Ser Leu Ile Gln Leu Thr Ser Gln
1 5 10 15

Asn Ser Ser Pro Asn Gln Gln Arg Thr Gln Gln Gln Val Ile Gly Val
20 25 30

Met Gln Ser Gln Asn Ser Ser Ala Gly Asn Arg Gly Pro Arg Pro Leu
35 40 45

Glu Gln Val Thr
50

<210> 749
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.L79fs"

<400> 749
Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly
1 5 10 15

Arg Pro Phe Ser Ile Ile Cys Leu Lys Thr Gln Ser Gly Gln Val Leu
20 25 30

Arg Thr Ser Ala Asn Val Asn His Val Val Ile Leu Gln Ile Leu
35 40 45

<210> 750
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V206fs"

<400> 750
Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu Ser
1 5 10 15

Ser Gly Lys Trp Ser Ala Val Pro Pro His Val Lys Arg His Ala Val
20 25 30

Asn Leu

<210> 751
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L628fs"

<400> 751
Ser Ile Cys Ala Phe Gln Asn Ser Phe Leu Gly Gly Leu Pro Val Gly

1 5 10 15

Met Thr Ser Asn Gly Val Ala Leu Leu Thr Ser Ile Ile Cys His Pro
20 25 30

His Leu Arg Leu
35

<210> 752
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F630V"

<400> 752
Ile Cys Ala Phe Gln Asn Ser Phe Leu Gly Gly Leu Pro Val Gly Met
1 5 10 15

Thr Ser Asn Gly Val Ala Leu Leu Asn Val Val Tyr Asn Met Pro Ser
20 25 30

Thr Pro Ser Phe Val Gly Cys Leu Gln Asp Ile Lys Ile Asp Trp Asn
35 40 45

His Ile Thr Leu
50

<210> 753
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T1110M"

<400> 753
Gly Trp Glu Gly Pro Arg Cys Glu Ala His Val Asp Pro Cys His Ser
1 5 10 15

Ala Pro Cys Ala Arg Gly Arg Cys His Met Met His Pro Asp Gly Arg
20 25 30

Phe Glu Cys Arg Cys Pro Pro Gly Phe Gly Gly Pro Arg Cys Arg Leu
35 40 45

Pro Val Pro Ser
50

<210> 754
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1435H"

<400> 754
Phe Gly Met His Val Gln Glu Tyr Gly Ser Asp Cys Pro Pro Pro Asn
1 5 10 15

Thr Arg Arg Val Tyr Ile Ser Tyr Leu His His Ser Ile His Phe Phe
20 25 30

Arg Pro Arg Cys Leu Arg Thr Ala Val Tyr His Glu Ile Leu Ile Gly
35 40 45

Tyr Leu Glu Tyr
50

<210> 755
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1446H"

<400> 755
Cys Pro Pro Pro Asn Thr Arg Arg Val Tyr Ile Ser Tyr Leu Asp Ser
1 5 10 15

Ile His Phe Phe Arg Pro Arg Cys Leu His His Thr Ala Val Tyr His
20 25 30

Glu Ile Leu Ile Gly Tyr Leu Glu Tyr Val Lys Lys Leu Gly Tyr Val
35 40 45

Thr Gly His Ile
50

<210> 756
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P2094L"

<400> 756
Asp Leu Leu Arg Thr Leu Lys Ser Pro Ser Ser Pro Gln Gln Gln Gln
1 5 10 15

Gln Val Leu Asn Ile Leu Lys Ser Asn Leu Leu Gln Leu Met Ala Ala
20 25 30

Phe Ile Lys Gln Arg Thr Ala Lys Tyr Val Ala Asn Gln Pro Gly Met
35 40 45

Gln Pro Gln Pro
50

<210> 757
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.M48fs"

<400> 757
Pro Ala Cys Ser Cys Ala His Val Glu Cys Pro Pro Ala His Thr Cys
1 5 10 15

Arg Cys Gly Val Pro Ala Cys Ser His Thr Cys Pro Cys Gly Val Pro
20 25 30

Ala Cys Ser His Val Pro Met Trp Ser Ala Arg Leu Leu Thr His Val
35 40 45

Ser Met Trp Ser Ala His Leu Leu Met Cys Pro Cys Gly Val Pro Thr
50 55 60

Cys Ser His Val Pro Met Trp Ser Ala Thr Cys Ser His Thr Cys Pro
65 70 75 80

Cys Gly Val Pro Ala Cys Ser Arg Ala His Val Glu Cys Pro Pro Ala
85 90 95

His Thr Cys Arg Cys Gly Val Pro Ala Cys Ser His Val Pro Met Arg
100 105 110

Ser Ala Arg Leu Leu Thr Arg Ala His Ala Glu Cys Pro Pro Ala His
115 120 125

Thr Cys Pro Cys Gly Val Pro Ala Cys Ser His Val Pro Thr Trp Ser
130 135 140

Ala Arg Leu Leu Thr Arg Ala His Val Glu Cys Pro Pro Ala His Thr
145 150 155 160

Cys Gln Arg Gly Val Pro Ala
165

<210> 758
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="p.C143R"

<400> 758
Ser His Val Pro Met Arg Ser Ala Arg Leu Leu Thr Arg Ala His Ala
1 5 10 15

Glu Cys Pro Pro Ala His Thr Cys Pro Arg Arg Gly Val Pro Ala Cys
20 25 30

Ser His Val Pro Met Arg Ser Ala Arg Leu Leu Thr Arg Ala Asp Val
35 40 45

Glu Cys Pro Pro
50

<210> 759
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C174R"

<400> 759
Ser His Val Pro Met Arg Ser Ala Arg Leu Leu Thr Arg Ala Asp Val
1 5 10 15

Glu Cys Pro Pro Ala His Thr Cys Pro Arg Arg Gly Val Pro Ala Cys
20 25 30

Ser His Val Pro Thr Trp Ser Ala Arg Leu Ile Thr Arg Ala His Val
35 40 45

Glu Cys Ser Pro
50

<210> 760
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S180fs"

<400> 760
Leu Thr Arg Ala Asp Val Glu Cys Pro Pro Ala His Thr Cys Pro Cys
1 5 10 15

Gly Val Pro Ala Cys Ser His Val Pro Met Trp Ser Ala Arg Leu Leu
20 25 30

Thr Arg Ala Asp Val Glu Cys Leu Pro Ala His Thr Cys Pro Cys Gly
35 40 45

Val Phe Ala Cys Ser His Val Pro Met Arg Ser Ala Arg Leu Leu Thr
50 55 60

Arg Ala Asp Ala Glu Cys Pro Pro Ala His Thr Cys Pro Cys Gly Val
65 70 75 80

Pro Ala Cys Ser Arg Ala Asp Val Glu Cys Pro Pro Ala His Thr Cys
85 90 95

Pro Cys Gly Val Pro Ala Cys Ser Arg Ala Asp Val Gly Cys Pro Pro
100 105 110

Ala His Met Cys Arg Cys Gly Val Pro Ala Cys Ser His Val Pro Met
115 120 125

Trp Ser Ala Arg Leu Leu Thr Arg Ala Asp Val Glu Cys Pro Pro Ala
130 135 140

His Val Pro Ile Trp Ser Ala Arg Leu Leu Thr Arg Ala Ile Val Glu
145 150 155 160

Cys Pro Pro Ala His Thr His Ala Asp Val Glu Cys Pro Pro Ala His
165 170 175

Thr Cys Pro Cys Gly Val Pro Ala Cys Ser His Val Pro Met Trp Ser
180 185 190

Ala Arg Leu Leu Thr His Val Pro Met Trp Ser Ala Arg Leu Leu Thr
195 200 205

Arg Ala His Val Glu Cys Leu Pro Ala His Thr Arg Ala His Val Glu
210 215 220

Cys Pro Pro Ala His Thr Lys Pro Trp His Gly Gly Ser Val Gly Phe
225 230 235 240

Leu Ser Cys Arg Pro Ser Gln Thr Leu Leu Pro Tyr Ile Leu Leu Met
245 250 255

Val Ala Phe

<210> 761
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I190L"

<400> 761
Glu Cys Pro Pro Ala His Thr Cys Pro Cys Gly Val Pro Ala Cys Ser
1 5 10 15

His Val Pro Thr Trp Ser Ala Arg Leu Leu Leu Thr Arg Ala His Val
20 25 30

Glu Cys Ser Pro Ala His Thr Cys Arg Cys Gly Val Pro Ala Cys Ser
35 40 45

His Val Pro Met
50

<210> 762
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R222W"

<400> 762

Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly Asn Trp
1 5 10 15

Trp Gly His Ala Pro Tyr Lys His Gly Trp Trp Pro Cys Ser Ala Cys
20 25 30

Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys Tyr Lys Glu
35 40 45

Gly Ser Asp Arg
50

<210> 763
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A355P"

<400> 763
Arg Thr Ser Arg Ala Val Gln Glu Ala Gly Leu Gly Leu Ser Thr Gly
1 5 10 15

Leu Arg Leu Ala Glu Ser Arg Ala Glu Pro Pro Ala Leu Glu Lys Gln
20 25 30

Ala Leu Leu Gln Ala Gln Leu Glu Glu Gln Leu Arg Asp Lys Val Leu
35 40 45

Arg Glu Lys Asp
50

<210> 764
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.Q580H"

<400> 764
Asp Pro Leu Phe Ser Lys Ser Gly Gly Gly Gly Asn Phe Val Leu Ser
1 5 10 15

Thr Ser Leu Val Gly Tyr Leu Arg Val His His Gly Val Val Val Pro
20 25 30

Met Val His Asn Gly Tyr Gly Phe Phe Tyr His Ile Arg Asp Asp Arg
35 40 45

Phe Val Val Ala
50

<210> 765
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L32fs"

<400> 765
Thr Glu Glu Arg Thr Phe Gln Tyr Gln Asp Ser Leu Pro Ser Leu Pro
1 5 10 15

Val Pro Ser Leu Glu Glu Ser Leu Lys Asn Thr Leu Asn Gln Ser Pro
20 25 30

Glu His Ala Thr Arg
35

<210> 766
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S363L"

<400> 766
Asn Lys Thr Val Leu Ser Ser Ser Leu Asn Asn His Pro Gln Thr Ser
1 5 10 15

Val Pro Asn Ala Ser Ala Leu His Pro Leu Leu Leu Arg Leu Phe Ser
20 25 30

Leu Ser Asn Pro Ser Leu Ser Thr Thr Asn Leu Ser Gly Pro Ser Arg
35 40 45

Arg Arg Gln Pro
50

<210> 767
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R143G"

<400> 767
His Leu Thr Glu Ile His Ser Leu Asn Val Leu Glu Gly Ser Trp Ile
1 5 10 15

Leu Tyr Glu Met Pro Asn Tyr Arg Gly Gly Gly Gln Tyr Leu Leu Arg
20 25 30

Pro Gly Glu Tyr Arg Arg Phe Leu Asp Trp Gly Ala Pro Asn Ala Lys
35 40 45

Val Gly Ser Leu
50

<210> 768
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G159fs"

<400> 768
Tyr Glu Met Pro Asn Tyr Arg Gly Arg Gln Tyr Leu Leu Arg Pro Gly
1 5 10 15

Asp Tyr Arg Arg Tyr His Asp Trp Gly Val Gln Met Pro Lys Ser Ala
20 25 30

Leu

<210> 769
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.*315K"

<400> 769
Phe Lys Ser Leu Gly Met Ala Val Glu Asp Thr Val Ala Ala Lys Leu
1 5 10 15

Ile Tyr Asp Ser Trp Ser Ser Gly Lys Lys Lys Asn Lys Gly Thr
20 25 30

<210> 770
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R220C"

<400> 770
Asn Val Gln Leu Glu Thr Gly Asp Lys Ile Asn Phe Val Ile Asp Asn
1 5 10 15

Asn Lys His Thr Gly Ala Val Ser Ala Cys Cys Asn Ile Met Leu Leu
20 25 30

Lys Lys Lys Gln Ala Arg Cys Gln Gly Val Val Cys Ala Met Lys Glu
35 40 45

Ala Phe Gly Phe
50

<210> 771
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G298S"

<400> 771
Ser Phe Gly Leu Phe Tyr Lys Pro Ser Pro Asp Ala Gly Glu Glu Glu
1 5 10 15

Cys Ser Pro Val Leu Arg Glu Gly Leu Ser Ser Ser Leu His Thr Arg
20 25 30

His His Cys Gln Ile Pro Val Pro Asp Pro Ala Thr His Gly Gln Tyr
35 40 45

Ile Val Ser Val
50

<210> 772
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P468fs"

<400> 772
Ser Leu Trp Val Gly Trp Glu Pro Pro Asn Pro Trp Pro Gln Gly Tyr

1 5 10 15

Val Ile Glu Trp Gly Leu Gly Pro Pro Ala Arg Ala Ile Ala Thr Arg
20 25 30

Pro Gly Gly Trp Asn Arg Met Gly Glu Pro Arg Gly Phe Cys
35 40 45

<210> 773
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L362F"

<400> 773
Val Ser Leu Asn Glu Glu Phe Asn Arg Gly Arg Gly Leu Asn Val Gly
1 5 10 15

Ala Arg Ala Trp Asp Lys Gly Glu Val Phe Phe Met Phe Phe Cys Asp
20 25 30

Val Asp Ile Tyr Phe Ser Ala Glu Phe Leu Asn Ser Cys Arg Leu Asn
35 40 45

Ala Glu Pro Gly
50

<210> 774
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R117Q"

<400> 774
Ser Ser Asn Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu
1 5 10 15

His Ile Ser Leu Leu Leu Ile Glu Ser Gln Gln Leu Glu Pro Val Arg
20 25 30

Phe Leu Arg Ser Thr Phe Thr Asn Asn Leu Val Tyr Asp Thr Ser Asp
35 40 45

Ser Asp Asp Tyr
50

<210> 775
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1855Q"

<400> 775
Pro Thr Cys Val Val Pro Cys Gly Gly Asn Leu Thr Glu Arg Arg Gly
1 5 10 15

Thr Ile Leu Ser Pro Gly Phe Pro Glu Gln Gln Tyr Leu Asn Ser Leu
20 25 30

Asn Cys Val Trp Lys Ile Val Val Pro Glu Gly Ala Gly Ile Gln Ile
35 40 45

Gln Val Val Ser
50

<210> 776
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q691K"

<400> 776
Asp Pro Gly Thr Pro Leu Tyr Gly Ile Arg Glu Gly Asp Gly Phe Ser
1 5 10 15

Asn Arg Asp Val Leu Arg Phe Glu Cys Lys Lys Phe Gly Phe Glu Leu
20 25 30

Ile Gly Glu Lys Ser Ile Val Cys Gln Glu Asn Asn Gln Trp Ser Ala
35 40 45

Asn Ile Pro Ile
50

<210> 777
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H952Y"

<400> 777
Ala Glu Pro Gly His Ser Ile Lys Ile Thr Phe Glu Arg Phe Gln Thr
1 5 10 15

Glu Leu Asn Tyr Asp Val Leu Glu Val Tyr Tyr Asp Gly Pro Asn Leu
20 25 30

Leu Ser Pro Leu Leu Gly Ser Tyr Asn Gly Thr Gln Val Pro Gln Phe
35 40 45

Leu Phe Ser Ser
50

<210> 778
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.T1094K"

<400> 778
Gly Asp Val Arg Gly Pro Ser Gly Thr Ile Leu Ser Pro Gly Tyr Pro
1 5 10 15

Glu Phe Tyr Pro Asn Ser Leu Asn Cys Lys Lys Trp Thr Val Asp Val
20 25 30

Thr His Gly Lys Gly Val Gln Phe Asn Phe His Thr Phe His Leu Glu
35 40 45

Asp His His Asp
50

<210> 779
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E171K"

<400> 779
Ser Thr Lys Ser Val Phe Ser Leu Arg Leu Thr Ser Asp Phe Ala Val
1 5 10 15

Ser Ala His Gly Phe Lys Val Tyr Tyr Lys Lys Glu Leu Gln Ser Ser
20 25 30

Ser Cys Gly Asn Pro Gly Val Pro Pro Lys Gly Val Leu Tyr Gly Thr
35 40 45

Arg Phe Asp Val
50

<210> 780
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q174H"

<400> 780
Ser Val Phe Ser Leu Arg Leu Thr Ser Asp Phe Ala Val Ser Ala His
1   5   10   15

Gly Phe Lys Val Tyr Tyr Glu Glu Leu His His Ser Ser Ser Cys Gly
            20   25   30

Asn Pro Gly Val Pro Pro Lys Gly Val Leu Tyr Gly Thr Arg Phe Asp
        35   40   45

Val Gly Asp Lys
    50

<210> 781
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.F2383fs"

<400> 781
Leu Glu Ser Val Tyr Ser Thr Ser Asn Gln Ile Leu Ile Lys Phe His
1   5   10   15

Ser Asp Phe Thr Thr Ser Gly Phe Phe Cys Ala Gln Leu Ser Arg Leu
            20   25   30

Ser Thr Lys Gly Val Pro Thr Ser Thr Thr Cys Ala Gln Cys
        35   40   45

<210> 782
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.P2727T"

<400> 782
Leu Glu His Gly Arg Trp Arg Ile Val Asn Gly Ser His Tyr Glu Tyr
1 5 10 15

Lys Thr Lys Val Val Phe Ser Cys Asp Thr Thr Gly Tyr His Gly Leu
20 25 30

Gly Pro Ala Ser Ile Glu Cys Leu Pro Asn Gly Thr Trp Ser Trp Arg
35 40 45

Asn Glu Arg Pro
50

<210> 783
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T2810N"

<400> 783
Cys Asp Leu Gly Phe Met Leu Val Gly Ser Ala Val Arg Glu Cys Leu
1 5 10 15

Ser Ser Gly Leu Trp Ser Glu Ser Glu Asn Asn Arg Cys Leu Ala Gly
20 25 30

His Cys Gly Ile Pro Glu Leu Ile Val Asn Gly Gln Val Ile Gly Glu
35 40 45

Asn Tyr Gly Tyr
50

<210> 784
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D119N"

<400> 784
Ala Val Thr Gly Thr Ala Trp Leu Glu Ala Asp Ser Pro Gly Leu Gly
1 5 10 15

Gly Val Thr Ala Glu Ala Gly Ser Gly Asn Asn Ala Gln Ala Leu Pro
20 25 30

Ala Thr Leu Gln Ala Pro His Glu Val Leu Gly Gln Ser Ile Met Pro
35 40 45

Pro Ala Ile Pro
50

<210> 785
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.234_243EKLTEEATEE>E"

<400> 785
Asp Leu Ala Glu Met Ala Arg Glu Pro Ala Glu Glu Ala Ala Asp Glu
1 5 10 15

Lys Pro Pro Glu Glu Ala Ala Glu Glu Glu Pro Ala Ala Glu Glu Pro
20 25 30

Thr Ser Glu Glu Ala Val Ala Pro Glu Glu Val Thr Lys Ser Gln Pro
35 40 45

Glu Lys Trp Asp Glu Glu Ala Gln Asp Ala Ala Gly Glu Glu Glu Lys
50 55 60

Glu Gln Glu Lys Glu Lys Asp Val Glu Asn Lys Val Lys Asn
65 70 75

<210> 786
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A364V"

<400> 786
Ile Ile Gln Leu Ser Glu Val Asp Lys Thr Lys Glu Glu Leu Thr Glu
1 5 10 15

His Ile Lys Asn Leu Gln Thr Gln Gln Val Val Ser Leu Gln Ser Glu
20 25 30

Asn Ile Tyr Phe Glu Ser Glu Asn Gln Lys Leu Gln Gln Lys Leu Lys
35 40 45

Ile Met Thr Glu
50

<210> 787
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K202fs"

<400> 787
Glu Gln Gly Glu Leu Pro Pro Gln Glu Asp Pro Ser Trp Gln Lys Asp
1 5 10 15

Pro Asp Tyr Gln Pro Pro Ala Lys Lys Lys Gln Arg Lys Pro Lys Arg
20 25 30

Ala Asn Cys Val Ile Gln Arg Arg Ala Lys Met
35 40

<210> 788

<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K202fs"

<400> 788
Glu Gln Gly Glu Leu Pro Pro Gln Glu Asp Pro Ser Trp Gln Lys Asp
1 5 10 15

Pro Asp Tyr Gln Pro Pro Ala Lys Lys Gln Arg Lys Pro Lys Arg Ala
20 25 30

Asn Cys Val Ile Gln Arg Arg Ala Lys Met
35 40

<210> 789
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E423K"

<400> 789
Tyr Glu Cys His Ile Cys His Thr Arg Phe Thr Gln Ser Gly Thr Met
1 5 10 15

Lys Ile His Ile Leu Gln Lys His Gly Lys Lys Asn Val Pro Lys Tyr
20 25 30

Gln Cys Pro His Cys Ala Thr Ile Ile Ala Arg Lys Ser Asp Leu Arg
35 40 45

Val His Met Arg
50

<210> 790
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E126K"

<400> 790
Lys His Pro Val Arg Phe Phe Val His Lys Arg Pro His Val Asp Phe
1 5 10 15

Phe Leu Glu Val Val Ser Gln Trp Tyr Lys Lys Leu Val Val Phe Thr
20 25 30

Ala Ser Met Glu Ile Tyr Gly Ser Ala Val Ala Asp Lys Leu Asp Asn
35 40 45

Ser Arg Ser Ile
50

<210> 791
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.K856fs"

<400> 791
Ile Ile Arg Ile Gln Ser Pro Ala Gly Pro Arg His Pro Val Val Met
1 5 10 15

Trp Arg Met Lys Ala Pro Ala Lys Lys Asn Pro
20 25

<210> 792
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K335I"

<400> 792
Glu Ser Lys Leu Ile Ile Leu Ala Ser Gly Gly Pro Gln Ala Leu Val
1 5 10 15

Asn Ile Met Arg Thr Tyr Thr Tyr Glu Ile Ile Leu Leu Trp Thr Thr
20 25 30

Ser Arg Val Leu Lys Val Leu Ser Val Cys Ser Ser Asn Lys Pro Ala
35 40 45

Ile Val Glu Ala
50

<210> 793
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G34R"

<400> 793
Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser His
1 5 10 15

Trp Gln Gln Gln Ser Tyr Leu Asp Ser Arg Arg Ile His Ser Gly Ala
20 25 30

Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu Glu
35 40 45

Asp Val Asp Thr
50

<210> 794
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G34V"

<400> 794
Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser His
1 5 10 15

Trp Gln Gln Gln Ser Tyr Leu Asp Ser Val Val Ile His Ser Gly Ala
20 25 30

Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu Glu
35 40 45

Asp Val Asp Thr
50

<210> 795
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.H36P"

<400> 795
Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser His Trp Gln
1 5 10 15

Gln Gln Ser Tyr Leu Asp Ser Gly Ile Pro Pro Ser Gly Ala Thr Thr
20 25 30

Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu Glu Asp Val
35 40 45

Asp Thr Ser Gln
50

<210> 796

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S37A"

<400> 796
Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln
1 5 10 15

Gln Ser Tyr Leu Asp Ser Gly Ile His Ala Ala Gly Ala Thr Thr Thr
20 25 30

Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu Glu Asp Val Asp
35 40 45

Thr Ser Gln Val
50

<210> 797
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S37C"

<400> 797
Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln
1 5 10 15

Gln Ser Tyr Leu Asp Ser Gly Ile His Cys Cys Gly Ala Thr Thr Thr
20 25 30

Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu Glu Asp Val Asp
35 40 45

Thr Ser Gln Val
50

<210> 798
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S37F"

<400> 798
Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln
1 5 10 15

Gln Ser Tyr Leu Asp Ser Gly Ile His Phe Phe Gly Ala Thr Thr Thr
20 25 30

Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu Glu Asp Val Asp
35 40 45

Thr Ser Gln Val
50

<210> 799
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.N387K"

<400> 799
Gly Met Gln Ala Leu Gly Leu His Leu Thr Asp Pro Ser Gln Arg Leu
1 5 10 15

Val Gln Asn Cys Leu Trp Thr Leu Arg Lys Lys Leu Ser Asp Ala Ala
20 25 30

Thr Lys Gln Glu Gly Met Glu Gly Leu Leu Gly Thr Leu Val Gln Leu
35 40 45

Leu Gly Ser Asp
50

<210> 800
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T41A"

<400> 800
Pro Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu
1 5 10 15

Asp Ser Gly Ile His Ser Gly Ala Thr Ala Ala Thr Ala Pro Ser Leu
20 25 30

Ser Gly Lys Gly Asn Pro Glu Glu Glu Asp Val Asp Thr Ser Gln Val
35 40 45

Leu Tyr Glu Trp
50

<210> 801
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T41I"

<400> 801
Pro Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu
1 5 10 15

Asp Ser Gly Ile His Ser Gly Ala Thr Ile Ile Thr Ala Pro Ser Leu
20 25 30

Ser Gly Lys Gly Asn Pro Glu Glu Glu Asp Val Asp Thr Ser Gln Val
35 40 45

Leu Tyr Glu Trp
50

<210> 802
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S45P"

<400> 802
Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu Asp Ser Gly Ile
1 5 10 15

His Ser Gly Ala Thr Thr Thr Ala Pro Pro Pro Leu Ser Gly Lys Gly
20 25 30

Asn Pro Glu Glu Glu Asp Val Asp Thr Ser Gln Val Leu Tyr Glu Trp
35 40 45

Glu Gln Gly Phe
50

<210> 803
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D32N"

<400> 803
Leu Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val
1 5 10 15

Ser His Trp Gln Gln Gln Ser Tyr Leu Asn Asn Ser Gly Ile His Ser

20 25 30

Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu
35 40 45

Glu Glu Asp Val
50

<210> 804
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D32Y"

<400> 804
Leu Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val
1 5 10 15

Ser His Trp Gln Gln Gln Ser Tyr Leu Tyr Tyr Ser Gly Ile His Ser
20 25 30

Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu
35 40 45

Glu Glu Asp Val
50

<210> 805
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D32G"

<400> 805
Leu Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val
1 5 10 15

Ser His Trp Gln Gln Gln Ser Tyr Leu Gly Gly Ser Gly Ile His Ser
20 25 30

Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu
35 40 45

Glu Glu Asp Val
50

<210> 806
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D32V"

<400> 806
Leu Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val
1 5 10 15

Ser His Trp Gln Gln Gln Ser Tyr Leu Val Val Ser Gly Ile His Ser
20 25 30

Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu
35 40 45

Glu Glu Asp Val
50

<210> 807
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S33P"

<400> 807
Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser
1 5 10 15

His Trp Gln Gln Gln Ser Tyr Leu Asp Pro Pro Gly Ile His Ser Gly
20 25 30

Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu
35 40 45

Glu Asp Val Asp
50

<210> 808
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S33Y"

<400> 808
Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser
1 5 10 15

His Trp Gln Gln Gln Ser Tyr Leu Asp Tyr Tyr Gly Ile His Ser Gly
20 25 30

Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu
35 40 45

Glu Asp Val Asp
50

<210> 809
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.S33C"

<400> 809
Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser
1 5 10 15

His Trp Gln Gln Gln Ser Tyr Leu Asp Cys Cys Gly Ile His Ser Gly
20 25 30

Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu
35 40 45

Glu Asp Val Asp
50

<210> 810
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S33F"

<400> 810
Met Glu Leu Asp Met Ala Met Glu Pro Asp Arg Lys Ala Ala Val Ser
1 5 10 15

His Trp Gln Gln Gln Ser Tyr Leu Asp Phe Phe Gly Ile His Ser Gly
20 25 30

Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly Lys Gly Asn Pro Glu Glu
35 40 45

Glu Asp Val Asp
50

<210> 811
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I447fs"

<400> 811
Val His Leu Gly Ala Cys Gly Ala Leu Lys Asn Ile Ser Phe Gly Arg
1 5 10 15

Asp Gln Asp Asn Lys Ile Ala Ile Lys Thr Val Met Val Cys Leu Pro
20 25 30

Leu Cys Asp Cys Phe Glu Arg Leu Val Ile Trp Thr Leu Leu Lys Leu
35 40 45

Leu Pro Glu Pro Cys Gly Ile Phe His Pro Met Thr Gln Ser Lys Trp
50 55 60

Arg Leu Trp Thr Met His Cys Met Pro
65 70

<210> 812
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F105fs"

<400> 812
Asn Ser Gly His Phe Thr Ile Ile Tyr Asn Gln Gly Phe Glu Ile Val
1 5 10 15

Leu Asn Asp Tyr Lys Trp Phe Ala Phe Leu Ser Ile Lys Lys Arg Ala
20 25 30

Ala Arg

<210> 813
<211> 74
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P89fs"

<400> 813
Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr
1 5 10 15

Gly Glu Ile Gly Ile Gly Thr Pro Pro Pro Val Leu His Ser Arg Leu
20 25 30

Arg His Gly Leu Leu Gln Pro Val Gly Pro Leu His Pro Leu Gln Thr
35 40 45

Ala Gly His Arg Leu Leu Asp Pro Pro Gln Val Gln Gln Arg Gln Val
50 55 60

Gln His Leu Arg Glu Glu Trp Tyr Leu Val
65 70

<210> 814
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S420L"

<400> 814
Thr Ser Ser Thr Pro Pro Leu Pro Ser Asn Ala Ala Pro Pro Thr Ala
1 5 10 15

Gln Thr Pro Gly Ile Ala Pro Gln Asn Leu Leu Gln Ala Pro Pro Met
20 25 30

His Ser Leu His Ser Pro Cys Ala Asn Thr Ser Leu His Pro Gly Leu
35 40 45

Asn Pro Arg Ile
50

<210> 815
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R164C"

<400> 815
Leu Glu Met Glu Lys Leu Gln Leu Gln Ala Leu Glu Gln Glu His Lys
1 5 10 15

Lys Leu Ala Ala Arg Leu Glu Glu Glu Cys Cys Gly Lys Asn Lys Gln
20 25 30

Val Val Leu Met Leu Val Lys Glu Cys Lys Gln Leu Ser Gly Lys Val
35 40 45

Ile Glu Glu Ala
50

<210> 816
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G596C"

<400> 816
Glu His Leu Arg Asn Gly Arg Gly Phe Thr Val Arg Trp Glu Thr Gln
1 5 10 15

Gln Pro Glu Cys Gly Gly Ile Leu Thr Cys Cys Pro Tyr Gly Ser Ile
20 25 30

Lys Ser Pro Gly Tyr Pro Gly Asn Tyr Pro Pro Gly Arg Asp Cys Val
35 40 45

Trp Ile Val Val
    50

<210> 817
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.I2816M"

<400> 817
Gly Gly Gly Phe Tyr Ala Thr Trp Asn Thr Gln Thr Leu Gly Cys Gly
1   5   10   15

Gly Ile Phe His Ser Asp Asn Gly Thr Met Met Arg Ser Pro His Trp
            20   25   30

Pro Gln Asn Phe Pro Glu Asn Ser Arg Cys Ser Trp Thr Ala Ile Thr
        35   40   45

His Lys Ser Lys
    50

<210> 818
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="p.E485K"

<400> 818
Asp Val Phe Gln Lys Phe Tyr Ala Lys Met Leu Ala Lys Arg Leu Val
1   5   10   15

His Gln Asn Ser Ala Ser Asp Asp Ala Lys Lys Ala Ser Met Ile Ser
            20   25   30

Lys Leu Lys Gln Ala Cys Gly Phe Glu Tyr Thr Ser Lys Leu Gln Arg

35 40 45

Met Phe Gln Asp
50

<210> 819
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L371F"

<400> 819
Gln Ala Gln Pro Ser Phe Arg Arg Ser Arg Arg Phe Arg Pro Arg Ser
1 5 10 15

Glu Phe Ala Ser Gly Asn Thr Tyr Ala Phe Phe Tyr Val Arg Asp Thr
20 25 30

Leu Gln Pro Gly Met Arg Val Arg Met Leu Asp Asp Tyr Glu Glu Ile
35 40 45

Ser Ala Gly Asp
50

<210> 820
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D1726E"

<400> 820
Ser Pro Arg Cys Trp Pro Val Ser Pro Leu Cys Tyr Leu Tyr His Pro
1 5 10 15

Arg Lys Cys Leu Pro Thr Glu Phe Cys Glu Glu Ala Leu Asp Arg Phe
20 25 30

Ser Ser Phe Tyr Ser Gln Ser Gln Asn His Pro Val Leu Asp Met Gly
35 40 45

Pro His Arg Arg
50

<210> 821
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A439fs"

<400> 821
Leu Ser Gly Ser Ala Arg Arg Lys Gly Lys Asp Gln Pro Glu Ser Arg
1 5 10 15

Arg Pro Gly Ser Leu Pro Ala Pro Pro Ser Phe Ser Val Ala Pro Gln
20 25 30

Pro Gly Gly Ala Gly Phe Gln Tyr
35 40

<210> 822
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K364E"

<400> 822
Glu Glu Leu Glu Arg Lys Arg Gln Glu Met Met Glu Asn Ala Lys Trp
1 5 10 15

Arg Glu Glu Glu Arg Leu Asn Ile Leu Glu Glu Arg His Ala Lys Asp
20 25 30

Glu Glu Arg Glu Gln Arg Leu Glu Lys Leu Asp Ser Arg Asp Gly Lys
35 40 45

Phe Ile His Arg
50

<210> 823
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K122N"

<400> 823
Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
1 5 10 15

Val Arg Lys Ser Gln Arg Ser Arg Gln Asn Asn Lys Thr Thr
20 25 30

<210> 824
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E345Q"

<400> 824
Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly
1 5 10 15

Gly His Ser Ser Val Ser Thr Glu Ser Gln Gln Ser Ser Ser Phe His
20 25 30

Ser Ser

<210> 825
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q156H"

<400> 825
Met Leu Ala Arg Gly Ser Ala Ser Pro His Lys Ser Ser Pro Gln Pro
1 5 10 15

Leu Val Ala Thr Pro Ser Gln His His His His Gln Gln Gln Gln Gln
20 25 30

Ile Lys Arg Ser Ala Arg Met Cys Gly Glu Cys Glu Ala Cys Arg Arg
35 40 45

Thr Glu Asp Cys
50

<210> 826
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V43I"

<400> 826
Gln Thr Pro Ser Thr Ser Ser Thr Lys Gly Arg Lys Lys Gly Lys Thr
1 5 10 15

Pro Arg Gln Arg Arg Ser Arg Ser Gly Ile Ile Lys Gly Leu Lys Thr
20 25 30

Thr Arg Lys Ala Lys Arg Pro Leu Arg Gly Ser Ser Ser Gln Lys Ala
35 40 45

Gly Glu Thr Asn

50

<210> 827
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R198M"

<400> 827
Leu Leu His Leu Ser Gly Lys Met Pro Pro Gly Ile Asn Ser Ser Gln
1 5 10 15

Ser Leu Pro Val Asp Asn His Glu Lys Met Met Val Ile Gln Leu His
20 25 30

Leu Gln His Ser Ser Leu Leu Asp Phe Leu Asn Ala Gln Gly Gly Cys
35 40 45

Ile Ser His Val
50

<210> 828
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R498G"

<400> 828
Leu Val Arg Val Phe Leu Tyr Ser Leu Gly Arg Asn Pro Ala Leu Phe
1 5 10 15

Pro Arg Pro Glu Arg Tyr Asn Pro Gln Gly Gly Trp Leu Asp Ile Arg
20 25 30

Gly Ser Gly Arg Asn Phe Tyr His Val Pro Phe Gly Phe Gly Met Arg
35 40 45

Gln Cys Leu Gly
    50

<210> 829
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.F406L"

<400> 829
Asp Val Ile Asp Gly Tyr Pro Val Lys Lys Gly Thr Asn Ile Ile Leu
1   5   10   15

Asn Ile Gly Arg Met His Arg Leu Glu Leu Leu Phe Pro Lys Pro Asn
            20   25   30

Glu Phe Thr Leu Glu Asn Phe Ala Lys Asn Val Pro Tyr Arg Tyr Phe
        35   40   45

Gln Pro Phe Gly
    50

<210> 830
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S113I"

<400> 830
Trp Ile Ser Gly Glu Glu Thr Leu Ile Ile Ser Lys Ser Ser Ser Met
1   5   10   15

Phe His Ile Met Lys His Asn His Tyr Ile Ile Ser Arg Phe Gly Ser
            20   25   30

Lys Leu Gly Leu Gln Cys Ile Gly Met His Glu Lys Gly Ile Ile Phe
35 40 45

Asn Asn Asn Pro
50

<210> 831
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V483M"

<400> 831
Cys Ile Gly Glu Val Leu Ala Lys Trp Glu Ile Phe Leu Phe Leu Ala
1 5 10 15

Ile Leu Leu Gln Gln Leu Glu Phe Ser Met Met Pro Pro Gly Val Lys
20 25 30

Val Asp Leu Thr Pro Ile Tyr Gly Leu Thr Met Lys His Ala Arg Cys
35 40 45

Glu His Val Gln
50

<210> 832
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P112Q"

<400> 832
Leu Tyr Lys Ala Lys Tyr Gly Pro Met Trp Met Ser Tyr Leu Gly Pro
1 5 10 15

Gln Met His Val Asn Leu Ala Ser Ala Gln Gln Leu Leu Glu Gln Val
20 25 30

Met Arg Gln Glu Gly Lys Tyr Pro Val Arg Asn Asp Met Glu Leu Trp
35 40 45

Lys Glu His Arg
50

<210> 833
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A444E"

<400> 833
Ala Leu Lys Lys Thr Glu Ala Phe Ile Pro Phe Ser Leu Gly Lys Arg
1 5 10 15

Ile Cys Leu Gly Glu Gly Ile Ala Arg Glu Glu Glu Leu Phe Leu Phe
20 25 30

Phe Thr Thr Ile Leu Gln Asn Phe Ser Met Ala Ser Pro Val Ala Pro
35 40 45

Glu Asp Ile Asp
50

<210> 834
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H352R"

<400> 834
Val Gln Arg Arg Val Gln Gln Glu Ile Asp Asp Val Ile Gly Gln Val

1 5 10 15

Arg Arg Pro Glu Met Gly Asp Gln Ala Arg Arg Met Pro Tyr Thr Thr
20 25 30

Ala Val Ile His Glu Val Gln Arg Phe Gly Asp Ile Val Pro Leu Gly
35 40 45

Val Thr His Met
50

<210> 835
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V185F"

<400> 835
Gly Leu Met Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Glu
1 5 10 15

Leu Leu Gly Gln Asp Ser Pro Leu Glu Phe Phe Phe Gln His Val Ser
20 25 30

Leu Met Thr Leu Asp Thr Ile Met Lys Cys Ala Phe Ser His Gln Gly
35 40 45

Ser Ile Gln Val
50

<210> 836
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E434D"

<400> 836
His Ile Tyr Ala Leu His Arg Asn Ser Ala Val Trp Pro Asp Pro Glu
1 5 10 15

Val Phe Asp Ser Leu Arg Phe Ser Thr Asp Asp Asn Ala Ser Lys Arg
20 25 30

His Pro Phe Ala Phe Met Pro Phe Ser Ala Gly Pro Arg Asn Cys Ile
35 40 45

Gly Gln Gln Phe
50

<210> 837
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K332T"

<400> 837
Tyr Leu Leu Arg His Pro Glu Ala Met Ala Ala Val Arg Asp Glu Ile
1 5 10 15

Asp Arg Leu Leu Gln Ser Thr Gly Gln Thr Thr Lys Gly Ser Gly Phe
20 25 30

Pro Ile His Leu Thr Arg Glu Gln Leu Asp Ser Leu Ile Cys Leu Glu
35 40 45

Ser Ser Ile Phe
50

<210> 838
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E161K"

<400> 838
Ile Leu Gly Gln Asp Tyr Cys Phe Glu Val Thr Thr Ser Ser Gly Ser
1 5 10 15

Lys Cys Phe Ser Cys Arg Ser Ala Ala Lys Lys Arg Asp Lys Trp Met
20 25 30

Glu Asn Leu Arg Arg Ala Val His Pro Asn Lys Asp Asn Ser Arg Arg
35 40 45

Val Glu His Ile
50

<210> 839
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R539C"

<400> 839
Thr Met Gln Lys Arg Leu Lys Lys Glu Lys Lys Thr Lys Arg Lys Leu
1 5 10 15

Gln Glu Ala Leu Glu Phe Glu Ser Lys Cys Cys Arg Glu Gln Val Glu
20 25 30

Gln Ala Leu Lys Gln Ala Thr Thr Ser Asp Ser Gly Leu Arg Met Leu
35 40 45

Lys Asp Thr Gly
50

<210> 840
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.R539L"

<400> 840
Thr Met Gln Lys Arg Leu Lys Lys Glu Lys Lys Thr Lys Arg Lys Leu
1 5 10 15

Gln Glu Ala Leu Glu Phe Glu Ser Lys Leu Leu Arg Glu Gln Val Glu
20 25 30

Gln Ala Leu Lys Gln Ala Thr Thr Ser Asp Ser Gly Leu Arg Met Leu
35 40 45

Lys Asp Thr Gly
50

<210> 841
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V216I"

<400> 841
Ala Ile Lys Val Thr Glu Thr Arg Thr Gly Pro Leu Gly Cys Asn Ser
1 5 10 15

Tyr Asp Asn Leu Asp Ser Val Ser Ser Ile Ile Leu Leu Gln Ser Thr
20 25 30

Glu Ser Lys Leu His Leu Gln Gly Leu Gln Ile Ile Phe Pro Gln Tyr
35 40 45

Leu Gln Glu Lys
50

<210> 842
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S254Y"

<400> 842
Pro Phe Leu Lys Ile Glu Asp Glu Ser Arg Lys Phe Arg Pro Phe His
1 5 10 15

His Gln Phe Lys Ser Phe Pro Glu Ile Tyr Tyr Phe Leu Gly Pro Lys
20 25 30

Asp Ala Ser Pro Phe Glu Ala Pro Thr Thr Leu Gly Ser Met His His
35 40 45

Thr Arg Glu Ser
50

<210> 843
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R246H"

<400> 843
Arg Met Asp Pro Asp Met Phe Asn Gly Ser Ile Ala Trp His Ser Glu
1 5 10 15

Val Gly Leu Pro Val Tyr Ala His Ile His His Pro Arg Asp Val Glu
20 25 30

Ala Ile Pro Arg Ala Ser Thr Asn Pro Ser Asn Arg Lys Val Arg Ala
35 40 45

Leu Ala Phe Ser
50

<210> 844
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R446H"

<400> 844
Ala Ile Pro Ser Ser Ser Val Leu Pro Ser Ala Pro Arg Asp Val Val
1 5 10 15

Pro Val Leu Val Ser Ser Arg Phe Val His His Leu Ser Trp Arg Pro
20 25 30

Pro Ala Glu Ala Lys Gly Asn Ile Gln Thr Phe Thr Val Phe Phe Ser
35 40 45

Arg Glu Gly Asp
50

<210> 845
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R235fs"

<400> 845
Leu Asp Arg Glu Asn Arg Ser His Tyr Met Leu Gln Leu Glu Ala Tyr
1 5 10 15

Asp Gly Gly Ser Pro Pro Arg Arg Ala Arg Pro Cys Trp Thr
20 25 30

<210> 846
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F2149L"

<400> 846
Thr Arg Glu Asn Thr Tyr Val Glu Tyr Ser Ile Ile Ser Gly Asn Ser
1 5 10 15

Gln Asn Asn Phe His Val Glu Thr Lys Leu Leu Phe His Ser Glu Tyr
20 25 30

Pro Tyr Lys Gln Val Gly Tyr Leu Val Leu Leu His Ser Leu Asp Arg
35 40 45

Glu Ala Ser Ala
50

<210> 847
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S549Y"

<400> 847
His Gly Leu Ser Ile Val His Arg Asp Ile Lys Pro Glu Asn Leu Leu
1 5 10 15

Val Cys Glu Tyr Pro Asp Gly Thr Lys Tyr Tyr Leu Lys Leu Gly Asp
20 25 30

Phe Gly Leu Ala Thr Val Val Glu Gly Pro Leu Tyr Thr Val Cys Gly
35 40 45

Thr Pro Thr Tyr
50

<210> 848
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F28I"

<400> 848
Gly Val Leu Ile Pro His Thr Pro Ile Ala Val Asp Phe Trp Ser Leu
1 5 10 15

Arg Arg Ala Gly Thr Ala Arg Leu Phe Ile Ile Leu Ser His Met His
20 25 30

Ser Asp His Thr Val Gly Leu Ser Ser Thr Trp Ala Arg Pro Leu Tyr
35 40 45

Cys Ser Pro Ile
50

<210> 849
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R532Q"

<400> 849
Leu Val Val Met Gly Thr Leu Val Ala Leu Val Gly Leu Phe Val Leu
1 5 10 15

Leu Ala Phe Leu Gln Tyr Arg Arg Leu Gln Gln Lys Gly Tyr Thr Pro
20 25 30

Leu Met Glu Thr His Leu Ser Ser Lys Arg Tyr Thr Glu Glu Ala
35 40 45

<210> 850
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L275P"

<400> 850
Glu Lys Asp Gln Arg Ser Leu Asp Ile Asn Thr Ala Lys Cys Met Leu
1 5 10 15

Gly Leu Leu Leu Gly Lys Ile Trp Pro Pro Pro Phe Pro Val Phe His
20 25 30

Gln Phe Leu Glu Gln Ser Lys Tyr Lys Val Ile Asn Lys Asp Gln Trp
35 40 45

Cys Asn Val Leu
50

<210> 851
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I433fs"

<400> 851
Leu Val Cys Phe Arg Leu Lys Gly Ser Asn Lys Val Asn Glu Ala Leu
1 5 10 15

Leu Gln Arg Ile Asn Ser Ala Lys Lys Ser Thr Trp Phe His Val Thr
20 25 30

Ser Gly Thr Ser Leu Ser Cys Ala Leu Pro Ser Val Leu Ala Arg Trp
35 40 45

Asn Leu Pro Met Cys Ser Gly Pro Gly Asn Thr Ser Lys Ser Trp Arg
50 55 60

Pro Thr Cys Cys Glu Gln Arg Gly Ser Arg Ser Glu Ala Ser Cys Arg
65 70 75 80

Asn Gln Lys Leu Lys Arg Asp Ile Ser Glu Asn Trp Asn Lys Lys Gln
85 90 95

Ile Asn Ile Ile Leu Pro Ser Trp Asn Ser Ala Val Cys Gly Phe Pro
100 105 110

Cys Leu Ser Pro Lys Leu Ser Arg Gly Leu
115 120

<210> 852
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R275Q"

<400> 852
Val Asn Gly His Pro Leu Lys Ala Phe Val Asp Ser Gly Ala Gln Met
1 5 10 15

Thr Ile Met Ser Gln Ala Cys Ala Glu Gln Gln Cys Asn Ile Met Arg
20 25 30

Leu Val Asp Arg Arg Trp Ala Gly Val Ala Lys Gly Val Gly Thr Gln
35 40 45

Arg Ile Ile Gly
50

<210> 853
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A376T"

<400> 853
Pro Tyr Tyr Gly Ser Arg Leu Ala Ile Pro Ala Ala Gln Leu Val Val
1 5 10 15

Leu Pro Tyr Gln Met Leu Leu His Ala Thr Thr Thr Arg Gln Ala Ala
20 25 30

Gly Ile Arg Leu Gln Asp Gln Val Val Ile Ile Asp Glu Ala His Asn
35 40 45

Leu Ile Asp Thr
50

<210> 854
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K208fs"

<400> 854
Ala Glu Arg Leu Glu Gln Leu Glu Ser Gly Glu Glu Glu Leu Val Leu
1 5 10 15

Ala Glu Tyr Glu Ser Asp Glu Glu Lys Arg Trp Arg Ala Glu Trp Met
20 25 30

Arg Met Arg Met Thr Trp Arg Lys Asn Thr
35 40

<210> 855
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.*128Q"

<400> 855

Cys Leu Phe Leu Ser Leu Glu Pro Pro Pro Arg Asp His Ile Ser
1 5 10 15

His Cys Leu Leu Ser Ala Gln Phe His Gln Gln Lys
20 25

<210> 856
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.G163fs"

<400> 856
His Pro Glu Val Ala Arg Leu Thr Pro Tyr Glu Val Asp Glu Leu Arg
1 5 10 15

Arg Lys Lys Glu Ile Thr Val Arg Gly Glu Met Phe Val Leu Asn Pro
20 25 30

Cys Leu Pro Ser Ile Met Leu Thr Ser His Asn Met
35 40

<210> 857
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F149fs"

<400> 857
Leu Ala Phe Gln Ile Ser Lys Glu Tyr Glu Arg Phe Ser Lys Tyr Met
1 5 10 15

Pro Asn Val Lys Val Ala Val Phe Phe Trp Trp Ser Val Tyr Gln Glu
20 25 30

Gly

<210> 858
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R329L"

<400> 858
Phe Asn Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val
1 5 10 15

Leu Gly Ala Pro Val Lys Gly Lys Arg Leu Leu Gly Arg Gly Pro Lys
20 25 30

Gly Asp Lys Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp
35 40 45

Phe His His Val
50

<210> 859
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.W90C"

<400> 859
Asp Cys Tyr Cys Arg Ile Pro Ala Cys Ile Ala Gly Glu Arg Arg Tyr
1 5 10 15

Gly Thr Cys Ile Tyr Gln Gly Arg Leu Cys Cys Ala Phe Cys Cys
20 25 30

<210> 860
<211> 52

<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R499L"

<400> 860
Gly Arg Lys Lys Arg Lys Ile Pro Lys Leu Val Leu Arg Ile Asn Ala
1 5 10 15

Ile Tyr Glu Val Arg Arg Gly Lys Lys Leu Leu Val Lys Arg Leu Ser
20 25 30

Gln Ser Met Glu Ser Asn Ser Gly Lys Val Thr Asp Glu Asn Ser Glu
35 40 45

Ser Asp Ser Asp
50

<210> 861
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R688Q"

<400> 861
Glu Val Tyr Cys Ile Val Ser Arg Leu Gly Cys Phe Ser Leu Phe Ser
1 5 10 15

Arg Ile Leu Asp Glu Val Glu Lys Arg Gln Gln Gly Ile Ser Pro Ala
20 25 30

Leu Val Gln Pro Leu Met Arg Ser Val Met Glu Ala Pro Phe Pro Ala
35 40 45

Leu Gly Lys Thr
50

<210> 862
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P357H"

<400> 862
Leu Tyr Arg Tyr Ser Ile Ser Gly Pro His Val Leu Pro Ile Glu Lys
1 5 10 15

His Ile Ser His Phe Met His Lys Val His His Phe Pro Ser Pro Gln
20 25 30

Arg Pro Arg Ile Leu Val Gln Leu Ser Pro His Asp Asn Leu Ile Leu
35 40 45

Ser Gln Pro Val
50

<210> 863
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1081Q"

<400> 863
Glu Ser Glu Lys Ser Ser Pro Ala Val Ser Arg Ser Lys Thr Phe Thr
1 5 10 15

Gly Arg Phe Lys Gln Gln Thr Pro Ser Gln Gln Thr His Lys Glu Arg
20 25 30

Ser Thr Ser Leu Ser Ala Leu Val Arg Ser Ser Pro His Gly Ser Leu
35 40 45

Gly Ser Val Val
50

<210> 864
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G1023E"

<400> 864
Gly Glu Leu Gly Asp Thr Gly Val Met Gln Ile Pro Lys Asn Leu Leu
1 5 10 15

Glu Met Thr Phe Glu Cys Gln Asn Leu Glu Glu Lys Leu Thr Thr Val
20 25 30

Gln Ile Gly His Asp Asn Ser Gly Leu Leu Ala Lys Trp Leu Val Asp
35 40 45

Cys Val Met Val
50

<210> 865
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E518K"

<400> 865
Ser Val Gln Asp Ala Pro Thr Lys Lys Glu Phe Val Ile Asn Pro Asn
1 5 10 15

Gly Lys Ser Glu Val Cys Ile Leu His Lys Lys Tyr Met Gln Arg Val
20 25 30

Leu Lys Val Arg Pro Val Tyr Asn Phe Phe Glu Cys Glu Asn Pro Ser

35 40 45

Glu Pro Phe Gly
50

<210> 866
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S13L"

<400> 866
Met Thr Asn Gln Glu Lys Trp Ala His Leu Ser Pro Leu Leu Glu Phe
1 5 10 15

Ser Gln Leu Gln Lys Tyr Ala Glu Tyr Ser Thr Lys Lys Leu Lys Asp
20 25 30

Val Leu Glu Glu Phe His Gly
35

<210> 867
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F49L"

<400> 867
Leu Pro Pro Glu Ser Thr Gln Val Arg Gly Tyr Asp Phe Asn Arg Gly
1 5 10 15

Val Asn Tyr Arg Ala Leu Leu Glu Ala Leu Leu Gly Thr Thr Gly Phe
20 25 30

Gln Ala Thr Asn Phe Gly Arg Ala Val Gln Gln Val Asn Ala Met Ile
35 40 45

Glu Lys Lys Leu
    50

<210> 868
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.I218T"

<400> 868
Leu Gly Leu Asn Lys Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile
1   5   10   15

Arg Val Asn Cys Leu Ala Pro Gly Leu Thr Thr Lys Thr Ser Phe Ser
            20   25   30

Arg Met Leu Trp Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr
        35   40   45

Leu Arg Ile Arg
    50

<210> 869
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R410Q"

<400> 869
Asp Ile Gly Lys Leu Val Gly Cys Ala Ile Ile His Val Asn Gly Asp
1   5   10   15

Ser Pro Glu Glu Val Val Arg Ala Thr Gln Gln Leu Ala Phe Glu Tyr
            20   25   30

Gln Arg Gln Phe Arg Lys Asp Val Ile Ile Asp Leu Leu Cys Tyr Arg
35 40 45

Gln Trp Gly His
50

<210> 870
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V40G"

<400> 870
Arg Lys Met Thr Pro Ser Tyr Glu Ile Arg Ala Val Gly Asn Lys Asn
1 5 10 15

Arg Gln Lys Phe Met Cys Glu Val Gln Gly Gly Glu Gly Tyr Asn Tyr
20 25 30

Thr Gly Met Gly Asn Ser Thr Asn Lys Lys Asp Ala Gln Ser Asn Ala
35 40 45

Ala Arg Asp Phe
50

<210> 871
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E121K"

<400> 871
Glu Arg Ser Leu Asn Leu Ser Glu Lys Glu Val Leu Asp Leu Phe Glu
1 5 10 15

Lys Met Met Glu Asp Met Asn Leu Asn Lys Lys Glu Lys Lys Ala Pro
20 25 30

Leu Arg Asn Lys Asp Phe Thr Thr Lys Arg Glu Met Val Val Gln Tyr
35 40 45

Ile Ser Ala Thr
50

<210> 872
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1705K"

<400> 872
Lys Ala Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn
1 5 10 15

Thr Ile Thr Asp Cys Tyr Gln Arg Leu Lys Lys Phe Leu Gly Asp Ala
20 25 30

Ile Leu Asp Tyr Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln
35 40 45

His Ser Pro Gly
50

<210> 873
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G79C"

<400> 873
Val Cys Thr Leu Gln Ile Thr Asp Thr Thr Gly Ser His Gln Phe Pro

1 5 10 15

Ala Met Gln Arg Leu Ser Ile Ser Lys Cys Cys His Ala Phe Ile Leu
20 25 30

Val Phe Ser Val Thr Ser Lys Gln Ser Leu Glu Glu Leu Gly Pro Ile
35 40 45

Tyr Lys Leu Ile
50

<210> 874
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R780K"

<400> 874
Cys Ser Gly Met Asp Asn Asp Phe His His Tyr Gly Leu Ala Ser Pro
1 5 10 15

Ile Tyr Thr His Phe Thr Ser Pro Ile Lys Lys Arg Tyr Ala Asp Val
20 25 30

Ile Val His Arg Leu Leu Ala Val Ala Ile Gly Ala Asp Cys Thr Tyr
35 40 45

Pro Glu Leu Thr
50

<210> 875
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G732L"

<400> 875
Glu Lys Val Leu Pro Cys Ile Val Ile Lys Phe Arg Tyr Leu Trp Leu
1 5 10 15

Phe Trp Phe Leu Ala Leu Thr Val Gly Leu Leu Ala Tyr Ile Val Cys
20 25 30

Ile Asn Pro Lys Met Lys Leu Pro Ser Leu Glu Leu Ser Glu Phe Gln
35 40 45

Val Phe Arg Ser Ser
50

<210> 876
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R763C"

<400> 876
Ile Asn Pro Lys Met Lys Leu Pro Ser Leu Glu Leu Ser Glu Phe Gln
1 5 10 15

Val Phe Arg Ser Ser His Pro Phe Glu Cys Cys Tyr Asp Ala Glu Tyr
20 25 30

Lys Lys Leu Phe Met Phe Glu Arg Val His His Gly Glu Glu Leu His
35 40 45

Met Pro Ile Thr
50

<210> 877
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F1021S"

<400> 877
Val Ala Gly Thr Val Leu Leu Thr Val Gly Leu Leu Val Leu Leu Glu
1 5 10 15

Trp Gln Leu Asn Thr Ala Glu Ala Leu Ser Ser Leu Ser Ala Ser Val
20 25 30

Gly Leu Ser Val Asp Phe Thr Val Asn Tyr Cys Ile Ser Tyr His Leu
35 40 45

Cys Pro His Pro
50

<210> 878
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R230H"

<400> 878
Lys Pro Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys
1 5 10 15

Gly Ser His Gly Leu Glu Ile Phe Gln His His Cys Asp Cys Ala Lys
20 25 30

Gly Leu Ser Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala
35 40 45

Arg Leu His Val
50

<210> 879
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.A350V"

<400> 879
Leu Ala Thr Gln Glu Pro Thr Asp Asn Gln Val Arg Leu Arg Lys Arg
1 5 10 15

Lys Glu Ile Arg Glu Asp Arg Asp Arg Val Val Arg Leu Asp Ser Met
20 25 30

Val Leu Leu Ile Met Lys Leu Asp Gln Leu Asp Gln Asp Ile Glu Asn
35 40 45

Ala Leu Ser Thr
50

<210> 880
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S741T"

<400> 880
Ile Ser Ala Leu Asn Gly Asn Arg Ile Asn Val Pro Met Val Arg Lys
1 5 10 15

Arg Ser Val Ser Asn Ser Thr Gln Thr Thr Thr Ser Ser Ser Ser Gln
20 25 30

Ser Glu Thr Ser Ser Ala Val Ser Thr Pro Ser Pro Val Thr Arg Thr
35 40 45

Arg Ser Leu Ser
50

<210> 881
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E222D"

<400> 881
Ile Ser Leu Ser Glu Ile Lys Asp Ala Pro Lys Val Asn Ala Val Asp
1 5 10 15

Thr Leu Asn Val Lys Asp Ile Ala Pro Asp Asp Lys Gln Leu Leu Asn
20 25 30

Ser Ala Val Ile Ala Gln Gln Arg Arg Lys Pro Asp Pro Pro Lys Asp
35 40 45

Glu Asn Glu Arg
50

<210> 882
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A83V"

<400> 882
Arg Ala Arg Pro Gly Pro Gly Arg Glu Glu Arg Gly Gly Gly Val Gly
1 5 10 15

Thr Arg Ser Arg Arg Thr Ala Ala Arg Val Val Asn Ser Pro Glu Glu
20 25 30

Glu Val Val Arg Gly Ala Glu Gly Gly Ala Glu Leu Leu Pro Phe Pro
35 40 45

Arg Asp Arg Gly
50

<210> 883
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S624L"

<400> 883
Lys Arg Arg Val Glu Arg Lys Glu Arg Ala Arg Leu Lys Thr Val Lys
1 5 10 15

Phe Asn Ala Lys Pro Gly Val Ile Asp Leu Leu Lys Gly Ser Phe Asn
20 25 30

Asp Lys Arg Lys Lys Ser Phe Ile Phe Ser Arg Lys Phe Pro Phe Tyr
35 40 45

Lys Asn Lys Glu
50

<210> 884
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G377fs"

<400> 884
Gly Leu Leu Gly Pro Glu Thr Lys Ala Lys Ala Arg Thr Tyr His Tyr
1 5 10 15

Leu Gln Val Pro Gln Asp Asp Trp Gly Val Thr Pro Pro Val Ala Arg
20 25 30

Met Gly Arg Ser Pro Ala Ala Gly Cys Gly Ala Ala Ala Thr Ser Lys
35 40 45

Pro Trp Gly Met Arg Arg Ala Glu Thr Gln Thr Ala Ala Pro Arg His
50 55 60

Leu Pro Lys Gln Ser Pro Asp Ala Ser Pro Pro Val Ala Pro Pro Ala
65 70 75 80

Trp Thr Arg Pro Gly Ser Thr Ala Val Ser His Pro Gly Ser Thr Pro
85 90 95

Gly Ala Pro Ser Leu Ala Thr Ala Val Pro Ser Pro Leu Asp Ser Ser
100 105 110

Ala Met Ser
115

<210> 885
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D318H"

<400> 885
Pro Arg Ser Phe Glu Cys Thr Cys Pro Arg Gly Phe Tyr Gly Leu Arg
1 5 10 15

Cys Glu Val Ser Gly Val Thr Cys Ala His His Gly Pro Cys Phe Asn
20 25 30

Gly Gly Leu Cys Val Gly Gly Ala Asp Pro Asp Ser Ala Tyr Ile Cys
35 40 45

His Cys Pro Pro
50

<210> 886
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R1521L"

<400> 886
Ser Arg Ala Ser Thr Ala Gly Ser Glu Ser Thr Leu Ala Leu Arg Leu
1 5 10 15

Val Asn Gly Gly Asp Arg Cys Arg Gly Leu Leu Val Glu Val Leu Tyr
20 25 30

Gln Gly Ser Trp Gly Thr Val Cys Asp Asp Tyr Trp Asp Thr Asn Asp
35 40 45

Ala Asn Val Val
50

<210> 887
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K1772N"

<400> 887
Asp His Cys Arg Lys Leu Val Glu Pro Gln Ile Ser Glu Leu Asn His
1 5 10 15

Arg Phe Ala Ala Ile Ser His Arg Ile Asn Asn Thr Gly Lys Ala Ser
20 25 30

Ile Pro Leu Lys Glu Leu Glu Gln Phe Asn Ser Asp Ile Gln Lys Leu
35 40 45

Leu Glu Pro Leu
50

<210> 888
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R3195H"

<400> 888
Asn Val Pro Leu Cys Val Asp Met Cys Leu Asn Trp Leu Leu Asn Val
1   5   10   15

Tyr Asp Thr Gly Arg Thr Gly Arg Ile His His Val Leu Ser Phe Lys
            20   25   30

Thr Gly Ile Ile Ser Leu Cys Lys Ala His Leu Glu Asp Lys Tyr Arg
        35   40   45

Tyr Leu Phe Lys
    50

<210> 889
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R44H"

<400> 889
Ala Gly Val Gly Pro Gly Leu Pro Gly Ala Gly Ala Pro Ala Arg Pro
1   5   10   15

Ser Pro Gly Arg Pro Pro Gly Ala Gly His His Leu Arg Thr Gly Pro
            20   25   30

Gly Gln Val Arg Gly Arg Leu Leu Ala Val Gly Pro Lys Ser Arg Val
        35   40   45

Phe Gln Ser Val
    50

<210> 890
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S45T"

<400> 890
Pro Gly Val Pro Pro Gln Gly Arg Ala Gly Gly Phe Gly Lys Ala Ser
1 5 10 15

Gly Ala Leu Val Gly Ala Ala Ser Gly Thr Thr Ser Ala Gly Gly Ser
20 25 30

Ser Arg Gly Gly Gly Ser Gly Ser Gly Ala Ser Asp Leu Gly Ala Gly
35 40 45

Ser Lys Lys Ser
50

<210> 891
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T106S"

<400> 891
Arg Gly Gly Pro Gln Pro Arg Pro Pro Leu Ala Pro Gln Ala Ser Pro
1 5 10 15

Ala Gly Thr Gly Pro Arg Glu Arg Cys Ser Ser Pro Ala Gly Gly Gly
20 25 30

Ala Glu Pro Arg Lys Leu Ser Arg Thr Pro Lys Cys Ala Arg Cys Arg
35 40 45

Asn His Gly Val
50

<210> 892
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D2412E"

<400> 892
Gly Gly Gly Val Lys Leu Val Val Lys Pro Arg Arg Gln Ser Glu Asn
1 5 10 15

Ile Ser Ala Pro Pro Val Leu Ser Glu Glu Glu Ile Asp Lys His Arg
20 25 30

Arg Arg Phe Asn Met Arg Met Leu Val Pro Gly Arg Pro Val Lys Asp
35 40 45

Ala Thr Pro Pro
50

<210> 893
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C1853F"

<400> 893
Gly Ala Pro Ala Gly Pro Ala Gly Thr Gly Lys Thr Glu Thr Thr Lys
1 5 10 15

Asp Leu Ala Lys Ala Leu Gly Leu Leu Phe Phe Val Val Thr Asn Cys
20 25 30

Gly Glu Gly Met Asp Tyr Arg Ala Val Gly Lys Ile Phe Ser Gly Leu
35 40 45

Ala Gln Cys Gly
50

<210> 894
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1888Q"

<400> 894
Asp Tyr Arg Ala Val Gly Lys Ile Phe Ser Gly Leu Ala Gln Cys Gly
1 5 10 15

Ala Trp Gly Cys Phe Asp Glu Phe Asn Gln Gln Ile Asp Ala Ser Val
20 25 30

Leu Ser Val Ile Ser Ser Gln Ile Gln Thr Ile Arg Asn Ala Leu Ile
35 40 45

His Gln Leu Thr
50

<210> 895
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1367C"

<400> 895
Gln Asp Ile Gly Pro Pro Ala Val Lys Met Leu Ile Ser Ala Glu Gly
1 5 10 15

Glu Gly Leu Val Leu Pro Lys Lys Ile Cys Cys Val Arg Ser Ala Val
20 25 30

Glu Gln Trp Leu Val Asn Val Glu Lys Ser Met Phe Asp Val Leu Lys
35 40 45

Lys Glu Arg Tyr

50

<210> 896
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E3367Q"

<400> 896
Leu Asn Leu Arg Ile Lys Tyr Ile Ile Asp His Phe Thr Leu Ser Ile
1 5 10 15

Tyr Asn Asn Val Cys Arg Ser Leu Phe Gln Gln Lys Asp Lys Leu Leu
20 25 30

Phe Ser Leu Leu Leu Thr Ile Gly Ile Met Lys Gln Lys Lys Glu Ile
35 40 45

Thr Glu Glu Val
50

<210> 897
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R3822L"

<400> 897
Gln Lys Leu Glu Ile Ser Ala Glu Thr Glu Val Gln Ile Asn Ser Ala
1 5 10 15

Arg Glu Glu Tyr Arg Pro Val Ala Thr Leu Leu Gly Ser Ile Leu Tyr
20 25 30

Phe Leu Ile Thr Glu Met Arg Leu Val Asn Glu Met Tyr Gln Thr Ser
35 40 45

Leu Arg Gln Phe
50

<210> 898
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R742Q"

<400> 898
Leu Phe Arg Glu Thr Glu Cys Met Ala Gln Met Gly Leu Glu Val Ser
1 5 10 15

Pro Leu Ala Thr Ser Leu Phe Gln Lys Gln Gln Asp Arg Tyr Lys Arg
20 25 30

Asn Phe Ser Asn Met Lys Met Met Leu Ala Glu Tyr Gln Arg Val Lys
35 40 45

Ser Lys Ile Pro
50

<210> 899
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R982H"

<400> 899
Glu Leu Leu Ser His Phe Asn His Gln Asn Met Asp Ala Leu Leu Lys
1 5 10 15

Val Thr Arg Asn Thr Leu Glu Ala Ile His His Lys Arg Ile His Ser
20 25 30

Ser His Thr Ile Asn Phe Arg Asp Ser Asn Ser Ala Ser Asn Met Lys
35 40 45

Gln Asn Ser Leu
50

<210> 900
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q1797E"

<400> 900
Thr Ile Glu Leu Asp Lys Pro Val Met Ala Glu Gly Asn Val Glu Val
1 5 10 15

Trp Leu Asn Ser Leu Leu Glu Glu Ser Glu Glu Ser Ser Leu His Leu
20 25 30

Val Ile Arg Gln Ala Ala Ala Asn Ile Gln Glu Thr Gly Phe Gln Leu
35 40 45

Thr Glu Phe Leu
50

<210> 901
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R224Q"

<400> 901
Phe Leu Ser Ser Leu Glu Gly Phe Val Asn Val Leu Ser Gly Ala Gln
1 5 10 15

Glu Ser Leu Lys Glu Lys Val Asn Leu Gln Gln Lys Cys Asp Ile Leu
            20   25   30

Glu Leu Lys Thr Leu Lys Glu Pro Thr Asp Tyr Leu Thr Leu Ala Asn
        35   40   45

Asn Pro Glu Thr
    50

<210> 902
<211> 52
<212> PRT
<213> Artificial Sequence

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R3197Q"

<400> 902
His Val Thr Pro Lys Ser Tyr Leu Ser Phe Ile Gln Gly Tyr Lys Phe
1   5   10   15

Ile Tyr Gly Glu Lys His Val Glu Val Gln Gln Thr Leu Ala Asn Arg
            20   25   30

Met Asn Thr Gly Leu Glu Lys Leu Lys Glu Ala Ser Glu Ser Val Ala
        35   40   45

Ala Leu Ser Lys
    50

<210> 903
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.D3236N"

<400> 903
Lys Glu Ala Ser Glu Ser Val Ala Ala Leu Ser Lys Glu Leu Glu Ala

1 5 10 15

Lys Glu Lys Glu Leu Gln Val Ala Asn Asn Lys Ala Asp Met Val
20 25 30

Leu Lys Glu Val Thr Met Lys Ala Gln Ala Ala Glu Lys Val Lys Ala
35 40 45

Glu Val Gln Lys
50

<210> 904
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R2961Q"

<400> 904
Leu Cys Lys Gly Arg Asp Ile Pro Cys Ser Asp Asp Cys Ser Leu Met
1 5 10 15

Gly Thr Leu Gly Glu Ala Val Thr Ile Gln Gln Thr Trp Asn Ile Ala
20 25 30

Gly Leu Pro Ser Asp Ser Phe Ser Ile Asp Asn Gly Ile Ile Ile Met
35 40 45

Asn Ala Arg Arg
50

<210> 905
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D1547N"

<400> 905
Leu Glu Ser Ile Phe Thr Gly Ser Glu Asp Ile Arg Ala Gln Leu Pro
1 5 10 15

Gln Asp Ser Lys Arg Phe Glu Gly Ile Asn Asn Ile Asp Phe Lys Glu
20 25 30

Leu Ala Tyr Asp Ala Gln Lys Ile Pro Asn Val Val Gln Thr Thr Asn
35 40 45

Lys Pro Gly Leu
50

<210> 906
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S2993R"

<400> 906
Lys Phe Pro Ala Ile Val Asn Cys Thr Ala Ile His Trp Phe His Glu
1 5 10 15

Trp Pro Gln Gln Ala Leu Glu Ser Val Arg Arg Leu Arg Phe Leu Gln
20 25 30

Asn Thr Glu Gly Ile Glu Pro Thr Val Lys Gln Ser Ile Ser Lys Phe
35 40 45

Met Ala Phe Val
50

<210> 907
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V231L"

<400> 907
Pro Asn Lys Pro Glu Leu Ala Leu Lys Pro Ser Ser Pro Leu Val Thr
1 5 10 15

Leu Glu Phe Asn Pro Lys Asp Ser His Leu Leu Leu Leu Gly Gly Cys
20 25 30

Tyr Asn Gly Gln Ile Ala Cys Trp Asp Thr Arg Lys Gly Ser Leu Val
35 40 45

Ala Glu Leu Ser
50

<210> 908
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K193fs"

<400> 908
Ala Val Val Trp Ser Ile Tyr Leu Glu Lys Gln Leu Asp Glu Leu Leu
1 5 10 15

Ser Arg Lys Lys Arg Glu Lys Lys Lys Arg Leu Ala Ala Arg Val Trp
20 25 30

Met Tyr Gln Asn Ser Val Leu Gln Lys Lys Met Lys Asp Cys
35 40 45

<210> 909
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.I80K"

<400> 909
Phe Lys Lys Leu Ala Leu Lys Leu His Pro Asp Lys Asn Pro Asn Asn
1 5 10 15

Pro Asn Ala His Gly Asp Phe Leu Lys Lys Lys Asn Arg Ala Tyr Glu
20 25 30

Val Leu Lys Asp Glu Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu
35 40 45

Lys Gly Leu Glu
50

<210> 910
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R135K"

<400> 910
Asp Leu Met Leu Glu Glu Ser Asp Lys Thr His Thr Thr Lys Met Glu
1 5 10 15

Asn Glu Glu Cys Asn Glu Gln Arg Glu Lys Lys Lys Lys Glu Glu Leu
20 25 30

Ala Ser Thr Ala Glu Lys Thr Glu Gln Lys Glu Pro Lys Pro Leu Glu
35 40 45

Lys Ser Val Ser
50

<210> 911
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E1248K"

<400> 911
Thr Pro Arg Leu Gln Ser Asn Thr Arg Ala Leu Tyr Gln Tyr Cys Pro
1 5 10 15

Ile Pro Ile Ile Asn Tyr Pro Gln Leu Lys Lys Asn Glu Leu Phe Cys
20 25 30

Asn Ile Tyr Tyr Leu Lys Gln Leu Cys Asp Thr Leu Arg Phe Pro Asp
35 40 45

Trp Pro Ile Lys
50

<210> 912
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E61K"

<400> 912
Leu Met Tyr His Pro Asp Lys Gln Ser Thr Asp Val Pro Ala Gly Thr
1 5 10 15

Val Glu Glu Cys Val Gln Lys Phe Ile Lys Lys Ile Asp Gln Ala Trp
20 25 30

Lys Ile Leu Gly Asn Glu Glu Thr Lys Arg Glu Tyr Asp Leu Gln Arg
35 40 45

Cys Glu Asp Asp
50

<210> 913
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D212N"

<400> 913
Cys Ala Ser Leu Thr Lys Lys Arg Leu Asp Lys Leu Glu Leu Arg Thr
1 5 10 15

Glu Pro Gly Phe His Trp Val Ile Ala Asn Asn Gly Glu Asp Thr Thr
20 25 30

Val Arg Ala Ser Thr His Cys Thr Tyr Asp Arg Val Val Leu His Gly
35 40 45

Glu Arg Cys Arg
50

<210> 914
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E378D"

<400> 914
Thr Leu Glu Leu Ser Gly Gly Ala Arg Ile Asn Arg Ile Phe His Glu
1 5 10 15

Arg Phe Pro Phe Glu Leu Val Lys Met Asp Asp Phe Asp Glu Lys Asp
20 25 30

Leu Arg Arg Glu Ile Ser Tyr Ala Ile Lys Asn Ile His Gly Val Arg
35 40 45

Thr Gly Leu Phe
50

<210> 915
<211> 55
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P791fs"

<400> 915
Gln Arg Arg Pro Val Ser Ser Ile His Pro Pro Gly Arg Pro Pro Ala
1 5 10 15

Val Arg Gly Pro Thr Pro Gly Pro Pro Pro Asp Ser Cys Ser Arg Gly
20 25 30

Gly Ser Ser Leu Leu Leu Gly Ala Pro Asn Pro Ile Pro Ala Trp Thr
35 40 45

Pro Glu Arg Val Cys Gln Gln
50 55

<210> 916
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.T78P"

<400> 916
Ser Ser Phe Val Glu Ile Val Thr Ile Pro Ser Leu Lys Glu Gly Glu
1 5 10 15

Arg Leu Phe Val Cys Ile Cys Glu Phe Pro Pro Ser Gln Glu Leu Asp
20 25 30

Asn Leu Pro Leu His Arg Gly Asp Leu Val Ile Leu Asp Gly Ile Pro
35 40 45

Thr Ala Gly Trp
50

<210> 917
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E432K"

<400> 917
Leu Thr Cys Phe Ser Val Tyr Cys Lys His Gly His Leu Cys Pro Ile
1 5 10 15

Asp Thr Gly Leu Ile Glu Lys Asn Ile Lys Lys Leu Phe Phe Ser Gly
20 25 30

Ser Ala Lys Pro Ile Tyr Asp Asp Asp Pro Ser Leu Glu Gly Gly Val
35 40 45

Asn Gly Lys Asn
50

<210> 918
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E51K"

<400> 918
Arg Arg Leu Lys Asp Leu Glu Arg Asp Ser Leu Thr Glu Lys Glu Cys
1 5 10 15

Val Lys Glu Lys Leu Asn Leu Leu His Lys Lys Phe Leu Gln Thr Glu
20 25 30

Ile Lys Asn Gln Leu Cys Asp Leu Glu Thr Lys Leu Arg Lys Glu Glu
35 40 45

Leu Ser Glu Glu

50

<210> 919
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R995Q"

<400> 919
Pro Glu His Tyr Arg Lys Tyr Ser Asp Tyr Ile Lys Gly Ser Asn Leu
1 5 10 15

Asp Ala Pro Glu Pro Tyr Arg Ile Gly Gln Gln Ile Lys Glu Ile Phe
20 25 30

Cys Pro Lys Lys Ser Asn Gly Arg Pro Asn Glu Thr Asp Ile Lys Ile
35 40 45

Arg Val Asn Lys
50

<210> 920
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E1531Q"

<400> 920
Arg His Asn His Trp Ala Gly Leu Tyr Gly Arg Leu Glu Trp Asp Gly
1 5 10 15

Phe Phe Ser Thr Thr Val Thr Asn Pro Gln Gln Pro Met Gly Lys Gln
20 25 30

Gly Arg Val Leu His Pro Glu Gln His Arg Val Val Ser Val Arg Glu
35 40 45

Cys Ala Arg Ser
50

<210> 921
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R736H"

<400> 921
Asn Asp Leu Ser Ile Val Asn Pro Ala Arg Lys Gly Leu Tyr Glu Gly
1 5 10 15

Thr Gly Arg Leu Phe Phe Glu Phe Tyr His His Leu Leu His Asp Ala
20 25 30

Arg Pro Lys Glu Gly Asp Asp Arg Pro Phe Phe Trp Leu Phe Glu Asn
35 40 45

Val Val Ala Met
50

<210> 922
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R882C"

<400> 922
Asp Ile Leu Trp Cys Thr Glu Met Glu Arg Val Phe Gly Phe Pro Val
1 5 10 15

His Tyr Thr Asp Val Ser Asn Met Ser Cys Cys Leu Ala Arg Gln Arg
20 25 30

Leu Leu Gly Arg Ser Trp Ser Val Pro Val Ile Arg His Leu Phe Ala
35 40 45

Pro Leu Lys Glu
50

<210> 923
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R882H"

<400> 923
Asp Ile Leu Trp Cys Thr Glu Met Glu Arg Val Phe Gly Phe Pro Val
1 5 10 15

His Tyr Thr Asp Val Ser Asn Met Ser His His Leu Ala Arg Gln Arg
20 25 30

Leu Leu Gly Arg Ser Trp Ser Val Pro Val Ile Arg His Leu Phe Ala
35 40 45

Pro Leu Lys Glu
50

<210> 924
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R92W"

<400> 924
Thr Gln Asp Leu Thr Gly Asp Gly Asp Gly Glu Asp Gly Asp Gly Ser
1 5 10 15

Asp Thr Pro Val Met Pro Lys Leu Phe Trp Trp Glu Thr Arg Thr Arg
20 25 30

Ser Glu Ser Pro Ala Val Arg Thr Arg Asn Asn Asn Ser Val Ser Ser
35 40 45

Arg Glu Arg His
50

<210> 925
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E864K"

<400> 925
Ser Lys Met Phe Thr Glu Phe Ile Leu Asn Val Pro Met Gly Leu Leu
1 5 10 15

Thr Ile Gln Lys Leu Tyr Cys Leu Ile Lys Lys Ile Val His Ser Asp
20 25 30

Leu Phe Thr Gln His Asp Cys Arg Glu Ile Leu Leu Pro Met Met Thr
35 40 45

Asp Gln Leu Lys
50

<210> 926
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A1830V"

<400> 926
Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr Met Cys Val Glu Phe Leu

460

1 5 10 15

Trp Lys Ser Glu Arg Tyr Glu Leu Ile Val Val Asp Val Asn Lys Pro
20 25 30

Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe Lys Lys Leu Ser Asp
35 40 45

Leu Tyr Tyr Asp
50

<210> 927
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q169E"

<400> 927
Phe Glu Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu
1 5 10 15

Cys Ser Gln Lys Gly Gly Val Ile Lys Glu Glu Gly Trp Leu His Lys
20 25 30

Ala Asn Val Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg
35 40 45

Arg Tyr Phe Tyr
50

<210> 928
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1183C"

<400> 928
Glu Leu Phe Ser Leu Leu Thr Gln Leu Phe Gly Pro Tyr Pro Ser Leu
1 5 10 15

Leu Glu Lys Val Glu Gln Glu Thr Trp Cys Cys Glu Thr Gly Ile Ser
20 25 30

Phe Val Thr Ser Val Thr Arg Leu Met Glu Arg Leu Leu Asp Tyr Arg
35 40 45

Asp Cys Met Lys
50

<210> 929
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E177K"

<400> 929
Ile Asp His Gly Asn Arg Met Leu Gly Leu Asp Leu Val Val Arg Asp
1 5 10 15

Asp Asn Gly Asn Ile Leu Asp Pro Asp Lys Lys Thr Ser Thr Ile Ala
20 25 30

Leu Phe Lys Ala His Glu Val Ala Ser Lys Arg Ile Glu Glu Lys Ile
35 40 45

Gln Glu Glu Lys
50

<210> 930
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.L1111fs"

<400> 930
Thr Leu Ile Ser Met Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His
1 5 10 15

Glu His Tyr Leu Asn Leu Asn Leu Phe Leu
20 25

<210> 931
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A177fs"

<400> 931
His Lys Thr Leu Pro Lys Gln Thr Phe Glu Ser Glu Thr Leu Glu Cys
1 5 10 15

Ser Glu Pro Ala Ala Gln Ala Gly Pro Pro Pro Leu Lys Arg Ala Val
20 25 30

Arg Arg Val Trp Glu Arg Pro Arg His Cys Leu
35 40

<210> 932
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R274W"

<400> 932
Lys Met Ser Glu Arg Ala Ala Ser Leu Ser Thr Met Val Pro Leu Pro
1 5 10 15

Arg Ser Ala Tyr Trp Gln His Ile Thr Trp Trp Gln His Ser Thr Gly
20 25 30

Gln Leu Tyr Arg Leu Gln Asp Val Ser Ser Pro Leu Lys Leu His Arg
35 40 45

Thr Glu Thr Phe
50

<210> 933
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G461D"

<400> 933
Gly Gln Thr Ser Ala Gly Cys Pro Ser Gly Trp Leu Gly Thr Arg Arg
1 5 10 15

Arg Gly Leu Val Met Glu Ala Pro Gln Asp Asp Ser Glu Ala Thr Leu
20 25 30

Pro Gly Pro Ala Pro Gly Glu Pro Trp Glu Ala Gly Gly Pro His Ala
35 40 45

Gly Pro Pro Pro
50

<210> 934
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1196K"

<400> 934
Lys Ala Gly Ala Lys Leu Ser Leu Val Arg Val Asp Ser Asp Lys Thr

1 5 10 15

Gln Ala Ser Glu Ser Phe Ser Ser Asp Lys Lys Glu Ala Asp Leu Glu
20 25 30

Leu Gln Ala Leu Thr Thr Ser Arg Leu Leu Lys Gln Gln Arg Glu Arg
35 40 45

Gln Glu Ala Val
50

<210> 935
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y2048S"

<400> 935
Phe Glu Gln Lys Ala Met Leu Leu Lys Arg Gln Ala Phe Ala Val Phe
1 5 10 15

Ser Gly Glu Leu Asp Gln Tyr His Leu Ser Ser Leu Pro Leu Ile Gln
20 25 30

Glu Arg Leu Thr Asp Asn Leu Arg Val Gly Gln Thr Ser Ile Val Ala
35 40 45

Ala Gln Met Phe
50

<210> 936
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L768del"

<400> 936
Asn Arg Glu Arg Thr Ala Asn Glu Asn Thr Thr Pro Ser Pro Ala Gln
1 5 10 15

Pro Thr Glu Asn Gly Asp Arg Thr Pro Ala Asn Glu Lys Thr Thr Pro
20 25 30

Ser Leu Ala Glu Pro Thr Glu Asn Gly Lys Arg Thr Pro Phe Ala Asn
35 40 45

Glu Lys Thr Thr Ser
50

<210> 937
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V11L"

<400> 937
Met Trp Ser Gly Trp Trp Leu Trp Pro Leu Leu Leu Ala Val Cys Thr
1 5 10 15

Ala Asp Phe Phe Arg Asp Glu Ala Glu Arg Ile Met Arg Asp Ser Pro
20 25 30

Val Ile Asp Gly His
35

<210> 938
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V183I"

<400> 938
Thr Ala Ser Tyr Val Ile Tyr Asn Ile His Thr Arg Glu Val Trp Glu
1 5 10 15

Leu Asn Pro Pro Glu Val Glu Asp Ser Ile Ile Leu Gln Tyr Ala Ala
20 25 30

Trp Gly Val Gln Gly Gln Gln Leu Ile Tyr Ile Phe Glu Asn Asn Ile
35 40 45

Tyr Tyr Gln Pro
50

<210> 939
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L757F"

<400> 939
Thr Phe Thr Cys Gly Ser Ala Leu Ser Pro Ile Thr Asp Phe Lys Leu
1 5 10 15

Tyr Ala Ser Ala Phe Ser Glu Arg Tyr Phe Phe Gly Leu His Gly Leu
20 25 30

Asp Asn Arg Ala Tyr Glu Met Thr Lys Val Ala His Arg Val Ser Ala
35 40 45

Leu Glu Glu Gln
50

<210> 940
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.G165R"

<400> 940
Gln Ala Thr Leu Asp Tyr Gly Met Tyr Ser Arg Glu Glu Glu Leu Leu
1 5 10 15

Arg Glu Arg Lys Arg Ile Gly Thr Val Arg Arg Ile Ala Ser Tyr Asp
20 25 30

Tyr His Gln Gly Ser Gly Thr Phe Leu Phe Gln Ala Gly Ser Gly Ile
35 40 45

Tyr His Val Lys
50

<210> 941
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F378L"

<400> 941
Ile Leu Lys Tyr Leu Thr Ser Lys Ile Phe Gly Ile Ala Asp Asp Ala
1 5 10 15

His Ile Gly Asn Leu Leu Thr Ser Lys Leu Leu Phe Ser Tyr Lys Asp
20 25 30

Phe Asp Thr Leu Leu Tyr Thr Cys Ala Ala Glu Phe Asp Phe Met Glu
35 40 45

Lys Glu Thr Pro
50

<210> 942
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V249L"

<400> 942
Met Leu Leu Val Thr His Ile Leu Arg Ala Thr Lys Leu Tyr Arg Gly
1 5 10 15

Ser Leu Ile Ala Leu Cys Ile Ser Asn Leu Leu Phe Phe Met Leu Pro
20 25 30

Trp Gln Phe Ala Gln Phe Val Leu Leu Thr Gln Ile Ala Ser Leu Phe
35 40 45

Ala Val Tyr Val
50

<210> 943
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M210V"

<400> 943
Ile Asn Ala Ile Lys Arg Phe His Leu Tyr Pro Glu Val Ile Ile Ala
1 5 10 15

Ser Trp Tyr Cys Thr Phe Met Gly Ile Val Val Asn Leu Phe Gly Leu
20 25 30

Glu Thr Lys Thr Cys Trp Asn Val Thr Arg Ile Glu Pro Leu Asn Glu
35 40 45

Val Gln Ser Cys
50

<210> 944
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R505H"

<400> 944
Ala Ser Cys Glu Phe Asp Cys Val Asp Glu Met Leu Thr Leu Ala Ala
1 5 10 15

Met Leu Thr Ala Ala Pro Gly Phe Thr His His Pro Pro Leu Ser Ala
20 25 30

Glu Glu Ala Ala Leu Arg Arg Ala Leu Glu His Thr Asp Gly Asp His
35 40 45

Ser Ser Leu Ile
50

<210> 945
<211> 52
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polypeptide"

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<223> /note="p.S275R"

<400> 945
Arg Ile Ala Gln Val Gln Ile Arg Arg Ile Ser Ser Leu Glu Arg Ala
1 5 10 15

Ala Glu His Ala Gln Ser Cys Arg Ser Arg Arg Ala Ala Cys Ala Pro
20 25 30

Asp Thr Ser Leu Arg Ala Ser Ile Lys Lys Glu Thr Lys Val Leu Lys
35 40 45

Thr Leu Ser Val
50

<210> 946
<211> 52
<212> PRT

<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.R128L"

<400> 946
Asn Pro Arg Thr Gly Glu Ile Asn Ile Thr Ser Val Val Asp Arg Glu
1 5 10 15

Ile Thr Pro Leu Phe Leu Ile Tyr Cys Leu Leu Ala Leu Asn Ser Arg
20 25 30

Gly Glu Asp Leu Glu Arg Pro Leu Glu Leu Arg Val Lys Val Met Asp
35 40 45

Ile Asn Asp Asn
50

<210> 947
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic
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<223> /note="p.R160G"

<400> 947
Cys Asp Ala Tyr Gln Lys Arg Leu Leu Gln Leu Gln Glu Gln Met Arg
1 5 10 15

Ala Leu Tyr Lys Ala Ile Ser Val Pro Gly Gly Val Arg Arg Ala Ser
20 25 30

Ser Lys Gly Gly Gly Gly Tyr Thr Cys Gln Ser Gly Ser Gly Trp Asp
35 40 45

Glu Phe Thr Lys
50

<210> 948
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A4410S"

<400> 948
Thr Ile Cys Gly Lys Ser Val Glu Arg Gln Asn Lys Leu Glu Glu Ala
1 5 10 15

Leu Leu Phe Ser Gly Gln Phe Thr Asp Ser Ser Leu Gln Ala Leu Ile
20 25 30

Asp Trp Leu Tyr Arg Val Glu Pro Gln Leu Ala Glu Asp Gln Pro Val
35 40 45

His Gly Asp Ile
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<210> 949
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<400> 949
Ile Thr Leu Thr Arg Ser Leu Ser Val Gln Asp Gly Leu Asp Glu Met
1 5 10 15

Leu Asp Trp Met Gly Asn Val Glu Ser Tyr Tyr Leu Lys Glu Gln Gly
20 25 30

Gln Val Pro Leu Asn Ser Thr Ala Leu Gln Asp Ile Ile Ser Lys Asn
35 40 45

Ile Met Leu Glu

50

<210> 950
<211> 36
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<220>
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<220>
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<223> /note="p.F101fs"

<400> 950
Lys Asp Cys Arg Tyr Ala Leu Tyr Asp Ala Ser Phe Glu Thr Lys Glu
1 5 10 15

Ser Arg Lys Glu Glu Leu Met Phe Phe Phe Val Gly Thr Arg Thr Ser
20 25 30

Thr Ser Glu Lys
35

<210> 951
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.F880L"

<400> 951
Ser Pro Glu Asp Lys Ser Arg Leu Met Phe Thr Met Tyr Asp Leu Asp
1 5 10 15

Glu Asn Gly Phe Leu Ser Lys Asp Glu Leu Leu Phe Thr Met Met Arg
20 25 30

Ser Phe Ile Glu Ile Ser Asn Asn Cys Leu Ser Lys Ala Gln Leu Ala
35 40 45

Glu Val Val Glu
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<210> 952
<211> 104
<212> PRT
<213> Artificial Sequence

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polypeptide"

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<223> /note="p.A601fs"

<400> 952
Tyr Gly Gly Gly Ser Ala Ser Ser Gln His Ser Glu Gly Ser Arg Ser
1 5 10 15

Ser Gly Ser Thr Arg Ser Asp Gly Gly Gln Gly Ala Arg Gly Gly Pro
20 25 30

Arg Ser Gly Pro Pro Ser Pro Ser Pro Ala Val Ala Val Ser Leu Ser
35 40 45

Pro Pro Ala Glu Gly Ala Ala Phe Gly Gly Val Gly Lys Gln Val Gly
50 55 60

Leu Ala Met Gly Ala Leu Leu His Pro Glu Ala Gln Leu Gly Val Pro
65 70 75 80

Leu Ile Ser Glu Pro Thr Gln Gly Ser Ile Pro Met Asp Arg Pro Leu
85 90 95

Ala Trp Pro Ser Pro Thr Thr Pro
100

<210> 953
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V66G"

<400> 953
Gly Asp Phe Lys Ser Val Leu Gln Arg Pro Ala Gly Ala Lys Tyr Phe
1 5 10 15

Phe Lys Ser Met Asp Gln Asp Phe Gly Gly Gly Val Lys Glu Glu Ile
20 25 30

Ser Asp Asp Asn Ala Arg Leu Pro Cys Phe Asn Gly Arg Val Val Ser
35 40 45

Trp Leu Val Ser
50

<210> 954
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E883D"

<400> 954
Lys Glu Trp Ile Val Ile Gly Gln Val Asp Met Glu Ala Leu Val Glu
1 5 10 15

Lys His Leu Phe Thr Val His Asp Trp Asp Asp Lys Asn Phe Lys Ala
20 25 30

Leu Lys Ile Lys Gly Lys Glu Val Glu Arg Leu Pro Ser Ala Val Lys
35 40 45

Val Asp Cys Leu
50

<210> 955
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.Q545fs"

<400> 955
Asp Val Pro His Lys Thr His Gln Ala Pro Ala Ser Ala Ser Ser Leu
1 5 10 15

Pro Gly Thr Gly Ala Gln Leu Pro Pro Ser Pro Asp Thr Leu Val Val
20 25 30

Pro His His Gln Pro His His His Pro Arg Ser
35 40

<210> 956
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K468fs"

<400> 956
Thr Ala Ser Arg Arg Gln Thr Phe Phe Asp Ser Lys Gly Phe Pro Lys
1 5 10 15

Asn Ile Thr Asn Asn Arg Gly Lys Lys Asp Thr Gln Ile Pro Arg Thr
20 25 30

Ser Arg Trp Cys
35

<210> 957
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M322L"

<400> 957
Asn Leu Lys Tyr Pro Gly Glu Asn Asp Gln Ser Phe Ser Gly Lys Lys

1 5 10 15

Cys Leu Lys Glu Gly Cys Thr Gly Asp Leu Leu Val Arg Met Leu Gln
20 25 30

Cys Asp Val Pro Gly Ile Val Lys Ile Leu Phe Glu Val Val Arg Lys
35 40 45

Asp Glu Tyr Ile
50

<210> 958
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I91S"

<400> 958
Pro Ile Thr Pro Val Lys Phe Val Asp Arg Gln Gln Ala Glu Pro Trp
1 5 10 15

Thr Pro Thr Ala Asn Leu Lys Met Leu Ser Ser Ser Ala Ala Ser Pro
20 25 30

Asp Ile Arg Asp Arg Glu Lys Lys Lys Gly Leu Phe Arg Pro Ile Glu
35 40 45

Asn Lys Asp Asp
50

<210> 959
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V109fs"

<400> 959
Cys Ile Leu Ile Ile Asn His Asp Thr Gly Glu Cys Arg Leu Glu Lys
1 5 10 15

Leu Ser Ser Asn Ile Thr Val Lys Lys Gln Glu Leu Lys Glu Ala Val
20 25 30

Lys Phe Ser Ile Val Lys Asn Asn Ser Asn Asn Lys Cys Gly Ile Gln
35 40 45

Pro Gly Leu Pro Ile Leu
50

<210> 960
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E187K"

<400> 960
Glu Glu Asp Ala Ala Trp Gln Ala Glu Glu Val Leu Arg Gln Gln Lys
1 5 10 15

Leu Ala Asp Arg Glu Lys Arg Ala Ala Lys Lys Gln Gln Arg Lys Lys
20 25 30

Met Glu Lys Glu Ala Gln Arg Leu Met Lys Lys Glu Gln Asn Lys Ile
35 40 45

Gly Val Lys Leu
50

<210> 961
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D353G"

<400> 961
Ser Tyr Lys Ser Lys Gln Phe Cys Lys Gly Thr Pro Gly Arg Phe Ile
1 5 10 15

Tyr Thr Ala Leu Asn Glu Pro Thr Ile Gly Gly Tyr Gly Phe Gln Arg
            20 25 30

Leu Gln Lys Val Ile Pro Arg His Pro Gly Asp Pro Glu Arg Leu Pro
        35 40 45

Lys Glu Val Ile
    50

<210> 962
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<223> /note="p.L189V"

<400> 962
Tyr Cys Trp Leu Tyr Leu Phe Phe Phe Asn Gly Val Trp Val Leu Ile
1 5 10 15

Pro Gly Leu Leu Leu Trp Gln Ser Trp Val Val Glu Leu Lys Lys Met
            20 25 30

His Gln Lys Glu Thr Ser Ser Val Lys Lys Phe Gln
        35 40

<210> 963
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<221> source
<223> /note="p.Q196P"

<400> 963
Phe Phe Asn Gly Val Trp Val Leu Ile Pro Gly Leu Leu Leu Trp Gln
1 5 10 15

Ser Trp Leu Glu Leu Lys Lys Met His Pro Pro Lys Glu Thr Ser Ser
20 25 30

Val Lys Lys Phe Gln
35

<210> 964
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.D254N"

<400> 964
Asp Arg Gly Val Ser Pro Cys Glu Asp Phe Tyr Gln Phe Ser Cys Gly
1 5 10 15

Gly Trp Ile Arg Arg Asn Pro Leu Pro Asn Asn Gly Arg Ser Arg Trp
20 25 30

Asn Thr Phe Asn Ser Leu Trp Asp Gln Asn Gln Ala Ile Leu Lys His
35 40 45

Leu Leu Glu Asn
50

<210> 965
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.K55R"

<400> 965
His Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn
1 5 10 15

Ser Met Asn Gln Val Lys Leu Leu Lys Arg Arg Asp Pro Gly Asn Glu
20 25 30

Val Lys Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro
35 40 45

Cys Asn Met Pro
50

<210> 966
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E266K"

<400> 966
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
1 5 10 15

Leu Glu Cys Ala Lys Leu Val Trp Glu Lys Lys Ala Met Ser Arg Phe
20 25 30

Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr
35 40 45

Arg Gln Gly Glu
50

<210> 967
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L58F"

<400> 967
Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
1 5 10 15

Leu Ser Leu Ala Leu His Leu Leu Thr Phe Phe Cys Cys Tyr Leu Glu
20 25 30

Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly
35 40 45

Gly Ser Gly Thr
50

<210> 968
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L450R"

<400> 968
Ser Arg Ile Leu Lys Leu Thr Leu Tyr Asn Gln Asn Asp Pro Asn Arg
1 5 10 15

Cys Glu Leu Leu Ser Phe Leu Leu Val Arg Trp Asp Tyr Ile Gly Ile
20 25 30

Asn Met Ala Ser Leu Asn Ser Cys Ile Asn Pro Ile Ala Leu Tyr Leu
35 40 45

Val Ser Lys Arg
50

<210> 969
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N570fs"

<400> 969
Glu Arg Glu Asp Leu Tyr Ala Lys Ile Gln Ala Gly Glu Gly Glu Thr
1 5 10 15

Ala Val Leu Asn Gln Leu Gln Glu Lys Thr Ile His Tyr Arg Ser Lys
20 25 30

<210> 970
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T432L"

<400> 970
Gly Lys Pro Met Cys Val Glu Ser Phe Ser Asp Tyr Pro Pro Leu Gly
1 5 10 15

Arg Phe Ala Val Arg Asp Met Arg Gln Leu Leu Val Ala Val Gly Val
20 25 30

Ile Lys Ala Val Asp Lys Lys Ala Ala Gly Ala Gly Lys Val Thr Lys
35 40 45

Ser Ala Gln Lys Ala
50

<210> 971
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.Y418S"

<400> 971
Ser Leu Lys Ser Gly Asp Ala Ala Ile Val Glu Met Val Pro Gly Lys
1 5 10 15

Pro Met Cys Val Glu Ser Phe Ser Gln Ser Ser Pro Pro Leu Gly Arg
20 25 30

Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val Gly Val Ile Lys
35 40 45

Asn Val Glu Lys
50

<210> 972
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S43G"

<400> 972
Tyr Leu Ala Asp Lys Ser Tyr Ile Glu Gly Tyr Val Pro Ser Gln Ala
1 5 10 15

Asp Val Ala Val Phe Glu Ala Val Ser Gly Gly Pro Pro Pro Ala Asp
20 25 30

Leu Cys His Ala Leu Arg Trp Tyr Asn His Ile Lys Ser Tyr Glu Lys
35 40 45

Glu Lys Ala Ser
50

<210> 973
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E673K"

<400> 973
Thr Asp Cys Asp Glu Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro
1 5 10 15

Arg Tyr Met Met Leu Ala Arg Glu Ala Lys Lys Met Leu Phe Thr Gly
20 25 30

Gly Tyr Gly Leu Glu Lys Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr
35 40 45

Gln Ala Ala Glu
50

<210> 974
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E265Q"

<400> 974
Met Glu Gln Gln Ile Lys Ser Glu Lys Glu Gln Phe Leu Leu Lys Asp
1 5 10 15

Thr Glu Arg Phe Gln Ala Arg Ser Gln Gln Gln Leu Glu Gln Lys Leu
20 25 30

Leu Cys Lys Glu Gln Glu Leu Glu Gln Leu Thr Gln Lys Gln Lys Arg
35 40 45

Leu Glu Gly Gln
50

<210> 975
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R379K"

<400> 975
Asn Trp Lys Gln Phe Leu Thr Ser Phe His Glu Pro Gln Gly Leu Gln
1 5 10 15

Val Ser Ser Lys Gly Pro Leu Thr Lys Lys Lys Asn Ser Ile Asn Ser
20 25 30

Arg Asn Glu Ser His Lys Glu Asn Ile Ile Thr Lys Leu Phe Arg His
35 40 45

Thr Glu Asp His
50

<210> 976
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E1002K"

<400> 976
Asp Gln Ser Lys Thr Asn Tyr Ile Ser Ile Cys Lys Met Gln Glu Val
1 5 10 15

Leu Glu Glu Cys Gly Cys Ser Leu Thr Lys Lys Gly Glu Leu Thr His
20 25 30

Leu Leu Asn Ser Trp Gly Val Ser Arg His Asp Asn Ala Ile Asn Tyr
35 40 45

Leu Asp Phe Leu
50

<210> 977
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P596S"

<400> 977
Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile
1 5 10 15

Asp Gly Pro His Cys Val Lys Thr Cys Ser Ser Ala Gly Val Met Gly
20 25 30

Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys
35 40 45

His Leu Cys His
50

<210> 978
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P596L"

<400> 978
Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile
1 5 10 15

Asp Gly Pro His Cys Val Lys Thr Cys Leu Leu Ala Gly Val Met Gly
20 25 30

Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys
35 40 45

His Leu Cys His
50

<210> 979
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G598A"

<400> 979
Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly
1 5 10 15

Pro His Cys Val Lys Thr Cys Pro Ala Ala Ala Val Met Gly Glu Asn
20 25 30

Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu
35 40 45

Cys His Pro Asn
50

<210> 980
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G598V"

<400> 980
Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly
1 5 10 15

Pro His Cys Val Lys Thr Cys Pro Ala Val Val Val Met Gly Glu Asn
20 25 30

Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu
35 40 45

Cys His Pro Asn

50

<210> 981
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L62R"

<400> 981
Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe Leu Ser Leu Gln
1 5 10 15

Arg Met Phe Asn Asn Cys Glu Val Val Arg Arg Gly Asn Leu Glu Ile
20 25 30

Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys Thr Ile Gln
35 40 45

Glu Val Ala Gly
50

<210> 982
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E709K"

<400> 982
Gln Glu Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro
1 5 10 15

Asn Gln Ala Leu Leu Arg Ile Leu Lys Lys Lys Thr Glu Phe Lys Lys
20 25 30

Ile Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu
35 40 45

Trp Ile Pro Glu
50

<210> 983
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G719A"

<400> 983
Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu Arg Ile Leu Lys Glu
1 5 10 15

Thr Glu Phe Lys Lys Ile Lys Val Leu Ala Ala Ser Gly Ala Phe Gly
20 25 30

Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys Ile
35 40 45

Pro Val Ala Ile
50

<210> 984
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.ELREA746del"

<400> 984
Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
1 5 10 15

Lys Val Lys Ile Pro Val Ala Ile Lys Thr Ser Pro Lys Ala Asn Lys
20 25 30

Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn Pro His
35 40 45

Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile
50 55 60

Thr
65

<210> 985
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S768I"

<400> 985
Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu
1 5 10 15

Ile Leu Asp Glu Ala Tyr Val Met Ala Ile Ile Val Asp Asn Pro His
20 25 30

Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile
35 40 45

Thr Gln Leu Met
50

<210> 986
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L838M"

<400> 986

Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu
1 5 10 15

Glu Asp Arg Arg Leu Val His Arg Asp Met Met Ala Ala Arg Asn Val
20 25 30

Leu Val Lys Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala
35 40 45

Lys Leu Leu Gly
50

<210> 987
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L858R"

<400> 987
Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
1 5 10 15

Gln His Val Lys Ile Thr Asp Phe Gly Arg Arg Ala Lys Leu Leu Gly
20 25 30

Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys
35 40 45

Trp Met Ala Leu
50

<210> 988
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.L861Q"

<400> 988
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln His Val
1 5 10 15

Lys Ile Thr Asp Phe Gly Leu Ala Lys Gln Gln Leu Gly Ala Glu Glu
20 25 30

Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met Ala
35 40 45

Leu Glu Ser Ile
50

<210> 989
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R108K"

<400> 989
Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val Glu Arg
1 5 10 15

Ile Pro Leu Glu Asn Leu Gln Ile Ile Lys Lys Gly Asn Met Tyr Tyr
20 25 30

Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn Lys
35 40 45

Thr Gly Leu Lys
50

<210> 990
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R252C"

<400> 990
Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys Thr Gly
1 5 10 15

Pro Arg Glu Ser Asp Cys Leu Val Cys Cys Cys Lys Phe Arg Asp Glu
20 25 30

Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro Thr
35 40 45

Thr Tyr Gln Met
50

<210> 991
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A289T"

<400> 991
Cys Pro Pro Leu Met Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val
1 5 10 15

Asn Pro Glu Gly Lys Tyr Ser Phe Gly Thr Thr Thr Cys Val Lys Lys
20 25 30

Cys Pro Arg Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala
35 40 45

Cys Gly Ala Asp
50

<210> 992
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A289D"

<400> 992
Cys Pro Pro Leu Met Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val
1 5 10 15

Asn Pro Glu Gly Lys Tyr Ser Phe Gly Asp Asp Thr Cys Val Lys Lys
20 25 30

Cys Pro Arg Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala
35 40 45

Cys Gly Ala Asp
50

<210> 993
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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polypeptide"

<220>
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<223> /note="p.A289V"

<400> 993
Cys Pro Pro Leu Met Leu Tyr Asn Pro Thr Thr Tyr Gln Met Asp Val
1 5 10 15

Asn Pro Glu Gly Lys Tyr Ser Phe Gly Val Val Thr Cys Val Lys Lys
20 25 30

Cys Pro Arg Asn Tyr Val Val Thr Asp His Gly Ser Cys Val Arg Ala
35 40 45

Cys Gly Ala Asp
50

<210> 994
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.H304Y"

<400> 994
Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly Ala Thr Cys Val Lys Lys
1 5 10 15

Cys Pro Arg Asn Tyr Val Val Thr Asp Tyr Tyr Gly Ser Cys Val Arg
20 25 30

Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu Asp Gly Val Arg Lys
35 40 45

Cys Lys Lys Cys
50

<210> 995
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q9H"

<400> 995
Met Ala Ala Ala Lys Ala Glu Met His His Leu Met Ser Pro Leu Gln
1 5 10 15

Ile Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn
20 25 30

Tyr Pro Lys
35

<210> 996
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P332fs"

<400> 996
Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr
1 5 10 15

Pro Asn Arg Pro Ser Lys Thr Pro Pro Thr Asn Ala Leu Thr Leu Ala
20 25 30

Gln Trp Ser Pro Val Ile Ala Ala Ser Pro Ala Pro Thr Ser Ser Pro
35 40 45

Ala Thr Ser Ala Ser Thr Gln Ala Arg Ser Pro Ser Ser Ala Ala Ser
50 55 60

Ala Cys Ala Thr Ser Ala Ala Ala Thr Thr Ser Pro Pro Thr Ser Ala
65 70 75 80

Pro Thr Gln Ala Lys Ser Pro Ser Pro Ala Thr Ser Val Glu Glu Ser
85 90 95

Leu Pro Gly Ala Met Asn Ala Arg Gly Ile Pro Arg Ser Thr Cys Gly
100 105 110

Arg Arg Thr Arg Lys Gln Thr Lys Val Leu Trp Pro Leu Arg Pro Pro
115 120 125

Pro Leu Ser Leu Pro Thr Arg Pro Arg Leu Leu Pro Leu Thr Arg Pro
130 135 140

Arg Leu Leu Pro Leu Ile His Pro Arg Pro Pro Pro His Thr His Pro
145 150 155 160

Leu Cys Pro Pro Pro Ser Pro Leu Pro Ala Pro Arg Pro Thr His Pro
165 170 175

Leu Cys Thr Val Ala Ser Pro Pro Arg Arg Trp Pro Pro Arg Thr Pro
180 185 190

Leu Phe Pro Leu Leu Ser Arg Pro Arg Ser Ala Ala Ser Leu Pro Gln
195 200 205

Leu Ser Pro Thr Pro Ser Ala Pro Pro Gln Gly Phe Arg Thr
210 215 220

<210> 997
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E369K"

<400> 997
Ser Lys Thr Pro Val His Glu Arg Pro Tyr Pro Cys Pro Ala Glu Gly
1 5 10 15

Cys Asp Arg Arg Phe Ser Arg Ser Asp Lys Lys Leu Thr Arg His Ile
20 25 30

Arg Ile His Thr Gly His Lys Pro Phe Gln Cys Arg Ile Cys Met Arg
35 40 45

Asn Phe Ser Arg
50

<210> 998
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R390H"

<400> 998
Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly His
1 5 10 15

Lys Pro Phe Gln Cys Arg Ile Cys Met His His Asn Phe Ser Arg Ser
20 25 30

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
35 40 45

Ala Cys Asp Tyr
50

<210> 999
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H397N"

<400> 999
Arg His Ile Arg Ile His Thr Gly His Lys Pro Phe Gln Cys Arg Ile
1 5 10 15

Cys Met Arg Asn Phe Ser Arg Ser Asp Asn Asn Leu Thr Thr His Ile
20 25 30

Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Tyr Cys Gly Arg
35 40 45

Lys Phe Ala Arg
50

<210> 1000
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E44K"

<400> 1000
Gln Thr Val Ser Glu Gly Leu Lys Lys Leu Tyr Lys Ser Lys Leu Leu
1 5 10 15

Pro Leu Glu Glu His Tyr Arg Phe His Lys Lys Phe His Ser Pro Ala
20 25 30

Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val Gly
35 40 45

Gln Tyr Ser Thr
50

<210> 1001
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q704H"

<400> 1001
Leu Gln Lys Tyr Tyr Arg Gln Asn Pro Asp Ile Pro Gln Leu Glu Pro
1 5 10 15

Ser Asp Tyr Leu Lys Lys Leu Ala Ser His His Gly Asn Pro Pro Leu
20 25 30

Lys Glu Trp Gln Ser Leu Ala Gly Ser Pro Ser Ser Lys Leu
35 40 45

<210> 1002
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G9D"

<400> 1002
Met Pro Lys Asn Lys Gly Lys Gly Asp Asp Lys Asn Arg Arg Arg Gly
1 5 10 15

Lys Asn Glu Asn Glu Ser Glu Lys Arg Glu Leu Val Phe Lys Glu Asp

500

20 25 30

Gly Gln Glu
35

<210> 1003
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R139Q"

<400> 1003
Glu Val Thr Ile Pro Gly Glu Gly Lys Asp Arg Ile Phe Lys Val Ser
1 5 10 15

Ile Lys Trp Leu Ala Ile Val Ser Trp Gln Gln Met Leu His Glu Ala
20 25 30

Leu Val Ser Gly Gln Ile Pro Val Pro Leu Glu Ser Val Gln Ala Leu
35 40 45

Asp Val Ala Met
50

<210> 1004
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A8G"

<400> 1004
Met Ala Ala Ala Ala Ala Ala Gly Gly Gly Asp Ser Asp Ser Trp Asp
1 5 10 15

Ala Asp Ala Phe Ser Val Glu Asp Pro Val Arg Lys Val Gly Gly Gly
20 25 30

Gly Thr

<210> 1005
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R8H"

<400> 1005
Met Asn Ser Gln Pro Gln Thr His His Ser Pro Phe Phe Gln Arg Pro
1 5 10 15

Gln Ile Gln Pro Pro Arg Ala Thr Ile Pro Asn Ser Ser Pro Ser Ile
20 25 30

Arg Pro

<210> 1006
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L263F"

<400> 1006
Arg Leu Asp Asn Leu Leu Asn Met Ala Tyr Gly Val Lys Arg Phe Ser
1 5 10 15

Pro Met Thr Ile Asp Gly Met Thr Ser Phe Phe Ala Gly Ile Asn Ile
20 25 30

Pro Gly His Pro Gly Thr Gly Trp Cys Ile Phe Val Tyr Asn Leu Ala
35 40 45

Pro Asp Ala Asp
    50

<210> 1007
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.F305fs"

<400> 1007
Asp Ile Leu Ile His Pro Glu Leu Asn Glu Gly Leu Met Lys Trp Glu
1   5   10   15

Asn Arg His Glu Gly Val Phe Lys Phe Cys Ala Pro Arg Leu Trp Pro
            20   25   30

Asn Tyr Gly Ala Lys Arg Lys Arg Thr Ala Thr
        35   40

<210> 1008
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S415L"

<400> 1008
Lys Leu Thr Lys Ala Val Ser Ala Ser Ser Val Pro Ser Asn Ile His
1   5   10   15

Leu Gly Val Ala Pro Val Gly Ser Gly Leu Leu Ala Leu Thr Leu Gln
            20   25   30

Thr Ile Pro Leu Thr Thr Val Leu Thr Asn Gly Pro Pro Ala Ser Thr
        35   40   45

Thr Ala Pro Thr
50

<210> 1009
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T141M"

<400> 1009
Arg Lys Arg Pro Tyr Asp Ser Asp Asn Leu Gln His Glu Glu Leu Leu
1 5 10 15

Met Lys Leu Trp Asn Leu Leu Met Pro Met Met Lys Lys Leu Asn Ala
20 25 30

Arg Ile Ser Lys Gln Trp Ala Glu Ile Gly Phe Gln Gly Asp Asp Pro
35 40 45

Lys Thr Asp Phe
50

<210> 1010
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.D570H"

<400> 1010
Ile Gly Pro Glu Leu Ser Arg Arg Ile Tyr Leu Gln Met Thr Thr Leu
1 5 10 15

Gln Pro His Leu Ser Leu Asp Ser Ala His His
20 25

<210> 1011

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R27G"

<400> 1011
Ala Pro Arg Thr Leu Trp Ser Cys Tyr Leu Cys Cys Leu Leu Thr Ala
1 5 10 15

Ala Ala Gly Ala Ala Ser Tyr Pro Pro Gly Gly Gly Phe Ser Leu Tyr
20 25 30

Thr Gly Ser Ser Gly Ala Leu Ser Pro Gly Gly Pro Gln Ala Gln Ile
35 40 45

Ala Pro Arg Pro
50

<210> 1012
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K805R"

<400> 1012
Phe Ser Ala Asp Gly Lys Cys Leu Val Ser Val Gly Leu Asp Asp Phe
1 5 10 15

His Ser Ile Val Phe Trp Asp Trp Lys Arg Arg Gly Glu Lys Ile Ala
20 25 30

Thr Thr Arg Gly His Lys Asp Lys Ile Phe Val Val Lys Cys Asn Pro
35 40 45

His His Val Asp
50

<210> 1013
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R493H"

<400> 1013
Glu Glu Ser Glu Ser Thr Glu Thr Thr Gly Val Ala Phe Val Ser Phe
1 5 10 15

Val Gly Met Glu Ser Val Leu Asn Glu His His Phe Phe Lys Asp His
20 25 30

Gln Ala Pro Leu Thr Thr Ser Glu Ile Lys Leu Lys Met Asn Ser Arg
35 40 45

Val Val Gly Gly
50

<210> 1014
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R631Q"

<400> 1014
Ser His Val Gly Ile Ile Ile Ser Leu Val Cys Leu Val Leu Ala Ile
1 5 10 15

Ala Thr Phe Leu Leu Cys Arg Ser Ile Gln Gln Asn His Asn Thr Tyr
20 25 30

Leu His Leu His Leu Cys Val Cys Leu Leu Leu Ala Lys Thr Leu Phe
35 40 45

Leu Ala Gly Ile
50

<210> 1015
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S75L"

<400> 1015
Gly Phe Ser Ser Phe Ser Glu Ile Ile Thr Thr Pro Met Glu Thr Cys
1 5 10 15

Asp Asp Ile Asn Glu Cys Ala Thr Leu Leu Leu Lys Val Ser Cys Gly
20 25 30

Lys Phe Ser Asp Cys Trp Asn Thr Glu Gly Ser Tyr Asp Cys Val Cys
35 40 45

Ser Pro Gly Tyr
50

<210> 1016
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R514L"

<400> 1016
Thr Pro Glu Pro Thr Arg Lys Pro Trp Glu Arg Thr Asn Thr Met Asn
1 5 10 15

Gly Ser Lys Ser Pro Val Ile Ser Arg Leu Leu Asp Ser Pro Arg Lys
20 25 30

Asn Gln Ile Val Phe Asp Asn Arg Ser Tyr Asp Ser Leu His Arg Pro
35 40 45

Lys Ser Thr Pro
50

<210> 1017
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R373H"

<400> 1017
Pro Phe Tyr Arg Asn Gln Gln Val Gln Arg Gly Pro Arg Trp Asn Phe
1 5 10 15

Phe Ala Trp Glu Arg Lys Gln Val Ala His His Pro Gly Asn Pro Val
20 25 30

Tyr His Lys Ala Tyr Pro Pro Thr Ser Arg Gly Asn Tyr Pro Asn Tyr
35 40 45

Ala Gly Asn Pro
50

<210> 1018
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R356W"

<400> 1018
Gln Phe Glu Gln Ile Val Ala Val Tyr His Ser Ala Ser Lys Gln Lys
1 5 10 15

Ala Trp Asp His Phe Thr Lys Ala Gln Trp Trp Lys Asn Ile Ser Val

20 25 30

Trp Cys Lys Gln Ala Glu Glu Ile Arg Asn Ile His Asn Asp Glu Leu
35 40 45

Met Gly Ile Arg
50

<210> 1019
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F289C"

<400> 1019
Glu Glu Ser Val Asp Asp Lys Trp Thr Arg Thr Thr Phe Glu Lys Ser
1 5 10 15

Val Pro Met Ser Thr Tyr Leu Val Cys Cys Cys Ala Val His Gln Phe
20 25 30

Asp Ser Val Lys Arg Ile Ser Asn Ser Gly Lys Pro Leu Thr Ile Tyr
35 40 45

Val Gln Pro Glu
50

<210> 1020
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G738E"

<400> 1020
Tyr Gln Asp Phe Arg Ile Pro Leu Ser Pro Val His Lys Cys Ser Phe
1 5 10 15

Tyr Lys Asn Asn Thr Lys Val Ser Tyr Glu Glu Phe Leu Ser Pro Pro
20 25 30

Gln Leu Asn Lys Asn Ser Ser Gly Ile Tyr Ser Glu Ala Leu Leu Thr
35 40 45

Thr Asn Ile Val
50

<210> 1021
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G204fs"

<400> 1021
Asn Phe Ile Lys Tyr Gly Trp Val Gly Arg Trp Phe Arg Pro Arg Lys
1 5 10 15

Gly Thr Leu Gly Ala Met Asp Leu Gly Val Pro Leu Pro Arg Ser Leu
20 25 30

Leu Arg Gln Pro Val Gln Leu Arg Thr Glu Pro Ala Arg Ser Ser Cys
35 40 45

Ile Ser Thr Ala Ser Thr Thr Glu Ser Thr Pro Thr Ala Ser Ser Ala
50 55 60

Met Ala Val Thr Arg Ser Ser Arg Gly Cys Trp Pro Ala Pro Ser Arg
65 70 75 80

Pro Thr Ala Ser Thr Pro Ala Gly Arg Gly Ala Phe Pro Pro Lys Cys
85 90 95

Cys Ser Gly Met Cys Thr Ser His His Ala Pro Trp Pro Ser Gly Pro
100 105 110

Arg Thr Ser Thr Ala Val Pro Gly Ser Ala Cys Gln Gly Ala Val Thr
115 120 125

Pro Thr Ser Ala Glu Ile Trp Phe Leu Gly Ser Ser Ala Ser Pro Pro
130 135 140

Ala Pro Ser Pro Asp Ala Leu Ser Met Gly Ser Ser Ser Pro Gln Trp
145 150 155 160

Leu Gly Thr Leu Trp Pro Ser Leu Pro Ser Ser Thr Leu Trp Thr Phe
165 170 175

Cys Gly Leu Arg Trp Gly Cys Pro Trp Pro Pro Cys Ser Ser Trp Arg
180 185 190

Gln Pro Gln
195

<210> 1022
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E327K"

<400> 1022
His Thr Glu His Val Tyr Arg Val Tyr Val Thr Thr Phe Leu Gly Phe
1 5 10 15

Gly Gly Asn Phe Ala Arg Gln Arg Tyr Lys Lys Asp Leu Val Leu Asn
20 25 30

Glu Thr Leu Asn Lys Asn Arg Leu Leu Gly Gln Lys Thr Gly Leu Ser
35 40 45

Pro Asp Asn Pro
50

<210> 1023
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<220>
<221> source
<223> /note="p.G332fs"

<400> 1023
Leu Asn Pro Thr Ala His Tyr Asn Val Phe Val Glu Val Val Leu Ala
1 5 10 15

Asp Pro Asn His Trp Arg Phe Gln Gly Ala Asn Gly
20 25

<210> 1024
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C1164Y"

<400> 1024
Tyr Lys Tyr Cys Ser Lys Leu Ser Glu Val Phe Glu Gln Glu Ile Asp
1 5 10 15

Pro Val Met Gln Ser Leu Gly Tyr Cys Tyr Tyr Gly Arg Lys Leu Glu
20 25 30

Phe Ser Pro Gln Thr Leu Cys Cys Tyr Gly Lys Gln Leu Cys Thr Ile
35 40 45

Pro Arg Asp Ala
50

<210> 1025
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.D1399N"

<400> 1025
Phe Gly Met His Val Gln Glu Tyr Gly Ser Asp Cys Pro Pro Pro Asn
1 5 10 15

Gln Arg Arg Val Tyr Ile Ser Tyr Leu Asn Asn Ser Val His Phe Phe
20 25 30

Arg Pro Lys Cys Leu Arg Thr Ala Val Tyr His Glu Ile Leu Ile Gly
35 40 45

Tyr Leu Glu Tyr
50

<210> 1026
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A896S"

<400> 1026
Ser Tyr Ser Ala Gly Asp Ser Gly Asp Ala Ala Ala Gln Pro Ala Phe
1 5 10 15

Thr Gly Ile Lys Gly Lys Glu Gly Ser Ser Ser Leu Thr Glu Gly Ala
20 25 30

Lys Glu Glu Gly Gly Glu Glu Val Ala Lys Ala Val Leu Glu Gln Glu
35 40 45

Glu Thr Ala Ala
50

<210> 1027
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D369N"

<400> 1027
Lys Val Phe Ser Tyr His Arg Tyr Gln Arg Val Glu Met Asn Glu Asn
1 5 10 15

Ala Leu Val Glu Leu Lys Lys Leu Phe Asn Asn Ala Lys Ser Glu His
20 25 30

Leu His Gln Thr Leu Ala Leu His Ser Tyr Thr Ser Val Leu Ser Arg
35 40 45

Leu Gln Val Glu
50

<210> 1028
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R2289L"

<400> 1028
Met Ala Leu Ser Ser Leu Phe Met Glu Val Leu Met Met Met Asn Asn
1 5 10 15

Ala Thr Ile Pro Thr Ala Glu Phe Leu Leu Leu Gly Ser Ile Arg Thr
20 25 30

Trp Ile Gly Gln Lys Met His Gly Leu Val Val Leu Pro Leu Leu Thr
35 40 45

Ala Ala Cys Gln
50

<210> 1029
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G111V"

<400> 1029
Ile Tyr Arg Gly Glu Glu Ala Ser Arg Val His Val Glu Leu Gln Phe
1 5 10 15

Thr Val Arg Asp Cys Lys Ser Phe Pro Val Val Gly Ala Gly Pro Leu
20 25 30

Gly Cys Lys Glu Thr Phe Asn Leu Leu Tyr Met Glu Ser Asp Gln Asp
35 40 45

Val Gly Ile Gln
50

<210> 1030
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A184T"

<400> 1030
Leu Val Ser Gly Ser Val Lys Leu Asn Val Glu Arg Cys Ser Leu Gly
1 5 10 15

Arg Leu Thr Arg Arg Gly Leu Tyr Leu Thr Thr Phe His Asn Pro Gly
20 25 30

Ala Cys Val Ala Leu Val Ser Val Arg Val Phe Tyr Gln Arg Cys Pro
35 40 45

Glu Thr Leu Asn
50

<210> 1031
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P868fs"

<400> 1031
Glu Arg Pro Tyr Trp Asp Met Ser Gly Gln Asp Val Ile Lys Ala Val
1 5 10 15

Glu Asp Gly Phe Arg Leu Pro Pro Pro Gly Thr Val Leu Thr Phe Cys
20 25 30

Thr Asp

<210> 1032
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P460fs"

<400> 1032
Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr
1 5 10 15

Ser Leu Ser Val Ser Trp Ser Ile Pro Arg Arg Ser Arg Ala Glu Cys
20 25 30

Gly Ser Thr Arg Ser Leu Thr Ala Arg Arg Glu Thr Pro Thr Ala Thr
35 40 45

Met Cys Ala Ala Pro Arg Val Ser Pro
50 55

<210> 1033
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.T802R"

<400> 1033
Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg Trp Thr Ser
1 5 10 15

Pro Glu Ala Ile Ala Tyr Arg Lys Phe Arg Arg Ser Ala Ser Asp Val
20 25 30

Trp Ser Tyr Gly Ile Val Leu Trp Glu Val Met Ser Tyr Gly Glu Arg
35 40 45

Pro Tyr Trp Glu
50

<210> 1034
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D952H"

<400> 1034
Thr Thr Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile
1 5 10 15

Ala Tyr Arg Lys Phe Ser Ser Ala Ser His His Ala Trp Ser Tyr Gly
20 25 30

Ile Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Glu
35 40 45

Met Ser Asn Gln
50

<210> 1035
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R392H"

<400> 1035
Ser Gly Arg Gly Ala Cys Thr Arg Cys Gly Asp Asn Val Gln Tyr Ala
1 5 10 15

Pro Arg Gln Leu Gly Leu Thr Glu Pro His His Ile Tyr Ile Ser Asp
20 25 30

Leu Leu Ala His Thr Gln Tyr Thr Phe Glu Ile Gln Ala Val Asn Gly
35 40 45

Val Thr Asp Gln
50

<210> 1036
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R337H"

<400> 1036
Lys Ala Cys Gln Ala Cys Pro Arg Gly Leu Tyr Lys Ser Ser Ala Gly
1 5 10 15

Asn Ala Pro Cys Ser Pro Cys Pro Ala His His Ser His Ala Pro Asn
20 25 30

Pro Ala Ala Pro Val Cys Pro Cys Leu Glu Gly Phe Tyr Arg Ala Ser
35 40 45

Ser Asp Pro Pro
50

<210> 1037
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G54fs"

<400> 1037
Ala Leu Glu Glu Val Leu Leu Asp Thr Thr Gly Glu Thr Ser Glu Ile
1 5 10 15

Gly Trp Leu Thr Tyr Pro Pro Gly Gly Gly Thr Arg
20 25

<210> 1038
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P132fs"

<400> 1038
Ile Leu Asn Arg Tyr Pro His Phe Lys Thr Lys Ile Glu Gly Leu Asp
1 5 10 15

Ile His Phe Ile His Val Lys Pro Pro Ser Cys Pro Gln Ala Ile Pro
20 25 30

Arg Ser Pro Cys
35

<210> 1039
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R282Q"

<400> 1039
Thr Thr Glu Asp Leu Glu Ala Tyr Ile Tyr Val Phe Ser Gln Pro Gly
1 5 10 15

Ala Leu Ser Gly Pro Ile Asn His Tyr Gln Gln Asn Ile Phe Ser Cys
20 25 30

Leu Pro Leu Lys His His Met Val Thr Thr Pro Thr Leu Leu Leu Trp
35 40 45

Gly Glu Asn Asp
50

<210> 1040
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G2015fs"

<400> 1040
Phe Gln Ala Met Gln Lys Gln Leu Ile Glu Lys Ala Glu Ala Leu Arg
1 5 10 15

Leu Leu Glu Val Gln Val Ala Thr Gly Val Ser Ser Thr His Ser Thr
20 25 30

Thr Thr Gly Ser His Trp Lys Gln Pro Thr Asp Gly Ala Val Cys Thr
35 40 45

Arg Thr Ser Met Arg Ser Phe Pro Thr Arg Ser Thr
50 55 60

<210> 1041
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D2378H"

<400> 1041
His Ser His Arg Val Pro Val Asp Val Ala Tyr Arg Arg Gly Tyr Phe
1 5 10 15

Asp Glu Glu Met Asn Arg Val Leu Ala His His Pro Ser Asp Asp Thr
20 25 30

Lys Gly Phe Phe Asp Pro Asn Thr His Glu Asn Leu Thr Tyr Leu Gln
35 40 45

Leu Leu Gln Arg
50

<210> 1042
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V1151L"

<400> 1042
Met Tyr Pro Ala Tyr Ala Lys Trp Val Gln Ser His Arg Asp Leu Pro
1 5 10 15

Ile Lys Leu Asn Gln Trp Cys Asn Val Leu Leu Arg Trp Glu Phe Lys
20 25 30

His Pro Gln Pro Phe Leu Arg Thr Arg Glu Phe Leu Trp Gln Glu Gly
35 40 45

His Ser Ala Phe
50

<210> 1043
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1335I"

<400> 1043
Gly Ile Thr Asn Ala Leu Ser Glu Glu Asp Lys Glu Ala Leu Ile Ala
1 5 10 15

Lys Cys Asn Asp Tyr Arg Arg Arg Leu Ile Ile Ser Val Asn Ile Arg
20 25 30

Val Arg Ala Asp Leu Arg Asp Asn Tyr Ser Pro Gly Trp Lys Phe Asn
35 40 45

His Trp Glu Leu
50

<210> 1044
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L755S"

<400> 1044
Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn
1 5 10 15

Val Lys Ile Pro Val Ala Ile Lys Val Ser Ser Arg Glu Asn Thr Ser
20 25 30

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly
35 40 45

Val Gly Ser Pro
50

<210> 1045
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D769Y"

<400> 1045
Glu Asn Val Lys Ile Pro Val Ala Ile Lys Val Leu Arg Glu Asn Thr
1 5 10 15

Ser Pro Lys Ala Asn Lys Glu Ile Leu Tyr Tyr Glu Ala Tyr Val Met
20 25 30

Ala Gly Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu
35 40 45

Thr Ser Thr Val
50

<210> 1046
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.774_775insAYVM"

<400> 1046
Ala Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu
1 5 10 15

Ile Leu Asp Glu Ala Tyr Val Met Ala Ala Tyr Val Met Tyr Val Met
20 25 30

Ala Gly Val Gly Ser Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu
35 40 45

Thr Ser Thr Val Gln Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu
50 55 60

Leu Asp
65

<210> 1047
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.776_776G>VC"

<400> 1047
Ala Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu
1 5 10 15

Ile Leu Asp Glu Ala Tyr Val Met Ala Val Cys Val Cys Val Gly Ser
20 25 30

Pro Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln
35 40 45

Leu Val Thr Gln Leu Met Pro
50 55

<210> 1048
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V842I"

<400> 1048
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
1 5 10 15

Met Ser Tyr Leu Glu Asp Val Arg Leu Ile Ile His Arg Asp Leu Ala

20 25 30

Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp
35 40 45

Phe Gly Leu Ala
50

<210> 1049
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M916I"

<400> 1049
Leu Glu Ser Ile Leu Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp
1 5 10 15

Ser Tyr Gly Val Thr Val Trp Glu Leu Ile Ile Thr Phe Gly Ala Lys
20 25 30

Pro Tyr Asp Gly Ile Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys
35 40 45

Gly Glu Arg Leu
50

<210> 1050
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S310Y"

<400> 1050
Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro
1 5 10 15

Tyr Asn Tyr Leu Ser Thr Asp Val Gly Tyr Tyr Cys Thr Leu Val Cys
20 25 30

Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys
35 40 45

Glu Lys Cys Ser
50

<210> 1051
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S310F"

<400> 1051
Pro Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro
1 5 10 15

Tyr Asn Tyr Leu Ser Thr Asp Val Gly Phe Phe Cys Thr Leu Val Cys
20 25 30

Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys
35 40 45

Glu Lys Cys Ser
50

<210> 1052
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M91I"

<400> 1052
Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile Arg
1 5 10 15

Glu Val Thr Gly Tyr Val Leu Val Ala Ile Ile Asn Glu Phe Ser Thr
20 25 30

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
35 40 45

Gly Lys Phe Ala
50

<210> 1053
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V104M"

<400> 1053
Trp Ile Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe
1 5 10 15

Ser Thr Leu Pro Leu Pro Asn Leu Arg Met Met Val Arg Gly Thr Gln
20 25 30

Val Tyr Asp Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr
35 40 45

Asn Ser Ser His
50

<210> 1054
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.V104L"

<400> 1054
Trp Ile Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe
1 5 10 15

Ser Thr Leu Pro Leu Pro Asn Leu Arg Leu Leu Val Arg Gly Thr Gln
20 25 30

Val Tyr Asp Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr
35 40 45

Asn Ser Ser His
50

<210> 1055
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D297Y"

<400> 1055
Leu Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val
1 5 10 15

Ala Ser Cys Pro His Asn Phe Val Val Tyr Tyr Gln Thr Ser Cys Val
20 25 30

Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys
35 40 45

Met Cys Glu Pro
50

<210> 1056
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K692R"

<400> 1056
Asp Leu Ser Glu Lys Glu Ala Ser Leu Leu Asp Leu Lys Glu His Ala
1   5   10   15

Ser Ser Leu Ala Ser Ser Gly Leu Lys Arg Arg Asp Ser Arg Leu Lys
            20   25   30

Thr Leu Glu Ile Ala Leu Glu Gln Lys Lys Glu Glu Cys Leu Lys Met
        35   40   45

Glu Ser Gln Leu
    50

<210> 1057
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Y14C"

<400> 1057
Met Lys Leu Asn Val Asp Gly Leu Leu Val Tyr Phe Pro Cys Cys Asp
1   5   10   15

Tyr Ile Tyr Pro Glu Gln Phe Ser Tyr Met Arg Glu Leu Lys Arg Thr
            20   25   30

Leu Asp Ala Lys Gly His Gly Val
        35   40

<210> 1058
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.N238S"

<400> 1058
Leu Asp Pro Lys Ile Ala Asp Leu Val Ser Lys Glu Leu Ala Arg Lys
1   5   10   15

Ala Val Val Val Phe Asp Glu Ala His Ser Ser Ile Asp Asn Val Cys
            20   25   30

Ile Asp Ser Met Ser Val Asn Leu Thr Arg Arg Thr Leu Asp Arg Cys
        35   40   45

Gln Gly Asn Leu
    50

<210> 1059
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.D312N"

<400> 1059
Arg Leu Val Glu Gly Leu Arg Glu Ala Ser Ala Ala Arg Glu Thr Asp
1   5   10   15

Ala His Leu Ala Asn Pro Val Leu Pro Asn Asn Glu Val Leu Gln Glu
            20   25   30

Ala Val Pro Gly Ser Ile Arg Thr Ala Glu His Phe Leu Gly Phe Leu
        35   40   45

Arg Arg Leu Leu
    50

<210> 1060
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V780I"

<400> 1060
Ser Leu Pro Asp Lys Asn Glu Gln Val Leu Phe Cys Arg Leu Thr Asp
1 5 10 15

Glu Gln His Lys Val Tyr Gln Asn Phe Ile Ile Asp Ser Lys Glu Val
20 25 30

Tyr Arg Ile Leu Asn Gly Glu Met Gln Ile Phe Ser Gly Leu Ile Ala
35 40 45

Leu Arg Lys Ile
50

<210> 1061
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R505Q"

<400> 1061
Leu Val Phe Ser Gln Ser Arg Gln Ile Leu Asn Ile Ile Glu Arg Leu
1 5 10 15

Leu Lys Asn Arg His Phe Lys Thr Leu Gln Gln Ile Asp Gly Thr Val
20 25 30

Thr His Leu Leu Glu Arg Glu Lys Arg Ile Asn Leu Phe Gln Gln Asn
35 40 45

Lys Asp Tyr Ser
50

<210> 1062
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L445I"

<400> 1062
Leu Gly Asp Thr Ser Ile Leu Asp Asp Leu Phe Lys Ser His Gly Asn
1 5 10 15

Ser Pro Thr Gln Leu Pro Lys Lys Val Ile Ile Ser Gly Pro Met Glu
20 25 30

Lys Ala Lys Gln Arg Pro Lys Asp Phe Trp Asp Ile Leu Asn Glu Gln
35 40 45

Asn Asp Glu Ser
50

<210> 1063
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T295K"

<400> 1063
Thr Gln Asp Leu Gly Val Pro Val Met Gly Val Tyr Thr Trp His Gln
1 5 10 15

Asp Gly Leu Arg Gln Leu Pro His Leu Lys Lys Leu Ala Arg Asp Thr
20 25 30

Leu His Phe Leu Ala Leu Arg Trp Gly His Ile Arg Leu Pro Ala Ser
35 40 45

Gly Pro Arg Asp
50

<210> 1064

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A421T"

<400> 1064
Leu Leu Pro Glu Arg Pro Pro Tyr Leu Asp Lys Tyr Glu Lys Phe Phe
1 5 10 15

Arg Glu Ala Glu Glu Thr Asn Gly Gly Thr Thr Gln Ile Gln Pro Leu
20 25 30

Pro Ala Asp Cys Gly Ile Ser Ser Ala Thr Glu Lys Pro Asp Ser Lys
35 40 45

Thr Lys Met Asp
50

<210> 1065
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R300Q"

<400> 1065
Thr Leu Pro Lys Ser Pro Gln Pro Ser Val Pro Glu Gln Ser Asp Asn
1 5 10 15

Glu Leu Glu Gln Ala Gly Lys Ser Lys Gln Gln Gly Ser Ile Leu Gln
20 25 30

Leu Cys Glu Glu Ile Ala Gly Glu Ile Glu Ser Asp Asn Val Glu Val
35 40 45

Lys Lys Glu Ser
50

<210> 1066
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T99fs"

<400> 1066
Leu Ser Asp Ser Asp Ser Asn Leu Ser Gly Glu Asp Ser Lys Ala Leu
1 5 10 15

Ser Gln Lys Lys Ile Lys Lys Lys Lys Pro Arg Leu Lys Lys Lys Ser
20 25 30

Ile Gln Lys Ile
35

<210> 1067
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.PPPPPPSFPPPPPPPPGTQLPP430del"

<400> 1067
Gln Ser Tyr Met Asp Met Leu Asn Pro Glu Leu Gly Leu Pro Arg Gly
1 5 10 15

Thr Ile Gly Lys Pro Thr Pro Pro Pro Gly Tyr Pro Ala Pro Lys Pro
20 25 30

Pro Val Gly Pro Gln Ala Ala Asp Ile Tyr Met Gln Thr Lys Asn Lys
35 40 45

Leu Arg His Val Glu Thr Glu Ala Leu Lys Lys Glu Leu Ser Ser Cys
50 55 60

Asp Gly His Asp Gly Leu Arg Arg Gln Asp Ser Ser Arg Lys Pro Arg
65 70 75 80

Ala Phe Ser Lys Gln Pro Ser Thr Gly Asp Tyr Tyr Arg Gln Leu Gly
85 90 95

Arg Cys Pro Gly Glu Thr Leu Ala Ala Arg Pro Gly Met Ala His Ser
100 105 110

Glu

<210> 1068
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R627Q"

<400> 1068
Glu Glu Glu Gln Arg Trp Lys Glu Glu Glu Glu Ala Arg Leu Ala Ser
1 5 10 15

Met Pro Ala Trp Arg Trp Asp Leu Leu Gln Gln Lys Lys Leu Glu Glu
20 25 30

Glu

<210> 1069
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H64fs"

<400> 1069

Pro Leu Tyr Leu Ala Cys Gln Glu Gly His Leu Glu Val Thr Gln Tyr
1 5 10 15

Leu Val Gln Glu Cys Gly Ala Asp Pro Arg Pro Arg Arg His Asp Pro
20 25 30

Thr Ala Arg Arg Gly Ala Asp Gly Pro Gln Pro Gly His Arg Val Val
35 40 45

Gly Glu Leu His Arg Arg Glu Pro Val Gly Ala Gly Gln Arg Arg Arg
50 55 60

His Arg His Ala Leu Arg Gly Glu Pro Arg Pro Gln Gln Gly Ala Gln
65 70 75 80

Leu Ala Ala Ala Ala Arg Arg Gly Asp Leu Gly
85 90

<210> 1070
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.296_317PPPPSFPPPPPPPPGTQLPPPPP>P"

<400> 1070
Gln Ser Tyr Met Asp Met Leu Asn Pro Glu Leu Gly Leu Pro Trp Gly
1 5 10 15

Thr Ile Gly Lys Pro Ile Pro Pro Pro Pro Ser Tyr Pro Ser Pro Lys
20 25 30

Pro Pro Val Gly Pro Gln Ala Ala Asp Ile Tyr Met Gln Thr Lys Asn
35 40 45

Lys Leu Arg His Val Glu Thr Glu Ala Leu Lys Lys Glu Pro Ser Ser
50 55 60

Cys Asp Gly His Asp Gly Leu Arg Arg Gln Asp Ser Ser Arg Lys Pro
65 70 75 80

Arg Ala Phe Ser Lys Gln Pro Ser Thr Gly Asp Tyr Tyr Arg Gln Leu

85 90 95

Gly Arg Cys Pro Gly Glu Thr Leu Val Ala Arg Pro Gly Met Ala His
100 105 110

Arg Glu

<210> 1071
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D219N"

<400> 1071
Val Asn Ala Leu Val Ser His Leu Leu Val Val Glu Pro Glu Lys Leu
1 5 10 15

Tyr Ala Met Pro Asp Pro Ala Gly Pro Asn Asn Gly His Leu Pro Ala
20 25 30

Val Ala Thr Leu Cys Asp Leu Phe Asp Arg Glu Ile Val Val Thr Ile
35 40 45

Ser Trp Ala Lys
50

<210> 1072
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R816W"

<400> 1072
Leu Gln Val Asn Ser Leu Ile Gln Thr Gln Lys Ser Ala Glu Leu Ala
1 5 10 15

Ala Ala Leu Leu Ser Ile Tyr Met Glu Trp Trp Ala Glu Asp Leu Pro
20 25 30

Leu Arg Lys Gly Thr Lys His Leu Ser Pro Tyr Ala Thr Leu Thr Val
35 40 45

Gly Asp Ser Ser
50

<210> 1073
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S574F"

<400> 1073
Gln Ile Leu Pro Tyr Ala Asp Leu Thr Leu Glu Gln Arg Phe Gln Leu
1 5 10 15

Asp His Ser Gly Leu Asp Ser Leu Ile Phe Phe Met Arg Leu Val Leu
20 25 30

Arg Phe Leu Gln Val Glu Glu Arg Glu Leu Gly Ser Pro Tyr Thr Gly
35 40 45

Pro Glu Ala Leu
50

<210> 1074
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I281F"

<400> 1074
Leu Tyr Lys Lys Phe Asp Leu Arg Ala Asn Cys Glu Pro Gln Thr Tyr
1 5 10 15

Gly Ile Gly Leu Lys Glu Leu Trp Val Phe Phe Asp Glu Lys Asn Trp
20 25 30

Lys Pro Gly Arg Val Asp His Thr Val Gly Trp Pro Leu Asp Arg His
35 40 45

Thr Tyr Gly Gly
50

<210> 1075
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R369W"

<400> 1075
Tyr Val Tyr Gln Leu Leu Ser Asp Ser Arg Tyr Glu Asn Phe Ile Arg
1 5 10 15

Trp Glu Asp Lys Glu Ser Lys Ile Phe Trp Trp Ile Val Asp Pro Asn
20 25 30

Gly Leu Ala Arg Leu Trp Gly Asn His Lys Asn Arg Thr Asn Met Thr
35 40 45

Tyr Glu Lys Met
50

<210> 1076
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R588C"

<400> 1076
Gln His Asn Cys Gly Thr Pro Leu Pro Val Ser Ser Glu Lys Asp Met
1   5   10   15

Ile Arg Gln Met Met Ile Lys Ile Phe Cys Cys Cys Ile Glu Pro Glu
            20   25   30

Leu Asn Asn Leu Ile Ala Leu Gly Asp Lys Ile Asp Ser Phe Asn Ser
        35   40   45

Leu Tyr Met Leu
    50

<210> 1077
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R11P"

<400> 1077
Met Ala Met Glu Met Arg Leu Pro Val Ala Pro Pro Lys Pro Leu Ser
1   5   10   15

Glu Arg Leu Gly Arg Asp Thr Lys Lys His Leu Val Val Pro Gly Asp
            20   25   30

Thr Ile Thr Thr Asp
        35

<210> 1078
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source

<223> /note="p.L160fs"

<400> 1078
Cys Asp Leu Ile Cys Leu Asp Tyr Asp Gly Asn Ile Leu Asp Ala Cys
1 5 10 15

Thr Phe Ala Leu Leu Ala Ala Leu Lys Met Tyr Ser Cys Leu Lys Leu
20 25 30

Leu

<210> 1079
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K510R"

<400> 1079
Val Asp Thr Pro Pro Arg Lys Lys Lys Arg Lys His Arg Leu Trp Ala
1 5 10 15

Ala His Cys Arg Lys Ile Gln Leu Lys Arg Arg Asp Gly Ser Ser Asn
20 25 30

His Val Tyr Asn Tyr Gln Pro Cys Asp His Pro Arg Gln Pro Cys Asp
35 40 45

Ser Ser Cys Pro
50

<210> 1080
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y641F"

<400> 1080
Leu Ala Pro Ser Asp Val Ala Gly Trp Gly Ile Phe Ile Lys Asp Pro
1 5 10 15

Val Gln Lys Asn Glu Phe Ile Ser Glu Phe Phe Cys Gly Glu Ile Ile
20 25 30

Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr Asp Lys Tyr Met
35 40 45

Cys Ser Phe Leu
50

<210> 1081
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E117K"

<400> 1081
Thr Ser Pro Cys Gln Asn Gln Gly Lys Cys Lys Asp Gly Leu Gly Glu
1 5 10 15

Tyr Thr Cys Thr Cys Leu Glu Gly Phe Lys Lys Gly Lys Asn Cys Glu
20 25 30

Leu Phe Thr Arg Lys Leu Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln
35 40 45

Phe Cys His Glu
50

<210> 1082
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q426L"

<400> 1082
Asp Glu Ser Phe Thr Lys His Thr Val Asn Pro Asn Met Lys Glu Asp
1 5 10 15

Gly Ile Leu Gly Pro Ile Ile Arg Ala Leu Leu Val Arg Asp Thr Leu
20 25 30

Lys Ile Val Phe Lys Asn Met Ala Ser Arg Pro Tyr Ser Ile Tyr Pro
35 40 45

His Gly Val Thr
50

<210> 1083
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1332P"

<400> 1083
Leu Ser Gln Thr Asn Leu Ser Pro Ala Leu Gly Gln Met Pro Ile Ser
1 5 10 15

Pro Asp Leu Ser His Thr Thr Leu Ser Pro Pro Asp Phe Ser Gln Thr
20 25 30

Asn Leu Ser Pro Glu Leu Ser Gln Thr Asn Leu Ser Pro Ala Leu Gly
35 40 45

Gln Met Pro Leu
50

<210> 1084
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.S2269Y"

<400> 1084
Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
1 5 10 15

Thr Gly Val Thr Thr Gln Gly Val Lys Tyr Tyr Leu Leu Thr Ser Met
20 25 30

Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp
35 40 45

Thr Leu Phe Phe
50

<210> 1085
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D75H"

<400> 1085
Ser Ser Ser Arg Ile Asn Ile Pro Glu Arg Ala Ser Gly Pro Glu Gly
1 5 10 15

Asn Leu Asn Gln Ile Val Thr Glu Pro His His Ala Asn Phe Pro Gln
20 25 30

Phe Leu His Glu Gly Leu Ser Lys Pro Val Tyr Val Ile Asn Trp Phe
35 40 45

Met Ser Phe Gly
50

<210> 1086
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.H126N"

<400> 1086
Ala Arg Glu Trp Lys Gly Glu Thr Pro Arg Asn Lys Leu Met Arg Lys
1 5 10 15

Ala Tyr Glu Glu Leu Phe Trp Arg His Asn Asn Ile Lys Cys Val Arg
20 25 30

Gln Val Arg Arg Asp Asn Tyr Asp Ala Leu Arg Ser Val Leu Phe Gln
35 40 45

Ile Phe Ser Gln
50

<210> 1087
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.GGG156del"

<400> 1087
Leu Ser Arg Ala Ser Phe Asp Tyr Leu Arg Leu Val Val Arg Glu Leu
1 5 10 15

Glu Gln Gln Leu Ala Ala Val Arg Gly Met Ala Leu Pro Gln Pro Gln
20 25 30

Pro Gln Ser Leu Pro Leu Pro Pro Ser Leu Pro Ser Ala Leu Ala Pro
35 40 45

Val Pro Ser Leu Pro Ser Ala Pro Ala Pro Val
50 55

<210> 1088
<211> 50

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S269fs"

<400> 1088
Lys Ile Tyr Gly Lys Gln Ser Met Val Asp Glu Val Ser Gly Lys Val
1 5 10 15

Leu Glu Met Asp Ile Ser Lys Lys Lys His Tyr Asn Arg Lys Ile Ser
20 25 30

Ile Lys Lys Leu Asn Arg Met Lys Val Pro Leu Met Lys Leu Ile Thr
35 40 45

Arg Val
50

<210> 1089
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.L441fs"

<400> 1089
Ile Lys Gln Leu Gln Lys Gly Val Gln Gln Lys Arg Pro Ser Glu Ala
1 5 10 15

Gln Ser Val Ile Leu Arg Arg Tyr Phe Trp Asn
20 25

<210> 1090
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P467H"

<400> 1090
Asp Ser Glu Pro Arg Gln Glu Val Pro Met Tyr Thr Gly Ser Glu Pro
1 5 10 15

Arg Gln Glu Val Pro Met Tyr Thr Gly His His Glu Ser Arg Gln Glu
20 25 30

Val Pro Met Tyr Thr Gly Pro Glu Ser Arg Gln Glu Val Leu Ile Arg
35 40 45

Thr Asp Pro Glu
50

<210> 1091
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R382H"

<400> 1091
Leu Ser Ser Gln Pro Ile Gly Thr Lys Pro Ser Ser Ser Ser Gln Arg
1 5 10 15

Gly Ser Leu Arg Lys Val Ala Thr Gly His His Ser Ala Lys Asp Lys
20 25 30

Glu Thr Ala Ser Ala Ile Lys Ser Ser Glu Ser Pro Arg Asp Ser Val
35 40 45

Val Arg Lys Gln
50

<210> 1092
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F52L"

<400> 1092
Ile Pro Phe Pro Glu Thr Phe Asp Gly Asp Thr Asp Arg Leu Pro Glu
1 5 10 15

Phe Ile Val Gln Thr Ser Ser Tyr Met Leu Leu Val Asp Glu Asn Thr
20 25 30

Phe Ser Asn Asp Ala Leu Lys Val Thr Phe Leu Ile Thr Arg Leu Thr
35 40 45

Gly Pro Ala Leu
50

<210> 1093
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S645R"

<400> 1093
Lys Gly Ile Asp Gln Glu Gly Lys Met Val Leu Leu Ser Leu Lys Leu
1 5 10 15

Thr Pro Ser Glu Pro Cys Asp Pro Leu Arg Arg Ser Thr Leu Arg Glu
20 25 30

Pro Leu Asp Ile Arg Ser Ser Leu Lys Asp Ser His Thr Glu Glu Gln
35 40 45

Glu Glu Leu Ser
50

<210> 1094

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L648M"

<400> 1094
Asp Gln Glu Gly Lys Met Val Leu Leu Ser Leu Lys Leu Thr Pro Ser
1 5 10 15

Glu Pro Cys Asp Pro Leu Ser Ser Thr Met Met Arg Glu Pro Leu Asp
20 25 30

Ile Arg Ser Ser Leu Lys Asp Ser His Thr Glu Glu Gln Glu Glu Leu
35 40 45

Ser Val Leu Ser
50

<210> 1095
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R884H"

<400> 1095
Gly His Cys Leu Pro Asp Gly Arg Thr Glu Asn Thr Pro Gly Val Glu
1 5 10 15

Thr Lys Gly Leu Asn Leu Lys Ile Pro His His Val Ile Ala Leu Glu
20 25 30

Asn Pro Arg Thr Arg Ser Leu His Arg Ala Leu Glu Glu Thr Pro Lys
35 40 45

Gly Met Pro Lys
50

<210> 1096
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.W240C"

<400> 1096
Gly Tyr Cys Lys Pro Thr Ser Ser Glu Gly Ser Phe Tyr Ile Thr Ser
1 5 10 15

Glu Asn Cys Met Gln His Ala His Lys Cys Cys His Arg Asp Leu Cys
20 25 30

Leu Leu Leu Leu His Ala Tyr Arg Gly Leu Arg Leu His Phe Leu Val
35 40 45

Ile Met Arg Asp
50

<210> 1097
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q285H"

<400> 1097
Leu Val Ile Met Arg Asp Ile Pro Glu Leu Pro His Thr Glu Leu Glu
1 5 10 15

Ala Leu Ala Val Glu Glu Thr Leu Ser His His Leu Cys Ser Glu Leu
20 25 30

Gln Met Leu Asn Asn Pro Glu Lys Ile Ala Glu Gln Ile Ser Lys Asp
35 40 45

Leu Ala Trp Leu
50

<210> 1098
<211> 67
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P117fs"

<400> 1098
Leu Glu Ala Asp Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr
1 5 10 15

Gly Val Pro Ile Met Ala His Pro Pro Leu Ser Thr Val Thr Thr His
20 25 30

Trp Ser Ser Gly Trp Thr Leu Cys Trp Ala Leu Pro Lys Arg Ala Ser
35 40 45

Asn Trp Thr Ser Arg Thr Ser Arg Gln Trp Ala Pro Pro Trp Thr Ser
50 55 60

Cys Gly Ser
65

<210> 1099
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q95R"

<400> 1099
Lys Glu His Gln Gln Gln Gln Arg Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15

Gln Arg Gln Arg Gln Gln Gln Gln Arg Arg Arg Arg Gln Gln Glu
20 25 30

Pro Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu Ser Ser Pro Ala
35 40 45

Ala Gln Ala His
50

<210> 1100
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E158K"

<400> 1100
Val Cys Gly Gly Val Pro Glu Pro Thr Gly Leu Asp Ala Ala Cys Thr
1 5 10 15

Lys Leu Gln Ser Leu Gln Arg Leu Phe Lys Lys Pro Thr Thr Pro Ala
20 25 30

Pro Pro Leu Arg Pro Pro Asp Ser Leu Ser Arg Ala Pro Ala Glu Phe
35 40 45

Pro Ser Ala Lys
50

<210> 1101
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K165N"

<400> 1101
Asn Asp Arg Pro Arg Gln Pro Ala Pro Gly Asp Gly Ser Lys Glu Arg

1 5 10 15

Met Cys Gly Glu Glu Leu Glu Asp Thr Asn Asn Asp Asp Pro Glu Cys
20 25 30

Gly Val Glu Glu Glu Asp Ala Gly Leu Ala Gly Gln Pro Pro Gly Lys
35 40 45

Leu Thr Arg Ser
50

<210> 1102
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E56K"

<400> 1102
Asp Ala Leu Gln Pro Gly Ser Thr Arg Val Ala Lys Gly Trp Ser Gln
1 5 10 15

Gly Val Gly Glu Val Thr Ser Thr Ser Lys Lys Tyr Cys Ser Cys Val
20 25 30

Ser Ser Ser Arg Lys Leu Ile His Ser Gly Ile Gln Arg Ile His Arg
35 40 45

Asp Ser Pro Gln
50

<210> 1103
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D459N"

<400> 1103
Ser Tyr Ser Pro Gln Lys Lys Glu Pro Ser Lys Ala Glu Thr Glu Glu
1 5 10 15

Arg Val Ser Met Val Lys Thr Arg Asp Asn Asn Phe Lys Ile Tyr Asn
20 25 30

Glu Asp Val Ser Phe Leu Ser Val Asn Gln Asn Asn Tyr Ser Arg Asn
35 40 45

Pro Thr Gln Ser
50

<210> 1104
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A831T"

<400> 1104
Gln Val Phe Asp Ala Phe Thr Pro Arg Leu Gln Asp Ser Asn Lys Lys
1 5 10 15

Val Asn Gln Trp Ala Leu Glu Ser Phe Thr Thr Lys Met Ile Pro Leu
20 25 30

Leu Arg Glu Ser Leu His Pro Met Leu Leu Ser Ile Ile Ile Thr Val
35 40 45

Ala Asp Asn Leu
50

<210> 1105
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R109H"

<400> 1105
Lys Ala Ala Leu Asp Lys Ser Ala Pro Cys Arg Arg Ser Val Asp His
1   5   10   15

Arg Lys Tyr Leu Gln Lys Gln Leu Lys His His Phe Ser Gln Lys Tyr
            20   25   30

Ser Arg Leu Pro Arg Gly Leu Pro Gly Arg Ala Ala Glu Pro Tyr Leu
        35   40   45

Lys Arg Gly Ser
    50

<210> 1106
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R784W"

<400> 1106
Arg Ala Leu Gly Arg Gln Gln Ala Ser Ser Gln Cys Pro Gly Asp Ser
1   5   10   15

Lys Asp His Ile Ile Ala Thr Glu Glu Trp Trp Gly Gly Pro Gly Gln
            20   25   30

Ala Gly Ser Pro Pro Gly Ala Ala Gly Gln Gly Ser Gly Glu Gly Cys
        35   40   45

Gly Leu Trp Glu
    50

<210> 1107
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.IPPQAQELEIPL1556del"

<400> 1107
Leu Ile Pro Pro Gln Ala Gln Glu Leu Gly Ile Pro Leu Thr Pro Gln
1 5 10 15

Gln Val Gln Ala Leu Gly Ile Pro Leu Thr Pro Gln Gln Ala Gln Ala
20 25 30

Leu Gly Ile Pro Leu Thr Pro Gln Gln Ala Gln Glu Leu Gly Ile Pro
35 40 45

Leu Thr Pro Gln Gln Ala Gln Glu Leu Gly Ile Pro Leu Thr Pro Gln
50 55 60

Gln Ala Gln Ala Gln Gly Ile Pro Leu Thr Pro Gln Gln Ala Gln Ala
65 70 75 80

Leu Gly Ile Ser Leu Thr
85

<210> 1108
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.C51Y"

<400> 1108
Pro Arg Lys Ala Lys Ile Arg His Pro Val Ala Ser Phe Phe His Leu
1 5 10 15

Phe Phe Arg Val Ser Ala Ile Ile Val Tyr Tyr Leu Leu Cys Glu Leu
20 25 30

Leu Ser Ser Ser Phe Ile Thr Cys Met Val Thr Ile Ile Leu Leu Leu
35 40 45

Ser Cys Asp Phe

50

<210> 1109
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.D428fs"

<400> 1109
Asn Tyr Arg Arg Arg Cys Ala Cys Asp Asp Cys Ser Leu Ser His Ile
1 5 10 15

Leu Thr Cys Gly Ile Met Asp Pro Pro Arg His
20 25

<210> 1110
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D428fs"

<400> 1110
Asn Tyr Arg Arg Arg Cys Ala Cys Asp Asp Cys Ser Leu Ser His Ile
1 5 10 15

Leu Thr Cys Gly Ile Met Asp Pro Pro Ser Leu Met Thr Ser Thr Phe
20 25 30

Thr Ser Ser His Phe Lys Trp Ile Leu Leu Leu Thr Ile Leu Leu Arg
35 40 45

Gly Ala Arg Pro Val Cys His Leu Gln Ala Arg Gly Pro Ala Pro Ala
50 55 60

Leu Pro Ser Gln Phe Ser Ser Thr Pro Gly Ser Ser Ser Gln Thr Val
65 70 75 80

Ala Arg His Gln Leu Phe Val Val Met Met Lys Met Leu His His Cys
85 90 95

Gln Pro Asn Leu Leu Ile Phe Ile His
100 105

<210> 1111
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.EEEEYL135del"

<400> 1111
Ile Glu Glu Glu Glu Tyr Leu Gly Lys Glu Gly Tyr Leu Glu Glu Glu
1 5 10 15

Glu Tyr Leu Gly Lys Glu Glu His Leu Gly Lys Glu Gly Tyr Leu Glu
20 25 30

Lys Glu Asp Tyr Ile Glu Glu Val Asp Tyr Leu Gly Lys Lys Ala Tyr
35 40 45

Leu Glu Glu Glu Glu Tyr Leu Gly Lys Lys Ser Tyr Leu Glu Glu Glu
50 55 60

Lys Ala Leu Glu
65

<210> 1112
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y139H"

<400> 1112
Glu Tyr Leu Gly Lys Glu Gly Tyr Leu Glu Glu Glu Glu Tyr Leu Gly
1 5 10 15

Lys Glu Glu His Leu Glu Glu Glu Glu His His Leu Gly Lys Glu Gly
20 25 30

Tyr Leu Glu Lys Glu Asp Tyr Ile Glu Glu Val Asp Tyr Leu Gly Lys
35 40 45

Lys Ala Tyr Leu
50

<210> 1113
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L112F"

<400> 1113
Gln Gln Leu Lys Lys Ile Phe Gln Glu Tyr Gly Thr Val Gly Val Ser
1 5 10 15

Leu His Ile Gly Ile Ser Leu Ile Ser Phe Phe Gly Ile Phe Tyr Met
20 25 30

Val Val Ser Ser Gly Val Asp Met Pro Ala Ile Leu Leu Lys Leu Gly
35 40 45

Phe Lys Glu Ser
50

<210> 1114
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.A42fs"

<400> 1114
Gly Pro Ser Gln Pro Pro Val Arg Gln Gly Ala Leu Gln Gly Gly Leu
1 5 10 15

Leu Met Gly Tyr Ser Pro Ala Gly Gly Arg His Pro Pro Gly Ser Thr
20 25 30

Arg Tyr Pro Ser Phe Pro Leu Arg Leu Val Pro Leu Ser Leu Ile Gly
35 40 45

Pro

<210> 1115
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P36S"

<400> 1115
Arg Gly Leu Gly Ala Ala Glu Met Pro Gly Gln Gly Pro Gly Ser Asp
1 5 10 15

Trp Thr Glu Arg Ser Ser Ser Ala Glu Ser Ser Pro Ala Val Ala Gly
20 25 30

Thr Glu Gly Gly Gly Gly Gly Ser Ala Gly Tyr Ser Cys Tyr Gln Asn
35 40 45

Ser Lys Gly Ser
50

<210> 1116
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1231S"

<400> 1116
Asp Met Asp Asp Ile Phe Ser Ser Gly Ile Gln Ala Lys Thr Thr Lys
1 5 10 15

Pro Lys Ser Arg Ser Ala Gln Ala Ala Ser Ser Glu Pro Arg Phe Glu
            20 25 30

His Lys Val Ser Asn Ile Phe Asp Asp Pro Leu Asn Ala Phe Gly Gly
        35 40 45

Gln

<210> 1117
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P690fs"

<400> 1117
Pro Gly Gly Arg Gly Pro Gln Gly Ala Leu Gln Ser Pro Ser Ala Gln
1 5 10 15

Lys Arg Gly Leu Ser Pro Ser Pro Ser Cys Gln Gln Val Gln Glu Ala
            20 25 30

Thr Ser Leu Trp Lys Pro Ile Pro Cys
        35 40

<210> 1118
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S691del"

<400> 1118
Ser Pro Gly Gly Arg Gly Pro Gln Gly Ala Leu Gln Ser Pro Ser Ala
1 5 10 15

Gln Lys Arg Gly Leu Ser Pro Ser Pro Pro Ala Ser Lys Ser Lys Lys
20 25 30

Arg Pro Leu Phe Gly Ser Pro Ser Pro Ala Glu Lys Thr Pro His Pro
35 40 45

Gly Pro Gly Leu Arg
50

<210> 1119
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K9R"

<400> 1119
Met Glu Ala Tyr Glu Gln Val Gln Arg Arg Gly Pro Leu Lys Leu Lys
1 5 10 15

Gly Val Ala Glu Leu Gly Val Thr Lys Arg Lys Lys Lys Lys Lys Asp
20 25 30

Lys Asp Lys
35

<210> 1120
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R740C"

<400> 1120
Leu Gln Thr Lys Tyr Leu Gly Arg Gln Trp Arg Lys Ser Asn Met Lys
1   5   10   15

Thr Met Ser Ala Ile Tyr Gln Lys Val Cys Cys His Arg Met Asn Asp
            20   25   30

Asp Trp Ala Tyr Gly Asn Asp Ile Asp Ala Arg Pro Trp Asp Phe Gln
        35   40   45

Ala Glu Glu Cys
    50

<210> 1121
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.H416R"

<400> 1121
Arg Pro Pro Gly Thr Asp Gly Val Val Pro Ala Thr Val Asn Tyr Tyr
1   5   10   15

Val Thr Pro Val Gln Pro Leu Leu Ala Arg Arg Ala Tyr Pro Thr Trp
            20   25   30

Leu Pro Cys Asn
        35

<210> 1122
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>

<221> source
<223> /note="p.G372W"

<400> 1122
Gly Ser Ser Leu Arg Ser Glu Pro Ser Glu Thr Gly Val Ser Arg Leu
1 5 10 15

Arg Leu Ala Pro Pro Lys Thr Arg Arg Trp Trp Ser Ser Leu His Ala
20 25 30

Glu Pro Ser Lys Thr Gly Val Ser His Leu Ser Pro Glu Pro Pro Lys
35 40 45

Thr Glu Val Ser
50

<210> 1123
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R690L"

<400> 1123
Glu Asp Lys Phe Phe Ser Gln Glu Lys Tyr Trp Gly Arg Lys Phe His
1 5 10 15

Thr Pro Ser Asn Ser Tyr Thr Ala Gln Leu Leu Val Lys Met Lys Tyr
20 25 30

Gly Ala Trp Tyr Leu Lys Pro Lys Leu Trp Lys Lys Leu Arg Ser Asp
35 40 45

Glu Pro Leu Ile
50

<210> 1124
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L567F"

<400> 1124
Gln Arg Gly Arg Ile Arg Tyr Gly Pro Trp Tyr Phe Glu Pro Lys Leu
1   5   10   15

Gly Lys Lys Leu Arg Ser Asp Glu Pro Phe Phe Ile Asp Pro Lys Pro
            20   25   30

Val Leu Glu Lys Pro Asp Glu Pro Asp Ile Leu Asp Gly Leu Tyr Gly
        35   40   45

Pro Ile Ala Phe
    50

<210> 1125
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.W163C"

<400> 1125
Gly Lys Asp Met Pro Pro Asp Leu Leu Leu Gln Val Leu Lys Gln Leu
1   5   10   15

Asp Pro Glu Arg Lys Leu Glu Asp Ala Cys Cys Ala Arg Cys Glu Ala
            20   25   30

Arg Glu Lys Thr Thr Glu Val Pro Thr Glu Ser Gly Lys Tyr Pro Cys
        35   40   45

Gly Glu Ser Cys
    50

<210> 1126
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P388S"

<400> 1126
Val Ser Pro Leu Arg Gln Leu Pro Pro Glu Ala Gly Val Ser His Leu
1 5 10 15

Cys Pro Glu Pro Pro Lys Thr Arg Val Ser Ser Pro Leu Arg Pro Glu
20 25 30

Thr Pro Lys Asn Gly Val Ser Pro Leu Phe Pro Glu Pro Pro Lys Thr
35 40 45

Arg Ile Ser Asn
50

<210> 1127
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.I499V"

<400> 1127
Ile Ser Ser Gly Asn Ser Phe Pro Pro Gln Gln Ala Gly Ser Pro Leu
1 5 10 15

Lys Arg Pro Phe Ser Ala Ala Ala Ala Val Val Ala Ala Ala Ala Ala
20 25 30

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Pro Ala Pro
35 40 45

Ala Leu Ala Ala
50

<210> 1128
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A516P"

<400> 1128
Arg Pro Phe Ser Ala Ala Ala Ala Ile Ala Ala Ala Ala Ala Ala Ala
1 5 10 15

Ala Ala Ala Ala Ala Ala Ala Ala Ala Pro Pro Ala Pro Ala Pro Ala
20 25 30

Leu Ala Ala Ala Ala Ala Pro Ala Leu Ala Ala Ala Ala Ala Pro Ala
35 40 45

Leu Ala Ala Ala
50

<210> 1129
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.H317R"

<400> 1129
Ser Asp Ala Thr Val Glu Lys Asp Glu Ser His Ala Gly Lys Val Val
1 5 10 15

Leu Arg Ser Trp Tyr Glu Lys Asn Lys Arg Arg Ile Phe Pro Ala Ser
20 25 30

Arg Trp Glu Pro Tyr Asp Pro Glu Lys Lys Trp Asp Lys Tyr Thr Ile
35 40 45

Arg

<210> 1130
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A70T"

<400> 1130
Leu Gly Met Gln Ser Ile Pro Ile Ala Thr Ala Cys Thr Ile Tyr Pro
1 5 10 15

Lys Phe Phe Cys Glu Thr Ile Leu Asp Thr Thr Phe Asp Pro Tyr Leu
20 25 30

Ile Ala Met Ser Ser Ile Tyr Leu Ala Gly Lys Val Glu Glu Gln Pro
35 40 45

Leu Trp Ala His
50

<210> 1131
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R402C"

<400> 1131
Ala Gly Leu Lys Val Leu Phe Lys Lys Thr His Arg Ile Leu Arg Arg
1 5 10 15

Leu Phe Asn Leu Cys Lys Arg Cys His Cys Cys Gln Pro Arg Phe Arg
20 25 30

Leu Pro Lys Glu Arg Ser Leu Ser Tyr Trp Trp Asn Arg Ile Gln Ser
35 40 45

Leu Leu Tyr Cys

50

<210> 1132
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S425W"

<400> 1132
Trp Leu Thr Arg Ile Gln Ser Phe Leu Tyr Cys Asn Glu Asn Gly Leu
1 5 10 15

Leu Gly Ser Phe Ser Glu Glu Thr His Trp Trp Cys Thr Cys Pro Asn
20 25 30

Asp Gln Val Val Cys Thr Ala Phe Leu Pro Cys Thr Val Gly Asp Ala
35 40 45

Ser Ala Cys Leu
50

<210> 1133
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R457G"

<400> 1133
Gln Val Val Cys Thr Ala Phe Leu Pro Cys Thr Val Gly Asp Ala Ser
1 5 10 15

Ala Cys Leu Thr Cys Ala Pro Asp Asn Gly Gly Thr Arg Cys Gly Thr
20 25 30

Cys Asn Thr Gly Tyr Met Leu Ser Gln Gly Leu Cys Lys Pro Glu Val
35 40 45

Ala Glu Ser Thr
50

<210> 1134
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S19L"

<400> 1134
Met Gln Pro Pro Val Pro Gly Pro Leu Gly Leu Leu Asp Pro Ala Glu
1 5 10 15

Gly Leu Leu Leu Arg Arg Lys Lys Thr Ser Leu Trp Phe Val Gly Ser
20 25 30

Leu Leu Leu Val Ser Val Leu Ile Val Thr Val Gly Leu
35 40 45

<210> 1135
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P277T"

<400> 1135
Gly Phe Arg Leu Thr Pro Glu Pro Val Pro Thr Cys Ser Ser Tyr Pro
1 5 10 15

Leu Pro Leu Gln Pro Cys Ser Arg Phe Thr Thr Val Ala Pro Ser Ser
20 25 30

Ala Leu Ala Ser Ser Glu Asp Leu Gln Pro Pro Ser Pro Ser Ser Ser
35 40 45

Gly Ser Gly Leu
50

<210> 1136
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H445D"

<400> 1136
Pro Ser Ala Glu Val Trp Asn Glu Asn Lys Glu Arg Arg Glu Lys Lys
1 5 10 15

Asp Arg His Pro Ser Arg Lys Ser Ser Asp Asp His Arg Lys Ala Gly
20 25 30

Glu Ser His Arg Arg Arg Ala Gly Asp Lys Asn Gln Lys Ala Ser Ser
35 40 45

His Arg Ser Ala
50

<210> 1137
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L583M"

<400> 1137
Val Asp Ile Val Ala Lys Met Val Glu Lys Gln Asn Ile Glu Ala Lys
1 5 10 15

Val Glu Lys Ala Gln Gly Gly Gln Glu Met Met Glu Met Ile Ser Gly
20 25 30

Thr Met Thr Ser Glu Lys Thr Glu Met Ile Val Phe Glu Thr Lys Ser
35 40 45

Ile

<210> 1138
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G23V"

<400> 1138
Met Ser Asp Cys Cys Ser Ala Pro Gly Ile Ser Trp Glu Ala Gly Val
1 5 10 15

Gly Arg Pro Ala Val Pro Val Val Leu Glu Leu Gln Ile Arg Arg Gly
20 25 30

Ala Met Ser Glu Glu Thr Val Ser Glu Ser Gln Phe Ser Leu Lys Thr
35 40 45

Ala

<210> 1139
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P54L"

<400> 1139
Phe Leu Thr Leu Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro
1 5 10 15

Tyr Leu Ser Tyr Phe His Cys Asp Asp Leu Leu Pro Ser Pro Ser Pro

20 25 30

Gly Lys Arg Lys Cys Pro Val Gly Arg Arg Arg Arg Pro Arg Gly Arg
35 40 45

Met Lys Asn His
50

<210> 1140
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R304S"

<400> 1140
Ala Ser Ser Arg Trp Gln Glu Thr Ala Arg Thr Ser Cys Ala Phe Asn
1 5 10 15

Ser Ser Val Gln Gln Asp Pro Leu Ser Ser Ser His Pro Pro Glu Thr
20 25 30

Cys Gln Met Glu Ala Gly Ser Leu Phe Leu Leu Ser Ser Asp Gly Gln
35 40 45

Asn Val Val Gly
50

<210> 1141
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1265S"

<400> 1141
Asn Ser Gln Gly Ile Ser Ser Gly Asp Met Gly Thr Ser Gln Val Val
1 5 10 15

His Val His Leu Glu Asp Ser Gly Ile Ser Ser Val Ala Gln Lys Gln
20 25 30

Glu Pro Arg Val Pro Thr Cys Val Leu Gln Lys Cys Gln Val Thr Asn
35 40 45

Phe Pro Pro Ala
50

<210> 1142
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L222P"

<400> 1142
Pro Pro Gln Pro Val Ser Pro Leu Asp Ser Lys Phe Pro Ile Asp His
1 5 10 15

Ser Leu Pro Gln Gln Leu Pro Ser Pro Pro Pro Phe Pro Pro His His
20 25 30

Ile Gln Arg Ala Glu Pro Ser Leu Gln Pro Glu Ala Ser Leu Ser Leu
35 40 45

Asn Thr Val Phe
50

<210> 1143
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W192L"

<400> 1143
Thr Trp Ala Val Pro Val Ser Glu Ser Asn Val Ala Lys Leu Thr Asn
1 5 10 15

Ile Tyr Arg Asp Gln Ser Phe Thr Thr Leu Leu Leu Val Ala Thr Asn
20 25 30

Thr Ser Thr Asn Asp Met Ile Ile Leu Gln Thr Leu His Trp Arg Met
35 40 45

Gln Leu Ser Ile
50

<210> 1144
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R206Q"

<400> 1144
Asp Glu Ser Asn Phe Asn His Phe Leu Asn Met Thr Glu Lys Gln Gly
1 5 10 15

Cys Ser Val Gln Arg Leu Arg Asn Ile Gln Gln Val Arg Thr Val Lys
20 25 30

Gly Gln Asp Tyr Leu Ser Lys Thr Gly Ala Lys Phe His Gly Lys Met
35 40 45

Glu Gln Lys Phe
50

<210> 1145
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.A141T"

<400> 1145
Ser Gly Gly Ser Val Thr Leu Ser Glu Ser Thr Ala Ile Ile Ser Tyr
1 5 10 15

Gly Thr Thr Gly Leu Val Thr Trp Asp Thr Thr Ala Leu Tyr Leu Ala
            20 25 30

Glu Trp Ala Ile Glu Asn Pro Ala Val Phe Thr Asn Arg Thr Val Leu
        35 40 45

Glu Leu Gly Ser
    50

<210> 1146
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.C120Y"

<400> 1146
Arg Ala Ser Cys Ser Pro Leu Ser Tyr Ala Gly Leu Gly Ser Asp Gly
1 5 10 15

Lys Trp Asn Leu Val Met Thr Arg Asn Tyr Tyr Phe Pro Thr Lys Ser
            20 25 30

Thr Trp Arg Trp Gln Cys
        35

<210> 1147
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source

<223> /note="p.S383L"

<400> 1147
Lys Val Gln Phe Glu Arg Lys His Ser Lys Ile His Ser Ile Arg Ser
1 5 10 15

Leu Ala Ser Gln Pro Thr Glu Leu Asn Leu Leu Glu Val Leu Glu Gln
20 25 30

Ser Gln Gln Ser Thr Ser Leu Thr Phe Gly Glu Gly Ala Glu Ser Pro
35 40 45

Gly Gly Gln Ser
50

<210> 1148
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R299L"

<400> 1148
Lys Arg Phe Leu Ile Lys Leu Arg Pro Asp Ala Asn Ser Ala Tyr Gln
1 5 10 15

Asp Thr Leu Glu Phe Leu Met Ala Ser Leu Leu Asp Phe Cys Lys Ser
20 25 30

Phe Trp Lys Ile Cys Val Glu His His Ala Phe Phe Arg Leu Phe Glu
35 40 45

Glu Pro Lys Pro
50

<210> 1149
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E261K"

<400> 1149
Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys
1 5 10 15

Asn Gly Val Asn Glu Ala Lys Ile Asp Lys Lys Ile Lys Asn Asp Asn
20 25 30

Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His
35 40 45

Gln Leu His Gly
50

<210> 1150
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K3fs"

<400> 1150
Met Lys Lys Asn Thr Cys Phe Pro Arg Val Ile Gly Tyr Lys Tyr Ala
1 5 10 15

Ser Ser Lys Ser Tyr Leu Ser Ile Leu Leu Glu Ser Val Ser Ile Ser
20 25 30

Thr His Gln Leu
35

<210> 1151
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q625E"

<400> 1151
Arg Phe Cys Ser Asn Ser Lys His Leu Leu Gly Lys Glu Ala Ile Lys
1 5 10 15

Gln Arg His Leu Gln Leu Leu Gly Tyr Glu Glu Val Val Gln Ile Pro
20 25 30

Tyr His Glu Ile Gly Met Leu Lys Ser Arg Arg Glu Leu Val Glu Tyr
35 40 45

Leu Gln Arg Lys
50

<210> 1152
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R4359L"

<400> 1152
Thr Lys Val Val Asp Leu Asp Pro Cys Leu Ser Lys Lys Pro Leu Glu
1 5 10 15

Glu Lys Pro Ser Gln Pro Tyr Ser Ala Leu Leu Glu Ser Leu Ser Glu
20 25 30

Val Gln Ser Leu Ser Ser Phe Gln Ser Glu Ser Cys Asp Asp Asn Gly
35 40 45

Tyr His Trp Asp
50

<210> 1153
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.H3574N"

<400> 1153
Pro Thr Ala Ile Pro Leu Glu Ile Phe Ile Val Thr Met Glu Asp Asp
1 5 10 15

Phe Pro Gly Gly Val Ile Gly Lys Ile Asn Asn Ala Thr Asp Gln Asp
20 25 30

Met Tyr Asp Val Leu Thr Phe Ala Leu Lys Ser Glu Gln Lys Ser Leu
35 40 45

Phe Lys Val Asn
50

<210> 1154
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A4159T"

<400> 1154
Gly Leu Arg Pro Val Val Val Pro Asn Ile Gln Ala Gly His Ser Tyr
1 5 10 15

Val Gly Lys Glu Glu Leu Ile Gly Ile Thr Thr Val Val Leu Phe Val
20 25 30

Ile Phe Ile Leu Val Val Leu Phe Ile Val Phe Arg Lys Lys Val Phe
35 40 45

Arg Lys Asn Tyr
50

<210> 1155
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R1266H"

<400> 1155
Val Val Gln Val Leu Asp Glu Asn Asp Asn Lys Pro Gln Phe Pro Glu
1 5 10 15

Lys Val Tyr Gln Ile Lys Leu Pro Glu His His Asp Arg Lys Lys Arg
20 25 30

Gly Glu Pro Ile Tyr Arg Ala Phe Ala Phe Asp Arg Asp Glu Gly Pro
35 40 45

Asn Ala Glu Ile
50

<210> 1156
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G1899V"

<400> 1156
Thr Asp Val Asn Asp Asn Pro Pro Val Phe Thr Gln Ala Val Phe Glu
1 5 10 15

Thr Ile Leu Leu Leu Pro Thr Tyr Val Val Val Val Glu Val Leu Lys
20 25 30

Val Ser Ala Thr Asp Pro Asp Ser Glu Val Pro Pro Glu Leu Thr Tyr
35 40 45

Ser Leu Met Glu
50

<210> 1157
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A836V"

<400> 1157
Gly Arg Ser Gly Ala Pro Ala Glu Arg Glu Ala Glu Pro Arg Val Lys
1 5 10 15

Glu Ser Arg Ser Pro Ala Lys Glu Glu Val Val Ala Lys Met Pro Ala
20 25 30

Arg Ala Ser Pro Pro His Ser Lys Ala Ala Pro Gly Asp Val Lys Val
35 40 45

Lys Glu Glu Arg
50

<210> 1158
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S102R"

<400> 1158
Arg Ile Gln Gln Ile Ile Tyr Cys His Lys Leu Thr Ile Ile Leu Thr
1 5 10 15

Lys Trp Arg Asn Thr Ala Arg His Lys Arg Arg Lys Lys Lys Glu Asp
20 25 30

Glu Leu Ile Leu Lys His Glu Leu Gln Leu Lys Lys Trp Lys Asn Arg
35 40 45

Leu Ile Leu Lys
50

<210> 1159
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V48G"

<400> 1159
Arg Asp Lys Gly Arg Ala Ala Gln Val Cys Thr Ala Trp Arg Asp Ala
1 5 10 15

Ala Tyr His Lys Ser Val Trp Arg Gly Gly Gly Glu Ala Lys Leu His
20 25 30

Leu Arg Arg Ala Asn Pro Ser Leu Phe Pro Ser Leu Gln Ala Arg Gly
35 40 45

Ile Arg Arg Val
50

<210> 1160
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M144I"

<400> 1160
Lys Gln Pro Cys Thr Asn Asp Met Ala Lys Ser Asn Ser Val Gly Gln
1 5 10 15

Asp Ser Cys Gln Asp Ser Glu Gly Asp Ile Ile Ile Phe Pro Ala Glu
20 25 30

Ser Ser Cys Ala Leu Pro Gln Glu Gly Ser Ala Gly Pro Gly Ser Pro
35 40 45

Gly Ser Ala Pro
50

<210> 1161
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F144fs"

<400> 1161
Lys Arg Phe Phe Ser Glu His Val Pro Cys Asn Gly Phe Ser Asp Ile
1 5 10 15

Glu Asn Leu Glu Gly Pro Glu Ile Phe Leu Arg Met Asn Trp Cys Val
20 25 30

Ser

<210> 1162
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M553V"

<400> 1162
His Leu Pro Ala Ser Arg Val Val Gly Thr Pro Glu Pro Ser Leu Gly
1 5 10 15

Ala Arg Ala Pro Gln Asp Pro Gly Gly Val Val Ala Gln Ala Cys Glu
20 25 30

Glu Tyr Leu Ser Gln Ile His Ser Cys Gln Thr Leu Gln Asp Arg Thr
35 40 45

Glu Lys Met Lys

50

<210> 1163
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G443fs"

<400> 1163
Thr Pro Gly Glu Asp Gly Gly Glu Pro Gly Asp Ala Val Ala Ala Ala
1 5 10 15

Glu Gln Pro Ala Gln Cys Gly Gln Gly Ala Ala Val Arg Ala Ala Arg
20 25 30

Gly Arg Glu Leu Gln Glu
35

<210> 1164
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G423V"

<400> 1164
Ser Asp Asp Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys
1 5 10 15

Leu Arg Thr Leu Val Gly His Thr Gly Val Val Val Trp Ser Ser Gln
20 25 30

Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys
35 40 45

Val Trp Asn Ala
50

<210> 1165
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R465C"

<400> 1165
Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
1 5 10 15

Thr Leu Tyr Gly His Thr Ser Thr Val Cys Cys Cys Met His Leu His
20 25 30

Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp
35 40 45

Asp Ile Glu Thr
50

<210> 1166
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R465H"

<400> 1166
Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
1 5 10 15

Thr Leu Tyr Gly His Thr Ser Thr Val His His Cys Met His Leu His
20 25 30

Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp
35 40 45

Asp Ile Glu Thr
    50

<210> 1167
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R479Q"

<400> 1167
Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu
1   5   10   15

His Glu Lys Arg Val Val Ser Gly Ser Gln Gln Asp Ala Thr Leu Arg
            20   25   30

Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His
        35   40   45

Val Ala Ala Val
    50

<210> 1168
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.R505G"

<400> 1168
Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His
1   5   10   15

Val Leu Met Gly His Val Ala Ala Val Gly Gly Cys Val Gln Tyr Asp
            20   25   30

Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp
35 40 45

Asp Pro Glu Thr
50

<210> 1169
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R505C"

<400> 1169
Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His
1 5 10 15

Val Leu Met Gly His Val Ala Ala Val Cys Cys Cys Val Gln Tyr Asp
20 25 30

Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp
35 40 45

Asp Pro Glu Thr
50

<210> 1170
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S546L"

<400> 1170
Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr
1 5 10 15

Leu Gln Gly His Thr Asn Arg Val Tyr Leu Leu Leu Gln Phe Asp Gly

20 25 30

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
35 40 45

Val Glu Thr Gly
50

<210> 1171
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S582L"

<400> 1171
Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn
1 5 10 15

Cys Ile His Thr Leu Thr Gly His Gln Leu Leu Leu Thr Ser Gly Met
20 25 30

Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val
35 40 45

Lys Ile Trp Asp
50

<210> 1172
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R689W"

<400> 1172
Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
1 5 10 15

Thr Lys Leu Val Cys Ala Val Gly Ser Trp Trp Asn Gly Thr Glu Glu
20 25 30

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
35 40 45

<210> 1173
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R14Q"

<400> 1173
Met Asn Gln Glu Leu Leu Ser Val Gly Ser Lys Arg Arg Gln Gln Thr
1 5 10 15

Gly Gly Ser Leu Arg Gly Asn Pro Ser Ser Ser Gln Val Asp Glu Glu
20 25 30

Gln Met Asn Arg Val Val Glu Glu
35 40

<210> 1174
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G298fs"

<400> 1174
Tyr Asp Lys Lys Val Thr Ile Tyr Asp Pro Arg Asp Arg Met Glu Thr
1 5 10 15

Arg Asp Ala Leu Met Gly Trp Gly Gly Ala Phe Glu Gly Leu
20 25 30

<210> 1175
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V233M"

<400> 1175
Ser Asn Ala Leu Glu Leu Val Val Thr Asp Ser Ile His Gln Asp Tyr
1 5 10 15

Thr Thr Gln Asn Leu Ile Arg Met Ala Met Met Ala Gly Leu Val Leu
20 25 30

Val Ala Leu Leu Ala Ile Leu Val Glu Asn Trp His Ser His Thr Ala
35 40 45

Leu Asn Lys Glu
50

<210> 1176
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V4019M"

<400> 1176
Val Tyr Tyr Glu Pro Glu Gln Thr Val Leu Ile Asp Asn Cys Arg Gln
1 5 10 15

Gln Cys Thr Cys His Val Gly Lys Val Met Met Val Cys Gln Glu His
20 25 30

Ser Cys Lys Pro Gly Gln Val Cys Gln Pro Ser Gly Gly Ile Leu Ser
35 40 45

Cys Val Thr Lys
    50

<210> 1177
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A1022S"

<400> 1177
Glu Ala Leu Cys Gly Leu Cys Gly Asn Phe Asn Gly Asp Pro Ala Asp
1   5   10   15

Asp Leu Ala Leu Arg Gly Gly Gly Gln Ser Ser Ala Asn Ala Leu Ala
            20   25   30

Phe Gly Asn Ser Trp Gln Glu Glu Thr Arg Pro Gly Cys Gly Ala Thr
        35   40   45

Glu Pro Gly Asp
    50

<210> 1178
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A2493V"

<400> 1178
Arg Phe Asp Phe Met Gly Thr Cys Val Tyr Val Leu Ala Gln Thr Cys
1   5   10   15

Gly Thr Arg Pro Gly Leu His Arg Phe Val Val Val Leu Gln Glu Asn
            20   25   30

Val Ala Trp Gly Asn Gly Arg Val Ser Val Thr Arg Val Ile Thr Val

35 40 45

Gln Val Ala Asn
50

<210> 1179
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V222G"

<400> 1179
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser
1 5 10 15

Ser Ser Pro Met Gly Ile Ile Val Ala Gly Gly Val Ile Ala Thr Ala
20 25 30

Val Ala Ala Ile Val Ala Ala Val Val Ala Leu Ile Tyr Cys Arg Lys
35 40 45

Lys Arg Ile Ser
50

<210> 1180
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P40A"

<400> 1180
Leu Phe Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu
1 5 10 15

Leu Tyr His Leu Thr Ala Val Ser Ser Ala Ala Ala Pro Gly Thr Pro
20 25 30

Ala Phe Trp Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Leu Ser Tyr
35 40 45

Asn Ser Leu Arg
50

<210> 1181
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V505L"

<400> 1181
Met Gln Gln Pro Glu Ser Ser Ala Asn Ile Arg Thr Leu Leu Glu Asn
1 5 10 15

Lys Asp Ser Gln Val Ile Tyr Ser Ser Leu Leu Lys Lys Ser
20 25 30

<210> 1182
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L620M"

<400> 1182
Ala Ile Met Asn Ala Leu Ile Glu Ala Gly Ala His Met Asp Ala Thr
1 5 10 15

Asn Ala Phe Lys Lys Thr Ala Tyr Glu Met Met Leu Asp Glu Lys Leu
20 25 30

Leu Ala Arg Gly Thr Met Gln Pro Phe Asn Tyr Val Thr Leu Gln Cys
35 40 45

Leu Ala Ala Arg
50

<210> 1183
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L474fs"

<400> 1183
Ser Glu Lys Pro Leu Ala Glu Gln Asp Trp Tyr His Gly Ala Ile Pro
1 5 10 15

Arg Ile Glu Ala Gln Glu Leu Leu Lys Asn Lys Glu Thr Phe Trp Cys
20 25 30

Glu Arg Val Met Gly Asn Leu Val Asn Met Ser Phe Leu Tyr Ile Leu
35 40 45

Met Asp Arg Gly Asp Ile Leu Ser Tyr Asn Met Leu Ile Thr Cys Ile
50 55 60

Asp Ser Arg Ala Leu Gly Phe Gln Thr Phe Leu Asn Leu
65 70 75

<210> 1184
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P92H"

<400> 1184
Cys Glu Val Asp Gln Gly Asp Gly Glu Glu Glu Glu Glu Glu Glu Arg
1 5 10 15

Gly Arg Gly Val Ser Leu Leu Gly Arg His His Lys Arg Lys Arg Val
20 25 30

Ile Thr Tyr Ala Gln Arg Gln Ala Ala Asn Ile Arg Glu Arg Lys Arg
35 40 45

Met Phe Asn Leu
50

<210> 1185
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P50L"

<400> 1185
Asn Cys Asn Ala Ser Pro Glu Pro Gly Ala Glu Ala Gly Ala Glu Ala
1 5 10 15

Gly Gly Gly Ala Asp Gly Phe Pro Ala Leu Leu Ala Cys Ser Leu Glu
20 25 30

Glu Lys Leu Ser Leu Cys Phe Arg Pro Ser Asp Pro Gly Ala Glu Pro
35 40 45

Pro Arg Thr Ala
50

<210> 1186
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E82K"

<400> 1186
Gly Ser Gln Gly Lys Lys Leu Leu Asn Leu Cys Ser Pro Leu Pro Cys

1 5 10 15

Met Ile Pro Leu Gln Pro Leu Gly Tyr Lys Lys Val Pro Ser Lys Thr
20 25 30

Leu Leu Ser Tyr Ser Glu Leu Trp Lys Ser Ser Leu Arg Ala Gly Gly
35 40 45

Gly Gly Gly Gly
50

<210> 1187
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E339Q"

<400> 1187
Asn Tyr Cys Gly Leu Pro Gly Glu Tyr Trp Leu Gly Asn Asp Lys Ile
1 5 10 15

Ser Gln Leu Thr Arg Met Gly Pro Thr Gln Gln Leu Leu Ile Glu Met
20 25 30

Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr Gly Gly Phe Thr
35 40 45

Val Gln Asn Glu
50

<210> 1188
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T229M"

<400> 1188
Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser Leu His Asp Val
1 5 10 15

Gly Glu Thr Val Pro Lys Pro Gly Val Met Met Pro Ser Lys Ser Thr
20 25 30

Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro Val Asn Lys Ser Lys
35 40 45

Thr Thr
50

<210> 1189
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A236V"

<400> 1189
Tyr Arg Glu Pro Ser Leu His Asp Val Gly Glu Thr Val Pro Lys Pro
1 5 10 15

Gly Val Thr Pro Ser Lys Ser Thr Ser Val Val Ser Ala Ile Met Asn
20 25 30

Gly Gly Lys Pro Val Asn Lys Ser Lys Thr Thr
35 40

<210> 1190
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G380R"

<400> 1190
Val Val Leu Pro Ala Glu Glu Glu Leu Val Glu Ala Asp Glu Ala Gly
1 5 10 15

Ser Val Tyr Ala Gly Ile Leu Ser Tyr Arg Arg Val Gly Phe Phe Leu
20 25 30

Phe Ile Leu Val Val Ala Ala Val Thr Leu Cys Arg Leu Arg Ser Pro
35 40 45

Pro Lys Lys Gly
50

<210> 1191
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R571fs"

<400> 1191
Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys Gly Asn
1 5 10 15

Leu Arg Glu Phe Leu Arg Ala Arg Arg Ala Pro Gly Pro Gly Leu Leu
20 25 30

Leu Arg His Leu Gln Ala Ala Arg Gly Ala Ala His Leu Gln Gly Pro
35 40 45

Gly Val Leu Cys Leu Pro Gly Gly Pro Gly His Gly Val Leu Gly Leu
50 55 60

Pro Glu Val His Pro Gln Gly Pro Gly Cys Pro Gln Cys Ala Gly Asp
65 70 75 80

Arg Gly Gln Arg Asp Glu Asp Arg Arg Leu Arg Ala Gly Pro Gly Arg
85 90 95

Ala Gln Pro Arg Leu Leu Gln Glu Asp Asp Gln Arg Pro Ala Ala Arg
100 105 110

Glu Val Asp Gly Ala
        115

<210> 1192
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P716H"

<400> 1192
Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu
1   5   10   15

Leu Lys Glu Gly His Arg Met Asp Lys His His Ala Asn Cys Thr His
            20   25   30

Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln
        35   40   45

Arg Pro Thr Phe
    50

<210> 1193
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.*807S"

<400> 1193
Ser Ser Gly Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala
1   5   10   15

Pro Pro Ser Ser Gly Gly Ser Arg Thr Ser Ser Arg Ala Thr Gly Pro
            20   25   30

Gln Gln Cys Glu Gly Ser Leu Ala Ala His Pro Ala Ala Gly Ala Gln

35 40 45

Pro Leu Pro Gly Met Arg Leu Ser Ala Asp Gly Glu Thr Ala Thr Gln
50 55 60

Ser Phe Gly Leu Cys Val Cys Val Cys Val Cys Val Cys Val Cys Ala
65 70 75 80

His Pro Arg Val Pro Val Cys Val Arg Ile Leu Pro Pro Gly Ala Glu
85 90 95

Val Pro Trp Val Ser Pro Leu Leu Cys Asn Gly Leu Leu Thr Gly Ala
100 105 110

Ala Ala Pro Arg Gly Leu Cys Ser Gly Gly Thr Gln Cys Arg Met
115 120 125

<210> 1194
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R248C"

<400> 1194
Arg Gly Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg
1 5 10 15

Gln Thr Tyr Thr Leu Asp Val Leu Glu Cys Cys Ser Pro His Arg Pro
20 25 30

Ile Leu Gln Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser
35 40 45

Asp Val Glu Phe
50

<210> 1195
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S249C"

<400> 1195
Gly Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln
1 5 10 15

Thr Tyr Thr Leu Asp Val Leu Glu Arg Cys Cys Pro His Arg Pro Ile
20 25 30

Leu Gln Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp
35 40 45

Val Glu Phe His
50

<210> 1196
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.H479fs"

<400> 1196
Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr Pro Lys Leu Tyr
1 5 10 15

Thr Asp Ile His Thr His Thr His Thr Leu Ser His Thr Leu Thr Arg
20 25 30

Gly Gly Gln Gly Pro Pro Ala His Pro Leu Ser Val Leu Asp Gly Thr
35 40 45

Val Ser Ala Val Gly Thr Gly Gly Pro Ala Arg Gln Ala Asp Trp Glu
50 55 60

Asp Gly Gly Arg Ser Cys Arg Arg Arg Gln Gly Thr His Gly Glu Glu
65 70 75 80

Glu Trp Pro Ala Pro Gln Ala Val Cys Val
85 90

<210> 1197
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R243L"

<400> 1197
Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn Ala Thr
1 5 10 15

Tyr Lys Val Asp Val Ile Gln Arg Thr Leu Leu Ser Lys Pro Val Leu
20 25 30

Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr
35 40 45

Ser Phe Gln Cys
50

<210> 1198
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V274L"

<400> 1198
Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr Thr
1 5 10 15

Ser Phe Gln Cys Lys Val Arg Ser Asp Leu Leu Lys Pro Val Ile Gln
20 25 30

Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr
35 40 45

Ile Asp Val Gly
50

<210> 1199
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G138fs"

<400> 1199
Leu Asp His Arg Ala Val Ser Gln Val Asn Arg Ile Asn Glu Thr Lys
1 5 10 15

His Ser Val Leu Gln Tyr Val Gly Gly Gly Asp Val Cys Gly Asn Ala
20 25 30

Gly Pro Glu Thr Ser Val Ala Glu Arg Glu Leu Glu Arg Asp Leu Leu
35 40 45

Gly

<210> 1200
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F100fs"

<400> 1200
Pro Gly Leu Pro Pro Thr Thr His Met Asn Gly Tyr Ser His Leu Gly
1 5 10 15

Lys Lys Lys Arg Met Arg Ser Phe Phe Gly Lys Leu Phe Arg Arg Ser

20 25 30

Lys Phe Glu Ala Lys Pro Thr Ser Gly Pro Trp Gln Pro Gly Arg Asn
35 40 45

Ile Thr Thr Lys Leu Ile Gln Arg Pro Leu Arg Ser Ser Leu Gly Ser
50 55 60

Arg Lys Thr Pro Pro Ser Leu Pro Phe Leu Gly Glu Glu Glu Leu
65 70 75

<210> 1201
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R254W"

<400> 1201
Ser Gly Asp Val Ser Lys Leu Ser Leu Ala Asp Ser Phe Leu Tyr Gly
1 5 10 15

Leu Ile Gln Val Pro Asn Tyr Ser Leu Trp Trp Ile Glu Ala Met Val
20 25 30

Leu Lys Lys Glu Phe Leu Pro Ser Cys Ser Ser Leu Tyr Thr Asp Ile
35 40 45

Thr Val Leu Arg
50

<210> 1202
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D184E"

<400> 1202
Ala Lys His Cys Val Lys Cys Asn Lys Ala Ile Thr Ser Gly Gly Ile
1 5 10 15

Thr Tyr Gln Asp Gln Pro Trp His Ala Glu Glu Cys Phe Val Cys Val
20 25 30

Thr Cys Ser Lys Lys Leu Ala Gly Gln Arg Phe Thr Ala Val Glu Asp
35 40 45

Gln Tyr Tyr Cys
50

<210> 1203
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K309fs"

<400> 1203
Asn Gly Pro Lys Glu Asp Ser Ser Leu Pro Thr Phe Lys Thr Ala Lys
1 5 10 15

Glu Gln Leu Trp Val Asp Gln Gln Lys Ser Thr Thr Asn Leu Ser Val
20 25 30

His Gln Gly Leu His Met Val Val
35 40

<210> 1204
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I522K"

<400> 1204
Leu Lys Asp Asp Leu Thr Lys Leu Lys Ser Phe Thr Val Met Leu Val
1 5 10 15

Asp Glu Arg Lys Asn Met Met Glu Lys Lys Lys Lys Gln Glu Glu Arg
20 25 30

Lys Val Asp Gly Leu Asn Lys Asn Phe Lys Val Glu Gln Gly Lys Val
35 40 45

Met Asp Val Thr
50

<210> 1205
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E161Q"

<400> 1205
Gly Pro Pro Glu Gly Trp Thr Glu Leu Thr Met Gly Val Gly Pro Trp
1 5 10 15

Arg Glu Glu Thr Trp Gly Glu Leu Ile Gln Gln Lys Cys Leu Glu Ser
20 25 30

Met Cys Gln Gly Glu Glu Ala Glu Leu Gln Leu Pro Gly His Ser Gly
35 40 45

Pro Pro Val Arg
50

<210> 1206
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R320L"

<400> 1206
Ala Gln Ala Ala Leu Gly Asn Leu Glu Lys Ala Thr Ala Asp Leu Lys
1 5 10 15

Lys Val Leu Ala Ile Asp Pro Lys Asn Leu Leu Ala Ala Gln Glu Glu
20 25 30

Leu Gly Lys Val Val Ile Gln Gly Lys Asn Gln Asp Ala Gly Leu Ala
35 40 45

Gln Gly Leu Arg
50

<210> 1207
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K159fs"

<400> 1207
Lys Gly Asn Lys Gly Arg Ser Lys Ser Pro Arg Glu Thr Gly Gly Lys
1 5 10 15

Arg His Glu Ser Ser Ser Glu Lys Lys Lys Glu Lys Asp Ile His Leu
20 25 30

Leu Ile Glu Lys Lys Asn Met Glu Lys Thr Ile Ile Thr Gln Val Lys
35 40 45

Lys Arg Lys Thr Arg Leu Lys Ile Leu Asp
50 55

<210> 1208
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.R2886H"

<400> 1208
Ala Ser Thr His Ala Asp Ile Ser Arg His Ser Gln Ala Val Gln Gly
1 5 10 15

Gln Ser Glu Gly Ser Arg Arg Ser Arg His His Gln Gly Ser Ser Val
            20 25 30

Ser Gln Asp Ser Asp Ser Glu Gly His Ser Glu Asp Ser Glu Arg Trp
        35 40 45

Ser Gly Ser Ala
    50

<210> 1209
<211> 52
<212> PRT
<213> Artificial Sequence

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      polypeptide"

<220>
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<223> /note="p.P3254H"

<400> 1209
Glu Arg Trp Ser Gly Ser Ala Ser Arg Asn His Arg Gly Ser Val Gln
1 5 10 15

Glu Gln Ser Arg His Gly Ser Arg His His His Arg Ser His His Glu
            20 25 30

Asp Arg Ala Gly His Gly His Ser Ala Asp Arg Ser Arg Gln Ser Gly
        35 40 45

Thr Arg His Ala
    50

<210> 1210
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L572F"

<400> 1210
Gly Ser Gly Ser Ser Gln Ser Ser Gly Tyr Gly Gln Tyr Gly Ser Arg
1 5 10 15

Glu Thr Ser Gly Phe Gly Gln His Gly Phe Phe Gly Ser Gly Gln Ser
20 25 30

Thr Gly Phe Gly Gln Tyr Gly Ser Gly Ser Gly Gln Ser Ser Gly Phe
35 40 45

Gly Gln His Gly
50

<210> 1211
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G1545V"

<400> 1211
His Thr His Gly Gln Ser Gly Ser Gln His Gly Glu Ser Glu Ser Ile
1 5 10 15

Ile His Asp Arg His Arg Ile Thr His Val Val Gln Thr Gly Asp Thr
20 25 30

Thr Arg His Ser Tyr Ser Gly His Glu Gln Thr Thr Gln Thr Gly Ser
35 40 45

Arg Thr Thr Gly
50

<210> 1212
<211> 54
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H1901fs"

<400> 1212
Arg Arg Ser Gly His Ser Glu Ser Ser Asp Ser Glu Val His Ser Gly
1 5 10 15

Gly Ser His Thr His Ser Gly His Thr Gln Pro Ser Gln Val Ser Thr
20 25 30

Trp Arg Val Arg Ile His Ser Ser Gln Glu Thr Pro Asn Tyr Ser Trp
35 40 45

Thr Asp Arg Arg Tyr His
50

<210> 1213
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L850fs"

<400> 1213
Ser His Thr Phe Gln Leu Trp Arg Ala Leu Gly Ala Gly Gln Pro Thr
1 5 10 15

Ser His Leu Val Leu Thr Thr Leu Leu Gly Leu Ser Ala Gly Ala Thr
20 25 30

Pro Ala His Arg Cys Gln Arg Gln Gln Pro Leu Pro Gln Gly Glu Asp
35 40 45

Leu Pro Ala Phe Ala Gly Cys His Glu His Ala Ala Arg Ala Ala Val
50 55 60

Cys Pro Gly Val Gln Ala Gly Arg Ala Gly Gly Leu Pro Gln Ala Leu
65 70 75 80

Pro Gly Pro Pro His Pro Asp Ala Leu Cys Leu Gly Ala Glu Pro Ala
85 90 95

Gln Arg Ala Pro Gln Ala Ala Gly Pro Gly Gly Gly Arg Ala Gln Pro
100 105 110

Pro Lys Leu Gln His Val Thr Gly Gly Thr Glu Glu Pro Ala Val His
115 120 125

His Gly Ala Leu Ala
130

<210> 1214
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V1240M"

<400> 1214
Gly Thr His Thr Ile Thr Tyr Ile Pro Leu Cys Pro Gly Ala Tyr Thr
1 5 10 15

Val Thr Ile Lys Tyr Gly Gly Gln Pro Met Met Pro Asn Phe Pro Ser
20 25 30

Lys Leu Gln Val Glu Pro Ala Val Asp Thr Ser Gly Val Gln Cys Tyr
35 40 45

Gly Pro Gly Ile
50

<210> 1215
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W529fs"

<400> 1215
Leu Asp Gly Val Tyr Ala Phe Glu Tyr Tyr Pro Ser Thr Pro Gly Arg
1 5 10 15

Tyr Ser Ile Ala Ile Thr Trp Gly Gly Thr Pro His Ser Lys Glu Pro
20 25 30

Leu

<210> 1216
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.W529fs"

<400> 1216
Phe Leu Asp Gly Val Tyr Ala Phe Glu Tyr Tyr Pro Ser Thr Pro Gly
1 5 10 15

Arg Tyr Ser Ile Ala Ile Thr Trp Gly Asp Thr Thr Phe Gln Arg Ala
20 25 30

Pro Leu Lys Phe Lys Leu Ala Leu Lys Arg Val Cys Arg Lys Ser Val
35 40 45

Leu Gly Ala Leu Gly Ser Met Val Gly Leu Ser Gly Gly Gln Arg Thr
50 55 60

Ser Trp
65

<210> 1217
<211> 78
<212> PRT
<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.600_601insFREYEYD"

<400> 1217
Leu Gln Met Val Gln Val Thr Gly Ser Ser Asp Asn Glu Tyr Phe Tyr
1 5 10 15

Val Asp Phe Arg Glu Tyr Glu Tyr Asp Phe Arg Glu Tyr Glu Tyr Asp
20 25 30

Phe Arg Glu Tyr Glu Tyr Asp Leu Lys Trp Glu Phe Pro Arg Glu Asn
35 40 45

Leu Glu Phe Gly Lys Val Leu Gly Ser Gly Ala Phe Gly Lys Val Met
50 55 60

Asn Ala Thr Ala Tyr Gly Ile Ser Lys Thr Gly Val Ser Ile
65 70 75

<210> 1218
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D835H"

<400> 1218
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr His Gly Lys Val Val
1 5 10 15

Lys Ile Cys Asp Phe Gly Leu Ala Arg His His Ile Met Ser Asp Ser
20 25 30

Asn Tyr Val Val Arg Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala
35 40 45

Pro Glu Ser Leu
50

<210> 1219
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D835Y"

<400> 1219
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr His Gly Lys Val Val
1 5 10 15

Lys Ile Cys Asp Phe Gly Leu Ala Arg Tyr Tyr Ile Met Ser Asp Ser
20 25 30

Asn Tyr Val Val Arg Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala
35 40 45

Pro Glu Ser Leu
50

<210> 1220
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D835E"

<400> 1220
Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr His Gly Lys Val Val
1 5 10 15

Lys Ile Cys Asp Phe Gly Leu Ala Arg Glu Glu Ile Met Ser Asp Ser
20 25 30

Asn Tyr Val Val Arg Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala
35 40 45

Pro Glu Ser Leu
    50

<210> 1221
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S751F"

<400> 1221
Cys Leu Glu Ala Leu Arg Leu Glu Glu Lys Glu Val Arg His His Arg
1   5   10   15

Ile Leu Glu Ala Lys Ser Ile Gln Thr Phe Phe Pro Thr Glu Glu Gly
            20   25   30

Gly Val Leu Thr Leu Pro Pro Val Asp Gly Leu Pro Gly Arg Pro Pro
        35   40   45

Cys Pro Pro Gly
    50

<210> 1222
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.P992T"

<400> 1222
Gly Ile Pro Leu Pro Pro Pro Leu Pro Gly Ala Gly Ile Pro Pro Pro
1   5   10   15

Pro Pro Leu Pro Gly Ala Gly Ile Pro Thr Thr Pro Pro Pro Leu Pro
            20   25   30

Gly Ala Gly Ile Pro Pro Pro Pro Pro Leu Pro Gly Ala Gly Ile Pro

35 40 45

Pro Pro Pro Pro
50

<210> 1223
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E927Q"

<400> 1223
His Phe Leu Asp Lys Ala Gly Ser Val Ser Leu Asp Ser Val Leu Ala
1 5 10 15

Asp Val Arg Ser Leu Gln Arg Gly Leu Gln Gln Leu Thr Gln Arg Glu
20 25 30

Phe Val Arg Gln Asp Asp Cys Met Val Leu Lys Glu Phe Leu Arg Ala
35 40 45

Asn Ser Pro Thr
50

<210> 1224
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F510L"

<400> 1224
Ala Ile Leu Thr Gln Trp Asp Arg Ser Leu Lys Pro Met Gln Thr Arg
1 5 10 15

Val Val Gly Arg Leu Gln Lys Pro Cys Leu Leu Phe Phe His Trp Leu
20 25 30

Lys Leu Phe Ala Ile Pro Ile Leu Leu Ile Ala Val Phe Leu Val Leu
35 40 45

Thr

<210> 1225
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S331R"

<400> 1225
Gln Lys Ile Pro Pro Val Asn Thr Asn Leu Glu Asn Leu Tyr Leu Gln
1 5 10 15

Gly Asn Arg Ile Asn Glu Phe Ser Ile Arg Arg Ser Phe Cys Thr Val
20 25 30

Val Asp Val Val Asn Phe Ser Lys Leu Gln Val Leu Arg Leu Asp Gly
35 40 45

Asn Glu Ile Lys
50

<210> 1226
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R290C"

<400> 1226
Arg Gly Glu Trp Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser
1 5 10 15

Ser Gly Ser Gly Pro Phe Thr Asp Val Cys Cys Ala Ala Val Tyr Gln
20 25 30

Pro Gln Pro His Pro Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp
35 40 45

Ser Gly Val Val
50

<210> 1227
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.TT58del"

<400> 1227
Pro Glu Pro Asp Thr Glu Pro Asp Ser Thr Ala Ala Val Pro Ser Gln
1 5 10 15

Pro Ala Pro Ser Ala Ala Thr Thr Thr Ala Val Thr Ala Ala Ala Ala
20 25 30

Ser Asp Asp Ser Pro Ser Glu Asp Glu Gln Glu Ala Val Gln Glu Val
35 40 45

Pro Arg Val Val Gln Asn Pro Pro
50 55

<210> 1228
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R652H"

<400> 1228

Gln Gly Thr Ser His Arg Pro Ser Leu Pro Ala Ser Leu Asn Asp Asn
1 5 10 15

Asp Leu Val Asp Ser Asp Glu Asp Glu His His Ala Val Gly Ser Leu
20 25 30

His Pro Lys Gly Ala Phe Ala Gln Pro Arg Pro Ala Leu Ser Pro Ser
35 40 45

Arg Gln Ser Pro
50

<210> 1229
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1180del"

<400> 1229
Ala Pro Gly Lys Ser Glu Pro Pro Ser Lys Arg Pro Leu Ser Ser Lys
1 5 10 15

Ser Gln Gln Ser Val Ser Ala Glu Asp Glu Glu Glu Asp Ala Gly Phe
20 25 30

Phe Lys Gly Gly Lys Glu Asp Leu Leu Ser Ser Ser Val Pro Lys Trp
35 40 45

Pro Ser Ser Ser Thr
50

<210> 1230
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S501fs"

<400> 1230
Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys
1 5 10 15

Ser Leu Tyr Glu Ser Trp Thr Lys Lys Val Leu Pro Gln Ser Ser Val
20 25 30

Ala Cys Pro Gly
35

<210> 1231
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A643S"

<400> 1231
His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp Ser Leu Phe
1 5 10 15

Ser Ala Val Lys Asn Phe Thr Glu Ile Ser Ser Ser Lys Phe Ser Glu
20 25 30

Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val Leu Arg Met Met
35 40 45

Asn Asp Gln Leu
50

<210> 1232
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C405fs"

<400> 1232
Gly Gln Phe Cys Ser Asn Ser Ser Ser Ile Arg Arg Thr Ala Pro Thr
1 5 10 15

Ala Ala Leu Pro Pro Arg Ala Arg Cys Gly Arg Ala Pro Val Gly Leu
20 25 30

Val Gly Ala Ala Glu Val Ser Gly Ser Gly Gly Gly Leu
35 40 45

<210> 1233
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R354W"

<400> 1233
Ser Gly Ile Tyr Ala His Ile Thr Lys His Tyr Pro Tyr Tyr Arg Thr
1 5 10 15

Ala Asp Lys Gly Trp Gln Asn Ser Ile Trp Trp His Asn Leu Ser Leu
20 25 30

Asn Arg Tyr Phe Ile Lys Val Pro Arg Ser Gln Glu Glu Pro Gly Lys
35 40 45

Gly Ser Phe Trp
50

<210> 1234
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P96fs"

<400> 1234
Asn Leu Leu Lys Ser Phe Gly Glu Ser Val Leu Arg Ser Val Ser Pro
1 5 10 15

Val Gln Asp Leu Asp Asp Asp Thr Pro His Pro Leu Pro Thr Leu Thr
20 25 30

Cys Pro Thr Met Pro Gly Arg Thr Pro Thr Ala Asn Pro Pro Thr Pro
35 40 45

Ser Ala Ala Ser Tyr Leu Trp Pro Ser Arg Thr Leu Gln Pro Ser Ala
50 55 60

Cys Gln
65

<210> 1235
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S135L"

<400> 1235
Arg Ser Lys Pro Tyr Thr Arg Arg Pro Lys Pro Pro Tyr Ser Tyr Ile
1 5 10 15

Ala Leu Ile Ala Met Ala Ile Arg Asp Leu Leu Ala Gly Gly Arg Leu
20 25 30

Thr Leu Ala Glu Ile Asn Glu Tyr Leu Met Gly Lys Phe Pro Phe Phe
35 40 45

Arg Gly Ser Tyr
50

<210> 1236
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R136L"

<400> 1236
Ser Val Gly Gly Ile Cys Gln Gln Phe Ser Leu Pro Glu Asn Ile Gln
1 5 10 15

Leu Ser Leu Phe Ser Ala Ser Phe Leu Leu Leu Asn Ile Asn Glu Tyr
20 25 30

Leu Ala Val Val Asp Ala Pro Pro Leu Asp Leu Arg Phe Asn Pro Ser
35 40 45

Gly Tyr Leu Leu
50

<210> 1237
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I22V"

<400> 1237
Met Ser Arg Ala Arg Ser His Leu Arg Ala Ala Leu Phe Leu Ala Ala
1 5 10 15

Ala Ser Ala Arg Gly Val Val Thr Thr Gln Val Ala Ala Arg Arg Gly
20 25 30

Leu Ser Ala Trp Pro Val Pro Gln Glu Pro Ser Met Glu Tyr Gln Asp
35 40 45

<210> 1238
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R455H"

<400> 1238
Asn Val Ile Asn Ile Asn His Gln Gly Arg Asp Gly His Thr Gly Leu
1 5 10 15

His Ser Ala Cys Tyr His Gly His Ile His His Leu Val Gln Phe Leu
20 25 30

Leu Asp Asn Gly Ala Asp Met Asn Leu Val Ala Cys Asp Pro Ser Arg
35 40 45

Ser Ser Gly Glu
50

<210> 1239
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R54Q"

<400> 1239
Pro Leu Val Val Leu Gly Val Thr Phe Val Leu Gly Val Leu Gly Asn
1 5 10 15

Gly Leu Val Ile Trp Val Ala Gly Phe Gln Gln Met Thr Arg Thr Val
20 25 30

Thr Thr Ile Cys Tyr Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr
35 40 45

Ala Thr Leu Pro
50

<210> 1240
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.C382F"

<400> 1240
Phe Met Ser Ser Asn Ala Ser Glu Val Lys Arg Ile Pro Glu Gly Glu
1 5 10 15

Lys Trp Glu Asp Gly Pro Cys Lys Val Phe Phe Glu Cys Arg Gly Ala
20 25 30

Gln Val Thr Cys Tyr Glu Pro Ser Cys Pro Pro Cys Pro Val Gly Thr
35 40 45

Leu Ala Leu Glu
50

<210> 1241
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E86del"

<400> 1241
Ala Ile Glu Met Asp Lys Gly Thr Tyr Ile His Ala Leu Asp Asn Gly
1 5 10 15

Leu Phe Thr Leu Gly Ala Pro His Lys Val Asp Glu Gly Pro Ser Pro
20 25 30

Pro Glu Gln Phe Thr Ala Val Lys Leu Ser Asp Ser Arg Ile Ala Leu
35 40 45

Lys Ser Gly Tyr Gly
50

<210> 1242
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I34T"

<400> 1242
Arg Ile Ala Leu Lys Ser Gly Tyr Gly Lys Tyr Leu Gly Ile Asn Ser
1 5 10 15

Asp Glu Leu Val Gly His Ser Asp Ala Thr Thr Gly Pro Arg Glu Gln
20 25 30

Trp Glu Pro Val Phe Gln Asn Gly Lys Met Ala Leu Leu Ala Ser Asn
35 40 45

Ser Cys Phe Ile
50

<210> 1243
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R37K"

<400> 1243
Leu Lys Ser Gly Tyr Gly Lys Tyr Leu Gly Ile Asn Ser Asp Glu Leu
1 5 10 15

Val Gly His Ser Asp Ala Ile Gly Pro Lys Lys Glu Gln Trp Glu Pro
20 25 30

Val Phe Gln Asn Gly Lys Met Ala Leu Leu Ala Ser Asn Ser Cys Phe
35 40 45

Ile Arg Cys Asn
50

<210> 1244
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q39K"

<400> 1244
Ser Gly Tyr Gly Lys Tyr Leu Gly Ile Asn Ser Asp Glu Leu Val Gly
1 5 10 15

His Ser Asp Ala Ile Gly Pro Arg Glu Lys Lys Trp Glu Pro Val Phe
20 25 30

Gln Asn Gly Lys Met Ala Leu Leu Ala Ser Asn Ser Cys Phe Ile Arg
35 40 45

Cys Asn Glu Ala
50

<210> 1245
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P42Q"

<400> 1245
Gly Lys Tyr Leu Gly Ile Asn Ser Asp Glu Leu Val Gly His Ser Asp
1 5 10 15

Ala Ile Gly Pro Arg Glu Gln Trp Glu Gln Gln Val Phe Gln Asn Gly
20 25 30

Lys Met Ala Leu Leu Ala Ser Asn Ser Cys Phe Ile Arg Cys Asn Glu
35 40 45

Ala Gly Asp Ile

50

<210> 1246
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M49V"

<400> 1246
Ser Asp Glu Leu Val Gly His Ser Asp Ala Ile Gly Pro Arg Glu Gln
1 5 10 15

Trp Glu Pro Val Phe Gln Asn Gly Lys Val Val Ala Leu Leu Ala Ser
20 25 30

Asn Ser Cys Phe Ile Arg Cys Asn Glu Ala Gly Asp Ile Glu Ala Lys
35 40 45

Ser Lys Thr Ala
50

<210> 1247
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A50P"

<400> 1247
Asp Glu Leu Val Gly His Ser Asp Ala Ile Gly Pro Arg Glu Gln Trp
1 5 10 15

Glu Pro Val Phe Gln Asn Gly Lys Met Pro Pro Leu Leu Ala Ser Asn
20 25 30

Ser Cys Phe Ile Arg Cys Asn Glu Ala Gly Asp Ile Glu Ala Lys Ser
35 40 45

Lys Thr Ala Gly
    50

<210> 1248
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.L52S"

<400> 1248
Leu Val Gly His Ser Asp Ala Ile Gly Pro Arg Glu Gln Trp Glu Pro
1   5   10   15

Val Phe Gln Asn Gly Lys Met Ala Leu Ser Ser Ala Ser Asn Ser Cys
            20   25   30

Phe Ile Arg Cys Asn Glu Ala Gly Asp Ile Glu Ala Lys Ser Lys Thr
        35   40   45

Ala Gly Glu Glu
    50

<210> 1249
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A53T"

<400> 1249
Val Gly His Ser Asp Ala Ile Gly Pro Arg Glu Gln Trp Glu Pro Val
1   5   10   15

Phe Gln Asn Gly Lys Met Ala Leu Leu Thr Thr Ser Asn Ser Cys Phe
            20   25   30

Ile Arg Cys Asn Glu Ala Gly Asp Ile Glu Ala Lys Ser Lys Thr Ala
35 40 45

Gly Glu Glu Glu
50

<210> 1250
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N55D"

<400> 1250
His Ser Asp Ala Ile Gly Pro Arg Glu Gln Trp Glu Pro Val Phe Gln
1 5 10 15

Asn Gly Lys Met Ala Leu Leu Ala Ser Asp Asp Ser Cys Phe Ile Arg
20 25 30

Cys Asn Glu Ala Gly Asp Ile Glu Ala Lys Ser Lys Thr Ala Gly Glu
35 40 45

Glu Glu Met Ile
50

<210> 1251
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I59V"

<400> 1251
Ile Gly Pro Arg Glu Gln Trp Glu Pro Val Phe Gln Asn Gly Lys Met
1 5 10 15

Ala Leu Leu Ala Ser Asn Ser Cys Phe Val Val Arg Cys Asn Glu Ala
20 25 30

Gly Asp Ile Glu Ala Lys Ser Lys Thr Ala Gly Glu Glu Glu Met Ile
35 40 45

Lys Ser Leu Ser
50

<210> 1252
<211> 52
<212> PRT
<213> Artificial Sequence

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<400> 1252
Trp Glu Pro Val Phe Gln Asn Gly Lys Met Ala Leu Leu Ala Ser Asn
1 5 10 15

Ser Cys Phe Ile Arg Cys Asn Glu Ala Glu Glu Asp Ile Glu Ala Lys
20 25 30

Ser Lys Thr Ala Gly Glu Glu Glu Met Ile Lys Ser Leu Ser His Ser
35 40 45

Leu Pro Ser Ser
50

<210> 1253
<211> 36
<212> PRT
<213> Artificial Sequence

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<223> /note="p.I10T"

<400> 1253
Met Ala Val Lys Leu Ser Asp Ser Arg Thr Thr Ala Leu Lys Ser Gly

1 5 10 15

Tyr Gly Lys Tyr Leu Gly Ile Asn Ser Asp Glu Leu Val Gly His Ser
20 25 30

Asp Ala Ile Gly
35

<210> 1254
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1254
Met Ala Val Lys Leu Ser Asp Ser Arg Ile Thr Thr Leu Lys Ser Gly
1 5 10 15

Tyr Gly Lys Tyr Leu Gly Ile Asn Ser Asp Glu Leu Val Gly His Ser
20 25 30

Asp Ala Ile Gly Pro
35

<210> 1255
<211> 39
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.K13N"

<400> 1255
Met Ala Val Lys Leu Ser Asp Ser Arg Ile Ala Leu Asn Asn Ser Gly
1 5 10 15

Tyr Gly Lys Tyr Leu Gly Ile Asn Ser Asp Glu Leu Val Gly His Ser
20 25 30

Asp Ala Ile Gly Pro Arg Glu
        35

<210> 1256
<211> 46
<212> PRT
<213> Artificial Sequence

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<223> /note="p.L20P"

<400> 1256
Met Ala Val Lys Leu Ser Asp Ser Arg Ile Ala Leu Lys Ser Gly Tyr
1   5   10   15

Gly Lys Tyr Pro Pro Gly Ile Asn Ser Asp Glu Leu Val Gly His Ser
            20   25   30

Asp Ala Ile Gly Pro Arg Glu Gln Trp Glu Pro Val Phe Gln
        35   40   45

<210> 1257
<211> 52
<212> PRT
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      polypeptide"

<220>
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<223> /note="p.D32V"

<400> 1257
Asp Ser Arg Ile Ala Leu Lys Ser Gly Tyr Gly Lys Tyr Leu Gly Ile
1   5   10   15

Asn Ser Asp Glu Leu Val Gly His Ser Val Val Ala Ile Gly Pro Arg
            20   25   30

Glu Gln Trp Glu Pro Val Phe Gln Asn Gly Lys Met Ala Leu Leu Ala
        35   40   45

Ser Asn Ser Cys
    50

<210> 1258
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<400> 1258
Glu Cys Ser Leu Ser Leu Asn Lys Lys Ser Arg Ser Ser Thr Pro Val
1   5   10   15

His Asn Ser Glu Ile Gln Glu Thr Cys Tyr Tyr Ala His His Arg Gly
            20   25   30

Arg Ser Arg Ala Cys Thr Gly Arg Ser Lys Arg His Arg Ser Arg Ala
        35   40   45

Leu Gly Val Gln
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<210> 1259
<211> 32
<212> PRT
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<400> 1259
Cys Lys Ala Thr Ser Ala Ala Leu Pro Gln Ser Gln Arg Ser Ser Thr
1   5   10   15

Pro Ser Ser Glu Ile Gly Ala Thr Pro Gln Ala Ala Pro Thr Thr Ser
            20   25   30

<210> 1260
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.E1093Q"

<400> 1260
Ala Pro Lys Tyr Thr Glu Pro Leu Leu Ser Pro Arg Asp Glu Pro Arg
1 5 10 15

Ser Asp Glu Cys Gly Ile Asn Pro Gly Gln Gln Lys Ile Ala Ser Ile
20 25 30

Pro Thr Lys Glu Glu Pro Gln Gly Gln Leu Ser Leu Glu Arg Asp Arg
35 40 45

Glu Val Thr Asn
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<210> 1261
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L47S"

<400> 1261
Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu Leu Gly Ser Gly Ile
1 5 10 15

Met Glu Leu Thr Asp Thr Glu Leu Ile Ser Ser Tyr Thr Arg Lys Arg
20 25 30

Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr Asp
35 40 45

Ser Asn Leu Phe

50

<210> 1262
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 1262
Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu
1 5 10 15

Glu Cys Arg Phe Cys Ile Ser Ile Asn Asn Asn Thr Trp Cys Ala Gly
20 25 30

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
35 40 45

Ile Gln Lys Thr
50

<210> 1263
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R430C"

<400> 1263
Gln Ser Gly Ala Arg Ile Glu Leu Gln Arg Asn Pro Pro Pro Asn Ala
1 5 10 15

Asp Pro Asn Met Lys Leu Phe Thr Ile Cys Cys Gly Thr Pro Gln Gln
20 25 30

Ile Asp Tyr Ala Arg Gln Leu Ile Glu Glu Lys Ile Gly Gly Pro Val
35 40 45

Asn Pro Leu Gly
50

<210> 1264
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S140fs"

<400> 1264
Asn Pro Ser Ala Gln Leu Pro Arg Ser Pro Arg Arg Gln Gly Gln Arg
1 5 10 15

Trp Ile Trp Phe Ser Met Glu Ser Pro Lys Pro Leu Leu Ala Ala Glu
20 25 30

Ser His Gly Arg Ile Leu Gln Ser His His Val Leu Pro Gln Arg Leu
35 40 45

Arg His Leu His Ala Leu Arg Leu Ala Gly Ala Val Val Arg Pro Ala
50 55 60

Cys Pro Pro Thr Ala Gln Pro Leu Gly Gln Asp Arg Ala Gly Gly Leu
65 70 75 80

Gly Ser Val Gln Leu Gly Ala Lys Leu Arg Gln Gly Ala Leu Leu Pro
85 90 95

Glu Pro Ala Gly Pro Ser Gln Gly Gly Arg Val Arg Thr Leu Pro Gln
100 105 110

Ala Pro Ala Pro Gly Asn His Asp Gly Asp Ala Val Pro Val Gln Val
115 120 125

Leu Ser Gly Leu Arg Glu Leu Leu Ala Pro Arg Leu His His Arg Glu
130 135 140

Ala Val Glu Glu Arg Pro Gly Gly Leu Gly Arg Ala Arg Gly Ala Gly
145 150 155 160

```
Pro Gln Gln Lys Gln Leu Arg Glu Val Pro Ala Thr Arg Arg Leu His
                165                 170                 175

Pro Arg Gly Arg Leu Pro Glu Pro Gln Gly Pro Gly Pro Val Pro Ala
            180                 185                 190

Gly Ala Gly Gln Gly Pro Arg Pro Leu Pro Glu Leu Leu Ser Leu Ala
        195                 200                 205

Gly Asp Ala Ala Ala Ser Leu Leu Gln Leu Gly Thr Arg Phe Leu Gln
    210                 215                 220

Gly Leu Leu Glu Thr Ala Gly Gly Ile Gln Val Pro Asp Thr Arg His
225                 230                 235                 240

Ser Gly Leu Val His Leu Arg Gly Trp Cys Gly Ala Trp Ala Ala Arg
                245                 250                 255

Asn Leu Ile Phe Leu Gly Pro His Leu Ser Gly Gly Leu Ile Tyr Leu
            260                 265                 270

Arg Thr Arg Leu Pro Glu Ala Ser Pro Ala
        275                 280
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<210> 1265
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.G324fs"

<400> 1265

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Asn Gln Glu Glu Leu Ala Ser Gly Thr Pro Pro Ala Arg Phe Pro Lys
1               5                   10                  15

Ala Pro Ser Lys Leu Thr Val Gly Gly His Gly Ala Lys Val Arg Lys
            20                  25                  30

Arg Lys Arg Glu Thr Arg Ile Gln Pro Pro Arg Asn Arg Ser His Cys
        35                  40                  45
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Leu Pro Cys Leu Pro Trp Val His Leu His Gln Asn Pro Thr Asp His
50 55 60

Gln Met Leu Thr
65

<210> 1266
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D367N"

<400> 1266
Leu Thr Ile Ile Leu Leu Ala Met Asn Lys Ile Glu Gly Asp Asn Ile
1 5 10 15

Ser Gly Val Cys Phe Val Gly Leu Tyr Asn Asn Val Asp Ala Leu Arg
20 25 30

Tyr Phe Val Leu Ala Pro Leu Cys Leu Tyr Val Val Val Gly Val Ser
35 40 45

Leu Leu Leu Ala
50

<210> 1267
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R416Q"

<400> 1267
Ile Ser Leu Asn His Val Arg Gln Val Ile Gln His Asp Gly Arg Asn
1 5 10 15

Gln Glu Lys Leu Lys Lys Phe Met Ile Gln Gln Ile Gly Val Phe Ser

20 25 30

Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu Gly Cys Tyr Val Tyr
35 40 45

Glu Gln Val Asn
50

<210> 1268
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R73H"

<400> 1268
Leu Ser Pro Lys His Ala Pro Asp Ile Pro Asp Asp Ser Thr Asp Asn
1 5 10 15

Ile Thr Ile Phe Thr Arg Ile Leu Asp His His Leu Leu Asp Gly Tyr
20 25 30

Asp Asn Arg Leu Arg Pro Gly Leu Gly Asp Ala Val Thr Glu Val Lys
35 40 45

Thr Asp Ile Tyr
50

<210> 1269
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R460Q"

<400> 1269
Pro Phe Ser Arg Ala Asn Ala Ala Glu Thr Ile Ser Ala Ala Arg Ala
1 5 10 15

Leu Pro Ser Ala Ser Pro Thr Ser Ile Gln Gln Thr Gly Tyr Met Pro
20 25 30

Arg Lys Ala Ser Val Gly Ser Ala Ser Thr Arg His Val Phe Gly Ser
35 40 45

Arg Leu Gln Arg
50

<210> 1270
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S126N"

<400> 1270
Arg Gln Ser Trp Lys Asp Glu Arg Leu Arg Phe Lys Gly Pro Met Gln
1 5 10 15

Arg Leu Pro Leu Asn Asn Leu Leu Ala Asn Asn Lys Ile Trp Thr Pro
20 25 30

Asp Thr Phe Phe His Asn Gly Lys Lys Ser Ile Ala His Asn Met Thr
35 40 45

Thr Pro Asn Lys
50

<210> 1271
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q224K"

<400> 1271
Ser Glu Val Val Tyr Val Trp Thr Asn Gly Ser Thr Lys Ser Val Val
1 5 10 15

Val Ala Glu Asp Gly Ser Arg Leu Asn Lys Lys Tyr His Leu Met Gly
20 25 30

Gln Thr Val Gly Thr Glu Asn Ile Ser Thr Ser Thr Gly Glu Tyr Thr
35 40 45

Ile Met Thr Ala
50

<210> 1272
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V314I"

<400> 1272
Ser Ala Arg His Ser Leu Pro Lys Val Ser Tyr Ala Thr Ala Met Asp
1 5 10 15

Trp Phe Ile Ala Val Cys Phe Ala Phe Ile Ile Phe Ser Ala Leu Ile
20 25 30

Glu Phe Ala Ala Val Asn Tyr Phe Thr Asn Leu Gln Thr Gln Lys Ala
35 40 45

Lys Arg Lys Ala
50

<210> 1273
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.R416C"

<400> 1273
Lys Ala Thr Met Tyr Ser Tyr Asp Ser Ala Ser Ile Gln Tyr Arg Lys
1 5 10 15

Pro Leu Ser Ser Arg Glu Ala Tyr Gly Cys Cys Ala Leu Asp Arg His
20 25 30

Gly Val Pro Ser Lys Gly Arg Ile Arg Arg Arg Ala Ser Gln Leu Lys
35 40 45

Val Lys Ile Pro
50

<210> 1274
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D500N"

<400> 1274
Arg Ser Leu Pro His Lys Lys Thr His Leu Arg Arg Arg Ser Ser Gln
1 5 10 15

Leu Lys Ile Lys Ile Pro Asp Leu Thr Asn Asn Val Asn Ala Ile Asp
20 25 30

Arg Trp Ser Arg Ile Val Phe Pro Phe Thr Phe Ser Leu Phe Asn Leu
35 40 45

Val Tyr Trp Leu
50

<210> 1275
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q412fs"

<400> 1275
Gly Ser Tyr Arg Ser Val Gly Val Glu Thr Gly Glu Thr Lys Lys Glu
1 5 10 15

Gly Ala Ala Arg Ser Gly Gly Gln Gly Ala Ser Val Pro Gly Ser Gly
20 25 30

Pro Ser Thr Gln Thr Pro Leu Thr Phe Thr Pro Ala Leu Cys Ser Leu
35 40 45

Arg Arg Leu Arg Pro Ser Met Ser Ser Thr Gly Arg His Thr Pro Cys
50 55 60

Glu His Arg Thr Gln Ala Thr Leu Ala Cys Pro Gly Ala Arg Arg Gln
65 70 75 80

Leu Pro Arg Asn Phe Leu Gly Glu Arg Ala Leu Gly Leu Pro Ser Pro
85 90 95

Leu Arg Val Ser Lys Trp Asp Asp Ser Arg Pro Arg Lys Thr Arg Gly
100 105 110

Ser Leu Gly Leu Pro Glu Leu
115

<210> 1276
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E205K"

<400> 1276
Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln Leu His Asn Phe
1 5 10 15

Pro Met Asp Glu His Ser Cys Pro Leu Lys Lys Phe Ser Ser Tyr Gly
20 25 30

Tyr Pro Lys Asn Glu Ile Glu Tyr Lys Trp Lys Lys Pro Ser Val Glu
35 40 45

Val Ala Asp Pro
50

<210> 1277
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A368V"

<400> 1277
Val Ser Tyr Val Lys Ala Val Asp Ile Tyr Leu Trp Val Ser Phe Val
1 5 10 15

Phe Val Phe Leu Ser Val Leu Glu Tyr Val Val Ala Val Asn Tyr Leu
20 25 30

Thr Thr Val Gln Glu Arg Lys Glu Arg Lys Leu Arg Glu Lys Phe Pro
35 40 45

Cys Met Cys Gly
50

<210> 1278
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L352I"

<400> 1278
Val Ala Trp Asn Pro His Lys Met Leu Met Ala Gly Ile Gln Cys Cys
1 5 10 15

Ala Leu Leu Val Lys Asp Lys Ser Asp Ile Ile Leu Lys Lys Cys Tyr
20 25 30

Ser Ala Lys Ala Ser Tyr Leu Phe Gln Gln Asp Lys Phe Tyr Asp Val
35 40 45

Ser Tyr Asp Thr
50

<210> 1279
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A271S"

<400> 1279
Glu Ser Leu Val Leu Leu Arg Arg Leu Leu Ala Trp Asp Leu Asp Asp
1 5 10 15

Val Leu Tyr Ala Lys Leu Asn Ala Arg Ser Ser Ala Ser Ser Arg Leu
20 25 30

Ala Ala Ile Pro Ala Ala Leu Ala Arg Ala Ala Arg Thr Trp Asn Ala
35 40 45

Leu Asp Ala Gly
50

<210> 1280
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G358C"

<400> 1280

Leu Glu Ile Val Thr Cys Ser His Val Gly His Val Phe Arg Lys Ala
1 5 10 15

Thr Pro Tyr Thr Phe Pro Gly Gly Thr Cys Cys His Val Ile Asn Lys
20 25 30

Asn Asn Arg Arg Leu Ala Glu Val Trp Met Asp Glu Phe Lys Asp Phe
35 40 45

Phe Tyr Ile Ile
50

<210> 1281
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D234E"

<400> 1281
Val Asn Arg Asp Trp Leu Gln Pro Leu Leu His Arg Val Lys Glu Asp
1 5 10 15

Tyr Thr Arg Val Val Cys Pro Val Ile Glu Glu Ile Ile Asn Leu Asp
20 25 30

Thr Phe Thr Tyr Ile Glu Ser Ala Ser Glu Leu Arg Gly Gly Phe Asp
35 40 45

Trp Ser Leu His
50

<210> 1282
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source

<223> /note="p.W317fs"

<400> 1282
Gly Ile Phe Val Ile Asp Lys Ser Trp Phe Asn His Leu Gly Lys Tyr
1 5 10 15

Asp Ala Gln Met Asp Ile Trp Gly Gly Arg Glu Phe
20 25

<210> 1283
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E395K"

<400> 1283
Ala Met Asp Arg His Tyr Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu
1 5 10 15

Met Ser Leu Arg Gly Gly Glu Asn Leu Lys Lys Leu Ser Phe Lys Ala
20 25 30

Trp Leu Cys Gly Gly Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly
35 40 45

His Ile Tyr Gln
50

<210> 1284
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A45T"

<400> 1284
Thr Ala Leu Leu Phe Ile Tyr Leu His His Asn His Val Ser Ser Trp
1 5 10 15

Gln Lys Lys Ser Gln Glu Pro Leu Ser Thr Thr Trp Ser Pro Gly Lys
20 25 30

Lys Val His Gln Gln Ile Ile Tyr Gly Ser Glu Gln Ile Pro Lys Pro
35 40 45

His Val Ile Val
50

<210> 1285
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R262I"

<400> 1285
Leu Glu Pro Leu Leu His Ala Ile Ala Lys Asp Pro Lys Met Val Val
1 5 10 15

Cys Pro Leu Ile Asp Val Ile Asp Asp Ile Ile Thr Leu Glu Tyr Lys
20 25 30

Pro Ser Pro Leu Val Arg Gly Thr Phe Asp Trp Asn Leu Gln Phe Lys
35 40 45

Trp Asp Asn Val
50

<210> 1286
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K567del"

<400> 1286
Trp Gly Tyr Arg Lys Asp Arg Thr Leu Phe His Pro Val Ser Asn Ser
1 5 10 15

Cys Met Asp Cys Asn Pro Ala Glu Lys Ile Phe Met Ala Arg Cys Asp
20 25 30

Pro Leu Ser Glu Thr Gln Gln Trp Ile Phe Glu His Ile Asn Met Thr
35 40 45

Val Leu Glu Lys Phe
50

<210> 1287
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P42A"

<400> 1287
Leu Leu Leu Leu Pro Pro Arg Leu Leu Ala Arg Pro Ser Leu Leu Leu
1 5 10 15

Arg Arg Ser Leu Ser Ala Ala Ser Cys Ala Ala Pro Ile Ser Leu Pro
20 25 30

Ala Ala Ala Ser Arg Ser Ser Met Asp Gly Ala Gly Ala Glu Glu Val
35 40 45

Leu Ala Pro Leu
50

<210> 1288
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.K807fs"

<400> 1288
Ile Glu Ser Met Gln Ile Asn Gly Ser Val Leu Lys Asn Gly Ser Leu
1 5 10 15

Thr Asn His Phe Ser Phe Glu Lys Lys Arg Pro Glu Trp Leu Ser
20 25 30

<210> 1289
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D189A"

<400> 1289
Ala Ala Pro Thr Leu Val Gln Leu Glu Glu Glu Ile Glu Glu Glu Val
1 5 10 15

Arg Arg Glu Leu Ala Leu Pro Pro Pro Ala Ala Pro Ser Pro Pro Ala
20 25 30

Pro Pro Arg Arg Gln Pro Cys His Phe Arg Asn Leu Asp Gln Met Val
35 40 45

Gln Ser Leu Val
50

<210> 1290
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G150fs"

<400> 1290
Cys Asp Arg Lys Gly Thr Gln Ala Cys Gln Asp Leu Met Gly Asn Phe

1 5 10 15

Phe Cys Leu Cys Lys Ala Gly Trp Gly Ala Gly Ser Ala Thr Lys Met
20 25 30

Ser Thr Asn Ala Ala Arg Arg Thr Gly Ala Ala Ser Arg Ser Ala Thr
35 40 45

Thr Ser Arg Val Ala Ser Thr Val Pro Ala Thr Ala Ala Ser Ser Ser
50 55 60

Pro Leu Met Ala Gly Pro Ala Lys Thr
65 70

<210> 1291
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R313S"

<400> 1291
Glu Glu Met Ser Glu Met Gln Lys Gln Leu Ala Asn Tyr Glu Arg Asp
1 5 10 15

Lys Gln Ile Leu Leu Cys Thr Lys Ala Ser Ser Leu Lys Val Arg Glu
20 25 30

Lys Glu Leu Lys Asp Leu Gln Trp Glu His Glu Val Leu Glu Gln Arg
35 40 45

Phe Thr Lys Val
50

<210> 1292
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N334fs"

<400> 1292
Ala Arg Arg Ala Gly Thr Ser Cys Ala Asn Cys Gln Thr Thr Thr Thr
1 5 10 15

Thr Leu Trp Arg Arg Asn Ala Asn Gly Gly Pro Cys Leu Gln Cys Leu
20 25 30

Trp Ala Leu Leu Gln Ala Ser Gln Tyr
35 40

<210> 1293
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H400fs"

<400> 1293
Cys Lys Lys Val His Asp Ser Leu Glu Asp Phe Pro Lys Asn Ser Ser
1 5 10 15

Phe Asn Pro Ala Ala Leu Ser Arg His Asn Val Leu Pro Glu Pro His
20 25 30

Leu Ala Leu Gln Pro Leu Gln Pro His Ala Asp His Ala His Ala Asp
35 40 45

Ala Pro Ala Ile Gln Pro Val Leu Trp Thr Thr Pro Pro Leu Gln His
50 55 60

Gly His Arg His Gly Leu Glu Pro Cys Ser Met Leu Thr Gly Pro Pro
65 70 75 80

Ala Arg Val Pro Ala Val Pro Phe Asp Leu His Phe Cys Arg Ser Ser
85 90 95

Ile Met Lys Pro Lys Arg Asp Gly Tyr Met Phe Leu Lys Ala Glu Ser
100 105 110

Lys Ile Met Phe Ala Thr Leu Gln Arg Ser Ser Leu Trp Cys Leu Cys
115 120 125

Ser Asn His
130

<210> 1294
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S408fs"

<400> 1294
Glu Asp Phe Pro Lys Asn Ser Ser Phe Asn Pro Ala Ala Leu Ser Arg
1 5 10 15

His Met Ser Ser Leu Ser His Ile Ser Ala Leu Gln Pro Leu Gln Pro
20 25 30

His Ala Asp His Ala His Ala Asp Ala Pro Ala Ile Gln Pro Val Leu
35 40 45

Trp Thr Thr Pro Pro Leu Gln His Gly His Arg His Gly Leu Glu Pro
50 55 60

Cys Ser Met Leu Thr Gly Pro Pro Ala Arg Val Pro Ala Val Pro Phe
65 70 75 80

Asp Leu His Phe Cys Arg Ser Ser Ile Met Lys Pro Lys Arg Asp Gly
85 90 95

Tyr Met Phe Leu Lys Ala Glu Ser Lys Ile Met Phe Ala Thr Leu Gln
100 105 110

Arg Ser Ser Leu Trp Cys Leu Cys Ser Asn His
115 120

<210> 1295
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S408fs"

<400> 1295
Glu Asp Phe Pro Lys Asn Ser Ser Phe Asn Pro Ala Ala Leu Ser Arg
1 5 10 15

His Met Ser Ser Leu Ser His Ile Ser Ala Leu Gln Pro Leu Gln Pro
20 25 30

His Ala Asp His Ala His Ala Asp Ala Pro Ala Ile Gln Pro Val Leu
35 40 45

Trp Thr Thr Pro Pro Leu Gln His Gly His Arg His Gly Leu Glu Pro
50 55 60

Cys Ser Met Leu Thr Gly Pro Pro Ala Arg Val Pro Ala Val Pro Phe
65 70 75 80

Asp Leu His Phe Cys Arg Ser Ser Ile Met Lys Pro Lys Arg Asp Gly
85 90 95

Tyr Met Phe Leu Lys Ala Glu Ser Lys Ile Met Phe Ala Thr Leu Gln
100 105 110

Arg Ser Ser Leu Trp Cys Leu Cys Ser Asn His
115 120

<210> 1296
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S430fs"

<400> 1296
Ile Ser Pro Phe Ser His Ser Ser His Met Leu Thr Thr Pro Thr Pro

1 5 10 15

Met His Pro Pro Ser Ser Leu Ser Phe Trp Thr Thr Pro Pro Leu Gln
20 25 30

His Gly His Arg His Gly Leu Glu Pro Cys Ser Met Leu Thr Gly Pro
35 40 45

Pro Ala Arg Val Pro Ala Val Pro Phe Asp Leu His Phe Cys Arg Ser
50 55 60

Ser Ile Met Lys Pro Lys Arg Asp Gly Tyr Met Phe Leu Lys Ala Glu
65 70 75 80

Ser Lys Ile Met Phe Ala Thr Leu Gln Arg Ser Ser Leu Trp Cys Leu
85 90 95

Cys Ser Asn His
100

<210> 1297
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H434fs"

<400> 1297
Phe Ser His Ser Ser His Met Leu Thr Thr Pro Thr Pro Met His Pro
1 5 10 15

Pro Ser Ser Leu Ser Phe Gly Pro His Pro Pro Leu Gln His Gly His
20 25 30

Arg His Gly Leu Glu Pro Cys Ser Met Leu Thr Gly Pro Pro Ala Arg
35 40 45

Val Pro Ala Val Pro Phe Asp Leu His Phe Cys Arg Ser Ser Ile Met
50 55 60

Lys Pro Lys Arg Asp Gly Tyr Met Phe Leu Lys Ala Glu Ser Lys Ile
65 70 75 80

Met Phe Ala Thr Leu Gln Arg Ser Ser Leu Trp Cys Leu Cys Ser Asn
85 90 95

His

<210> 1298
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H435fs"

<400> 1298
His Ser Ser His Met Leu Thr Thr Pro Thr Pro Met His Pro Pro Ser
1 5 10 15

Ser Leu Ser Phe Gly Pro His His Pro Leu Gln His Gly His Arg His
20 25 30

Gly Leu Glu Pro Cys Ser Met Leu Thr Gly Pro Pro Ala Arg Val Pro
35 40 45

Ala Val Pro Phe Asp Leu His Phe Cys Arg Ser Ser Ile Met Lys Pro
50 55 60

Lys Arg Asp Gly Tyr Met Phe Leu Lys Ala Glu Ser Lys Ile Met Phe
65 70 75 80

Ala Thr Leu Gln Arg Ser Ser Leu Trp Cys Leu Cys Ser Asn His
85 90 95

<210> 1299
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.M443I"

<400> 1299
Thr Thr Pro Thr Pro Met His Pro Pro Ser Ser Leu Ser Phe Gly Pro
1 5 10 15

His His Pro Ser Ser Met Val Thr Ala Ile Ile Gly
20 25

<210> 1300
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L328fs"

<400> 1300
Arg Arg Leu Ser Ala Ala Arg Arg Ala Gly Thr Ser Cys Ala Asn Cys
1 5 10 15

Gln Thr Thr Thr Thr Thr Leu Trp Arg Leu Glu Glu Glu Cys Gln Trp
20 25 30

Gly Pro Cys Leu Gln Cys Leu Trp Ala Leu Leu Gln Ala Ser Gln Tyr
35 40 45

<210> 1301
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G431fs"

<400> 1301
Gln Ala Glu Leu Lys Arg Leu Ser Glu Leu Leu Thr Glu Ser Ile Ser
1 5 10 15

Arg Gly Thr Phe Phe Val Pro Gly Gly Ala Gln Tyr Leu Leu Arg Ser
20 25 30

Lys Lys Glu Asp
35

<210> 1302
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L389fs"

<400> 1302
Val Ser Leu Leu Lys Arg Asn Asn Cys Gly Lys Ala Leu Asp Ile Ala
1 5 10 15

Arg Gln Ala Arg Asp Met Leu Gly Gly Met Gly Phe Leu Thr Ser Ile
20 25 30

Thr

<210> 1303
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R82C"

<400> 1303
Glu Glu Gln Leu Thr Thr Asp Glu Ile Leu Ile Arg Asp Thr Phe Arg
1 5 10 15

Thr Tyr Cys Gln Glu Arg Leu Met Pro Cys Cys Ile Leu Leu Ala Asn
20 25 30

Arg Asn Glu Val Phe His Arg Glu Ile Ile Ser Glu Met Gly Glu Leu

35 40 45

Gly Val Leu Gly
50

<210> 1304
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T307A"

<400> 1304
Arg Val Leu Lys Arg Lys Thr Phe Asn Lys Val Leu Gly His Val Asn
1 5 10 15

Asn Ile Leu Ile Ser Ala Val Leu Pro Ala Ala Ala Phe Arg Val Ala
20 25 30

Lys Lys Arg Ala Pro Lys Val Leu Gly Thr Thr Leu Val Val Gly Leu
35 40 45

Leu Ala Gly Val
50

<210> 1305
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E105fs"

<400> 1305
Gly Gln Thr Gly Gly Leu Thr Gln Pro Lys Lys Asp Glu Pro Lys Lys
1 5 10 15

Leu Pro Pro Arg Pro Gly Gly Pro Glu Thr Gln Ala Arg Thr Pro Ser
20 25 30

Pro Asn Lys Ala Gly Tyr Ser Pro Asp Cys Asp Pro Lys Arg Thr Ala
35 40 45

Ser Arg Arg Gln Gly Thr Pro Lys Ser Arg Ile Cys Pro Gln Leu Leu
50 55 60

Pro Ala Glu Glu Gly Gln Gly Ala Arg Ala Pro Thr Arg Ala Gln Gly
65 70 75 80

Ala Val Ser Pro Thr Pro His His Thr Pro Arg Val His Ala Leu Ala
85 90 95

Val Gln Asp Ala Val Arg Cys
100

<210> 1306
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G593fs"

<400> 1306
Ser Val Cys Ser Asp Asn Ser Tyr Asp Thr Tyr Ala Asn Ser Thr Ala
1 5 10 15

Thr Pro Val Gly Pro Arg Gly Gly Gly Gln Pro His Gln Asp Pro His
20 25 30

Arg Ala Glu Trp Ala Leu Ala Glu Asp Met Ser Val Pro Pro Val Pro
35 40 45

Asp Thr Glu Ala Gly Glu Pro Arg Arg Ala Gly Gly Ser Val Ser Glu
50 55 60

Leu Gly Val Leu Trp Glu Arg Ala Pro Gln Pro Pro Cys Gly Leu Gln
65 70 75 80

Pro Leu Val Ser Arg Ser Leu Ser
85

<210> 1307
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R268L"

<400> 1307
Arg Asp Ser Lys Glu Lys Asn Glu Arg Arg Leu Ala Tyr Gln Lys Arg
1 5 10 15

Lys Glu Ser Met Pro Arg Lys Ala Arg Leu Leu Phe Trp Gly Lys Ile
20 25 30

Val Ala Lys Asn Asn Lys Asn Met Ala Phe Lys Leu Lys Ser Lys Ser
35 40 45

Cys His Asp Leu
50

<210> 1308
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S509L"

<400> 1308
Val Met Ser Phe Gln Ser His Met Thr Leu Lys Pro Thr Cys Glu Ile
1 5 10 15

Phe His Lys Gln Asn Ser Lys Leu Asn Leu Leu Gly Ile Ser Pro Asp
20 25 30

Pro Thr Leu Pro Gln Glu Ser Ile Ser Ala Ser Leu Asn Ser Leu Leu
35 40 45

Leu Pro Lys Asn
    50

<210> 1309
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.A17fs"

<400> 1309
Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
1   5   10   15

Ala Pro Arg Leu Pro Arg Leu Ala Glu Glu Ala Gly
            20   25

<210> 1310
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q308K"

<400> 1310
Leu Gly Thr Val Leu Gln Val Gln Cys Thr Cys Arg Thr Ile Thr Gln
1   5   10   15

Ser Glu Glu Ser Leu Cys Lys Ile Phe Lys Lys His Met Leu His Arg
            20   25   30

Lys Ser Cys Phe Asn Tyr Pro Thr Leu Ser Asn Val Lys Gly Met Ala
        35   40   45

Leu Tyr Thr Arg
    50

<210> 1311

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A63V"

<400> 1311
Met Ser Glu Gln Asp Trp Ser Ala Ile Gln Asn Phe Cys Glu Gln Val
1 5 10 15

Asn Thr Asp Pro Asn Gly Pro Thr His Val Val Pro Trp Leu Leu Ala
20 25 30

His Lys Ile Gln Ser Pro Gln Glu Lys Glu Ala Leu Tyr Ala Leu Thr
35 40 45

Val Leu Glu Met
50

<210> 1312
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R227H"

<400> 1312
Pro Asn Phe Glu Glu Gly Gly Pro Thr Ser Val Gly Arg Lys His Glu
1 5 10 15

Phe Ile Arg Ser Glu Ser Glu Asn Trp His His Ile Phe Arg Glu Glu
20 25 30

Gln Asn Gly Glu Asp Glu Asp Gly Gly Trp Arg Leu Ala Gly Ser Arg
35 40 45

Arg Asp Gly Glu
50

<210> 1313
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V276fs"

<400> 1313
Leu Leu Lys Leu Lys Tyr Asp Glu Lys Ile Lys Asn Ile Arg Glu Glu
1 5 10 15

Ala Glu Arg Asn Ile Phe Lys Asp Val Leu Ile Gly Phe Gly Arg Cys
20 25 30

Phe Gln Lys Tyr Gly Ile Gly Phe Cys Arg Asn Val Ser Phe Ile Leu
35 40 45

Pro Asn Leu Leu
50

<210> 1314
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A544S"

<400> 1314
Ser Cys Cys Glu Lys Gly Asp Thr Phe Phe Val Leu Val Phe Gln Leu
1 5 10 15

Gly Arg Phe Thr Glu Glu Asp Lys Thr Ser Ser Val Ala Lys Leu Glu
20 25 30

Ala Ile Phe Gly Ala Asp Phe Thr Lys Tyr Ala Ile Met Leu Phe Thr
35 40 45

Arg Lys Glu Asp
50

<210> 1315
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G227fs"

<400> 1315
Ser Arg Ser Ser Lys Cys Pro Val Glu Ala Lys Val Thr Ser Gly Arg
1 5 10 15

Glu Thr Leu Arg Leu Arg Ser Gly Gly Leu Pro Gln Trp Arg Lys Arg
20 25 30

Pro Val Ser Leu Arg Arg Arg His Leu Gly Arg Leu Met Thr Cys Trp
35 40 45

Lys Ala Thr Trp Ala Phe Gly Thr Pro Ser Trp Arg Pro Pro Trp Trp
50 55 60

Arg Arg Pro Arg Arg Gln Arg Ala Pro Arg Ser Leu His Ala Val
65 70 75

<210> 1316
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R123L"

<400> 1316
Lys Val His Pro Asn Lys Ala Glu Phe Ile Arg Ala Lys Tyr Gln Met
1 5 10 15

Leu Ala Phe Val His Arg Leu Pro Cys Leu Leu Asp Asp Asp Ser Val
20 25 30

Thr Ala Lys Asp Leu Ser Lys Gln Leu His Ser Ser Val Arg Thr Gly
35 40 45

Asn Leu Glu Thr
50

<210> 1317
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A311fs"

<400> 1317
Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr
1 5 10 15

Asn Lys Gln Ala Ser Glu Gln Asn Trp Val Ile Thr Val Gln Asn Lys
20 25 30

Ile Glu Trp Gly Arg Arg Glu Ala Pro Ser Leu Thr Pro Met His Ser
35 40 45

Leu Leu Ile Ser Pro Met Ile Thr Arg Ile Leu Lys Asn
50 55 60

<210> 1318
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R160H"

<400> 1318
Leu Ile Phe Lys Leu Ile Ile Glu Phe Leu Phe Leu Tyr Leu Leu His

1 5 10 15

Thr Leu Trp His Gly Phe Asn Met Pro His His Leu Val Gln Cys Ala
20 25 30

Asn Val Ala Pro Cys Pro Asn Ile Val Asp Cys Tyr Ile Ala Arg Pro
35 40 45

Thr Glu Lys Lys
50

<210> 1319
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R22S"

<400> 1319
Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15

Ser Thr Val Leu Ser Ser Ser Ile Trp Leu Ser Val Val Phe Ile Phe
20 25 30

Arg Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu
35 40 45

<210> 1320
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I407M"

<400> 1320
Lys Met Pro Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp
1 5 10 15

Asp Ala Leu Lys Tyr Leu Gly Glu Pro Met Met Lys Ser Glu Lys Pro
20 25 30

Ile Asn Met Glu Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe
35 40 45

Gly Tyr Ile Leu
50

<210> 1321
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W272fs"

<400> 1321
Gln Glu Gln Leu Val His His Ile Asn Ser Glu His Ile His Gly Glu
1 5 10 15

Arg Lys Glu Phe Val Cys His Trp Gly Ala Ala Pro Gly Ser
20 25 30

<210> 1322
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P998L"

<400> 1322
Val His Ala Pro Arg Arg Cys Ser Asp Gly Gly Ala His Gly Tyr Gly
1 5 10 15

Arg Arg His Leu Gln Pro His Asp Ala Leu Leu Gly His Gly Val Arg
20 25 30

Arg Ala Ser Asp Pro Val Arg Thr Gly Ser Glu Gly Leu Ala Leu Pro
35 40 45

Arg Val Pro Arg
50

<210> 1323
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1033fs"

<400> 1323
Pro Val Arg Thr Gly Ser Glu Gly Leu Ala Leu Pro Arg Val Pro Arg
1 5 10 15

Phe Ser Ser Leu Ser Ser Cys Asn Pro Arg Arg Trp Pro Arg Pro Arg
20 25 30

Arg Ser Ala Val Ser Cys Phe Arg Ile Thr Arg Gly Pro Arg Ala Ala
35 40 45

Ser Pro Glu Thr Ser Thr Arg Pro Pro Val Leu Pro Ala Ser Pro Arg
50 55 60

Thr Ser Pro Trp Ser Pro
65 70

<210> 1324
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G92fs"

<400> 1324

Ile Pro Arg Gly Ser Asn Leu Arg Phe Met Thr Trp Asp Val Ala Leu
1 5 10 15

Ser Arg Thr Ala Arg Ala Trp Gly Lys Asn Val Cys Leu Arg Ile Ile
20 25 30

Phe Ile Tyr Lys Met Tyr Lys Trp Ser Ile Leu Asn Phe Met Val Leu
35 40 45

Val Lys Ile Cys Gly Ser Ala Leu Lys Met Asn Leu Leu Gln Val Leu
50 55 60

Leu Ser Glu Val Gly Met Gln Arg Arg Lys Cys Thr Ile Leu Lys Met
65 70 75 80

Ala Val Ala Leu Glu Thr Val Leu Ile Ile Phe Ser Leu Phe Gly Thr
85 90 95

Thr Leu Thr Lys Leu Val Val Leu Leu Leu His Val Gln Lys Leu Asp
100 105 110

Ile Leu Tyr Met Gln Gln Phe Ser Tyr Ala Thr Met Arg Gln Glu Glu
115 120 125

His

<210> 1325
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q223fs"

<400> 1325
Lys Leu Glu Leu Gln Gly Val Lys Gly Gly Val Asp His Ala Ala Ala
1 5 10 15

Phe Gly Arg Ile Ala Phe Ser Cys Pro Pro Glu Arg Val Ala Arg Leu
20 25 30

Arg Arg Leu Asp Glu Lys Gly Glu Pro Glu Asp Ser Asp Ser Pro Gly

35 40 45

Glu Pro Gly His Pro Arg Glu Ser Asn Ser Thr Gly Gly His Ser Gly
50 55 60

Arg Pro
65

<210> 1326
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L454I"

<400> 1326
Asp Thr Ile Ser Arg Ala Cys Phe Pro Leu Ala Phe Leu Ile Phe Asn
1 5 10 15

Ile Phe Tyr Trp Val Ile Tyr Lys Ile Ile Ile Arg His Glu Asp Ile
20 25 30

His Gln Gln Gln Asp
35

<210> 1327
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F132L"

<400> 1327
Ala Tyr Ser Glu Tyr Pro Asp Asp Ser Leu Asp Leu Asp Pro Ser Met
1 5 10 15

Leu Asp Ser Ile Trp Lys Pro Asp Leu Leu Leu Phe Ala Asn Glu Lys
20 25 30

Gly Ala Asn Phe His Glu Val Thr Thr Asp Asn Lys Leu Leu Arg Ile
35 40 45

Phe Lys Asn Gly
50

<210> 1328
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A178V"

<400> 1328
Ile Tyr Leu Asp Asp Asp Val Ile Val Gln Gly Asp Ile Gln Glu Leu
1 5 10 15

Tyr Asp Thr Thr Leu Ala Leu Gly His Val Val Ala Ala Phe Ser Asp
20 25 30

Asp Cys Asp Leu Pro Ser Ala Gln Asp Ile Asn Arg Leu Val Gly Leu
35 40 45

Gln Asn Thr Tyr
50

<210> 1329
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q389R"

<400> 1329
Arg His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala
1 5 10 15

Leu Arg Leu Ala Glu Leu Ala Arg Arg Arg Arg Arg Arg Gln Ala
20 25 30

Arg Arg Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys
35 40 45

Tyr Gln Ala Pro
50

<210> 1330
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G380fs"

<400> 1330
Cys Tyr Val Asp Met Ser Thr Val Asp Ala Asp Thr Val Thr Glu Leu
1 5 10 15

Ala Gln Val Ile Val Ser Arg Gly Gly Ala Leu Ser Gly Ser Pro Arg
20 25 30

Leu Arg Glu Ser Ala Ala Val
35

<210> 1331
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R200G"

<400> 1331
Lys Tyr Phe Leu Asp Asn Leu Asp Lys Leu Gly Glu Pro Asp Tyr Ile
1 5 10 15

Pro Ser Gln Gln Asp Ile Leu Leu Ala Gly Gly Arg Pro Thr Lys Gly
20 25 30

Ile His Glu Tyr Asp Phe Glu Ile Lys Asn Val Pro Phe Lys Met Val
35 40 45

Asp Val Gly Gly
50

<210> 1332
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P283Q"

<400> 1332
Lys Trp Phe Thr Asp Thr Ser Ile Ile Leu Phe Leu Asn Lys Lys Asp
1 5 10 15

Ile Phe Glu Glu Lys Ile Lys Lys Ser Gln Gln Leu Thr Ile Cys Phe
20 25 30

Pro Glu Tyr Thr Gly Pro Ser Ala Phe Thr Glu Ala Val Ala Tyr Ile
35 40 45

Gln Ala Gln Tyr
50

<210> 1333
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R844C"

<400> 1333
Gln Tyr Phe Leu Asp Lys Ile Asp Val Ile Lys Gln Ala Asp Tyr Val

1 5 10 15

Pro Ser Asp Gln Asp Leu Leu Arg Cys Cys Cys Val Leu Thr Ser Gly
20 25 30

Ile Phe Glu Thr Lys Phe Gln Val Asp Lys Val Asn Phe His Met Phe
35 40 45

Asp Val Gly Gly
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<210> 1334
<211> 52
<212> PRT
<213> Artificial Sequence

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<400> 1334
Gln Tyr Phe Leu Asp Lys Ile Asp Val Ile Lys Gln Ala Asp Tyr Val
1 5 10 15

Pro Ser Asp Gln Asp Leu Leu Arg Cys His His Val Leu Thr Ser Gly
20 25 30

Ile Phe Glu Thr Lys Phe Gln Val Asp Lys Val Asn Phe His Met Phe
35 40 45

Asp Val Gly Gly
50

<210> 1335
<211> 52
<212> PRT
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<400> 1335
Leu Ala Lys Ile Tyr Ala Met His Trp Gly Thr Asp Ser Arg Leu Leu
1 5 10 15

Val Ser Ala Ser Gln Asp Gly Lys Leu Thr Thr Ile Trp Asp Ser Tyr
20 25 30

Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg Ser Ser Trp Val Met
35 40 45

Thr Cys Ala Tyr
50

<210> 1336
<211> 46
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.T68fs"

<400> 1336
Cys Glu Glu His Ala Arg Ser Asp Pro Leu Leu Ile Gly Ile Pro Thr
1 5 10 15

Ser Glu Asn Pro Phe Lys Asp Lys Lys Leu Ala Ser Ser Tyr Ser Gly
20 25 30

Ile Glu Lys Gln Leu Leu Ala Ser Ser Gln Gln Arg Lys Leu
35 40 45

<210> 1337
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 1337
Ala Ile Ser Pro Thr His Pro Gly Glu Gly Leu Val Leu Arg Pro Leu
1 5 10 15

Cys Thr Ala Asp Leu Asn Arg Gly Phe Leu Arg Tyr Trp Val Ser
20 25 30

<210> 1338
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R1189Q"

<400> 1338
Val Lys Ala Val Leu Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro
1 5 10 15

Ser Gln Phe Glu Leu Pro Arg Glu Tyr Gln Gln Asn Arg Phe Leu His
20 25 30

Met His Glu Leu Gln Glu Trp Arg Ala Tyr Arg Asp Lys Leu Lys Phe
35 40 45

Trp Thr His Cys
50

<210> 1339
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q1536H"

<400> 1339
Lys Lys Glu Ser Asn Leu Glu Thr Glu Leu Lys Ser Gln Thr Ala Arg
1 5 10 15

Ile Met Glu Leu Glu Asp His Ile Thr His His Lys Thr Ile Glu Ile
20 25 30

Glu Ser Leu Asn Glu Val Leu Lys Asn Tyr Asn Gln Gln Lys Asp Ile
35 40 45

Glu His Lys Glu
50

<210> 1340
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L492I"

<400> 1340
Glu Leu Glu Glu Leu Arg His Glu Lys Glu Met Gln Arg Glu Glu Ile
1 5 10 15

Gln Lys Leu Met Gly Gln Ile His Gln Ile Ile Arg Ser Glu Leu Gln
20 25 30

Asp Met Glu Ala Gln Gln Val Asn Glu Ala Glu Ser Ala Arg Glu Gln
35 40 45

Leu Gln Asp Leu
50

<210> 1341
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R355W"

<400> 1341
Ile Leu Asn Thr Pro Asp Leu Arg Lys Gln Trp Leu Gln Glu Val Lys

1 5 10 15

Val Met Ala Asp Arg Ile Ile Gly Met Trp Trp Thr Gln Leu Val Ser
20 25 30

Asn Leu Lys Lys Glu Gly Ser Thr His Asn Trp Gln His Ile Thr Asp
35 40 45

Gln Ile Gly Met
50

<210> 1342
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S41L"

<400> 1342
Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser Ala Val Gln Arg
1 5 10 15

Gly Tyr Gly Asn Pro Ile Glu Ala Ser Leu Leu Tyr Gly Leu Asp Leu
20 25 30

Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro
35 40 45

Cys Gln Asn Tyr
50

<210> 1343
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K210fs"

<400> 1343
Phe Leu Ala Arg Leu Lys Gly Gln Asp Pro Gly Ala Pro Gln Leu Gln
1 5 10 15

Ser Glu Ser Lys Pro Pro Lys Lys Lys Glu Lys Glu Lys Glu Ala Glu
20 25 30

Arg Gly Gly Arg Ser Tyr Ser Ile
35 40

<210> 1344
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K210fs"

<400> 1344
Ala Phe Leu Ala Arg Leu Lys Gly Gln Asp Pro Gly Ala Pro Gln Leu
1 5 10 15

Gln Ser Glu Ser Lys Pro Pro Lys Lys Arg Lys Arg Lys Gly Gly Arg
20 25 30

Lys Arg Arg Lys Lys Leu Gln His Leu Lys Gly Met Met Gln Met Arg
35 40 45

Ser Thr Gln Asn Met Leu Ser Arg Thr Ser Glu Lys Ala Arg Arg Arg
50 55 60

Lys Gly Asp Ile Lys Lys Glu Arg Ser Gln Met Lys Glu Arg Val Gln
65 70 75 80

Leu Lys Gly Met Arg Arg Arg Thr Leu Gln Glu Gln Val Gly Leu Gly
85 90 95

Asn

<210> 1345
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="p.R347L"

<400> 1345
Leu Val Asn Asp Ala Val Leu Gln Ala His Leu Asn Gly Gln Lys Leu
1 5 10 15

Leu Glu Gln Val Asn Arg Ile Cys Gly Leu Leu Pro Val Arg Thr Pro
20 25 30

Thr Gln Ser Pro Arg Cys Ser Phe Asp Gln Ser Lys Glu Lys His Gly
35 40 45

Met Lys Thr Thr
50

<210> 1346
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A214T"

<400> 1346
Cys Val Ser Lys Tyr Thr Asp Gln Leu Lys Pro Phe Gly Asp Val Pro
1 5 10 15

Arg Lys Leu Lys Ile Gln Val Thr Arg Thr Thr Phe Ile Ala Ala Arg
20 25 30

Thr Phe Val Gln Gly Leu Thr Val Gly Arg Glu Val Ala Asn Arg Val
35 40 45

Ser Lys Val Ser
50

<210> 1347
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R717Q"

<400> 1347
Thr Arg Met Tyr Ala Leu Thr Ser Asp Ala Gln Pro Leu Leu Leu Ser
1 5 10 15

Thr Phe Ser Gly Asp Arg Arg Phe Ser Gln Gln Phe Gly Gly Val Leu
20 25 30

His Leu Ser Asp Leu Asp Asp Asp Gly Leu Asp Glu Ile Ile Met Ala
35 40 45

Ala Pro Leu Arg
50

<210> 1348
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.A50V"

<400> 1348
Ile Pro Tyr Ala Ser Leu Ile Ala Thr Ile Leu Leu Tyr Ala Gly Val
1 5 10 15

Ala Leu Phe Cys Gly Cys Gly His Glu Val Val Leu Ser Gly Thr Val
20 25 30

Asn Ile Leu Gln Thr Tyr Phe Glu Met Ala Arg Thr Ala Gly Asp Thr
35 40 45

Leu Asp Val Phe

50

<210> 1349
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I174M"

<400> 1349
Gly Gln Ser His His Asn Val Phe Pro Asp Gly Lys Pro Phe Pro His
1 5 10 15

His Pro Gly Trp Arg Arg Trp Asn Phe Met Met Tyr Val Phe His Thr
20 25 30

Leu Gly Gln Tyr Phe Gln Lys Leu Gly Arg Cys Ser Val Arg Val Ser
35 40 45

Val Asn Thr Ala
50

<210> 1350
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1350
Met Glu Cys Leu Leu Phe Pro Gly Ile Ser Ala Pro Gly Cys Lys Ile
1 5 10 15

Ala Thr

<210> 1351
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R443G"

<400> 1351
Thr Ala Leu Pro Leu Asn Phe Ser Arg Lys Phe Ile Asp Trp Lys Gly
1 5 10 15

Ile Pro Val Asn Lys Ser Gln Leu Lys Gly Gly Gly Tyr Ser Tyr Gln
20 25 30

Ile Lys Met Cys Pro Gln Asn Thr Ser Ile Pro Ile Arg Gly Arg Val
35 40 45

Leu Ile Gly Ser
50

<210> 1352
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.S1283Y"

<400> 1352
Lys Asp Gln Met Thr Ile Ser Leu Gly Lys Thr Pro Arg Thr Met Glu
1 5 10 15

Val Thr Glu Met Ser Pro Ser Lys Asn Tyr Tyr Phe Ile Ser Tyr Ser
20 25 30

Arg Gly Thr Pro Ser Leu Glu Met Thr Asp Thr Gly Phe Pro Glu Thr
35 40 45

Thr Lys Ile Ser
50

<210> 1353
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L630P"

<400> 1353
Pro Arg Thr Pro His Cys Val Gly Lys Lys Val Pro Gln Pro Val Gly
1 5 10 15

Ala Ala Asp Leu Ala Pro Asp Thr Ser Pro Pro Cys Arg Lys Glu Gly
20 25 30

Ser Ser Ala Ser Arg Ser Cys Arg Pro Gly Pro Gly His Leu Thr Arg
35 40 45

Arg Glu Glu Asp
50

<210> 1354
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R113Q"

<400> 1354
Leu Ser Asn Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly
1 5 10 15

Leu Ser Leu Leu Glu Arg Leu Asp Leu Gln Gln Asn Asn Leu Ile Ser
20 25 30

Ser Ile Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu
35 40 45

Asp Leu Thr Asn
    50

<210> 1355
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.G240C"

<400> 1355
Lys Ile Ser Lys Met Ser Leu Ala Asn Ile Tyr Leu Glu Ser Lys Gly
1   5   10   15

Ser Ser Val Cys Gln Val Thr Ala Ile Cys Cys Val Thr Val Ile Leu
            20   25   30

Leu Tyr Thr Ser Arg Ala Cys Tyr Asn Leu Phe Ile Leu Ser Phe Ser
        35   40   45

Gln Asn Lys Ser
    50

<210> 1356
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.F754L"

<400> 1356
Pro Val Pro Ser Gly Cys Ala Ser Leu Ser Ser Gln His Ser Tyr Phe
1   5   10   15

Asp Thr Glu Ser Ser Ser Ser Asp Glu Leu Leu Phe Cys Arg Cys His
            20   25   30

Arg Pro Tyr Cys Glu Ile Cys Phe Gln Ser Ser Ser Asp Ser Ser Asp

35 40 45

Ser Gly Thr Ser
50

<210> 1357
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D566N"

<400> 1357
Leu Ile Gly Trp Thr Ser Ser Val Cys Gln Asn Leu Glu Lys Gln Ile
1 5 10 15

Ser Leu Ile Gly Gln Gly Lys Thr Ser Asn Asn His Leu Ile Phe Asn
20 25 30

Met Cys Leu Ile Asp Arg Trp Asp Tyr Met Thr Ala Val Ala Glu Phe
35 40 45

Leu Phe Leu Leu
50

<210> 1358
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P762T"

<400> 1358
Asn Pro His Leu Gln Lys Lys Arg Cys Ser Lys Lys Gly Leu Gly Arg
1 5 10 15

Ser Ile Met Arg Arg Ile Thr Glu Ile Thr Thr Glu Thr Val Ser Arg
20 25 30

Gln Cys Ser Lys Glu Asp Lys Glu Gly Ala Asp His Gly Thr Ala Lys
35 40 45

Gly Thr Ala Leu
50

<210> 1359
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.G517fs"

<400> 1359
Ala Glu Ala Lys Ile Asn Leu Phe Gly Glu Glu Ala Leu Pro Gly Val
1 5 10 15

Leu Val Thr Ala Arg Thr Val Pro Gly Ala Ala Ser Gly Ala Ala Glu
20 25 30

Ala Ala Glu Leu Leu
35

<210> 1360
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R216H"

<400> 1360
Phe Thr Leu Phe Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile
1 5 10 15

Val Cys Phe Thr Tyr Phe Asn Ile Phe His His Ile Cys Gln Gln His
20 25 30

Thr Lys Asp Ile Ser Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly
35 40 45

Glu Thr Gly Glu
50

<210> 1361
<211> 110
<212> PRT
<213> Artificial Sequence

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<223> /note="p.AAAAATAAGGPDTGEWGPPA36del"

<400> 1361
Ala Ala Met Asn Ala Ser Ala Ala Ser Leu Asn Asp Ser Gln Val Val
1 5 10 15

Val Val Ala Ala Glu Gly Ala Ala Ala Leu Gly Ala Gly Gly Gly Ala
20 25 30

Asn Gly Ser Leu Glu Leu Ser Ser Gln Leu Ser Ala Gly Pro Pro Gly
35 40 45

Leu Leu Leu Pro Ala Val Asn Pro Trp Asp Val Leu Leu Cys Val Ser
50 55 60

Gly Thr Val Ile Ala Gly Glu Asn Ala Leu Val Val Ala Leu Ile Ala
65 70 75 80

Ser Thr Pro Ala Leu Arg Thr Pro Met Phe Val Leu Val Gly Ser Leu
85 90 95

Ala Thr Ala Asp Leu Leu Ala Gly Cys Gly Leu Ile Leu His
100 105 110

<210> 1362
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.R4142W"

<400> 1362
Arg Phe Thr Ile Gln Leu Ile Ser Ile Asp Glu Val Glu Ile Ser Pro
1 5 10 15

Val Lys Gly Ser Ala Ser Ile Ile Ile Trp Trp Gly Asp Lys Arg Ala
20 25 30

Ser Gly Glu Val Gly Ile Ala Pro Ser Ser Arg His Ile Leu Ile Gly
35 40 45

Glu Pro Ser Ala
50

<210> 1363
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G4307W"

<400> 1363
Gln Arg Val Asn Ile Thr Ile Ile Arg Ser Ser Gly Asp Phe Gly His
1 5 10 15

Val Arg Leu Trp Tyr Lys Thr Met Ser Trp Trp Thr Ala Glu Ala Gly
20 25 30

Leu Asp Phe Val Pro Ala Ala Gly Glu Leu Leu Phe Glu Ala Gly Glu
35 40 45

Met Arg Lys Ser
50

<210> 1364
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Y6152F"

<400> 1364
Ala Tyr Arg His Phe Trp Met Leu Val Leu Phe Val Ile Phe Asn Ser
1 5 10 15

Leu Gln Gly Leu Tyr Val Phe Met Val Phe Phe Phe Ile Leu His Asn
20 25 30

Gln Met Cys Cys Pro Met Lys Ala Ser Tyr Thr Val Glu Met Asn Gly
35 40 45

His Pro Gly Pro
50

<210> 1365
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S706L"

<400> 1365
Lys Glu Pro Cys Met Tyr Pro Ala Gly Gly Gly Ser Trp Lys Ser Arg
1 5 10 15

Pro Glu Glu Glu Glu Asp Ile Val Asn Leu Leu Trp Phe Trp Ser Arg
20 25 30

Lys Tyr Thr Lys Pro Glu Ala Ile Ile Gly Ser Trp Leu Trp Ala Thr
35 40 45

Glu Glu Ser Asn
50

<210> 1366
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V30I"

<400> 1366
Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg Leu
1 5 10 15

Cys Asp Lys Ala Glu Ala Trp Gly Ile Ile Ile Leu Glu Thr Val Ala
20 25 30

Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile
35 40 45

Leu Val Cys Lys
50

<210> 1367
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.231_239RKEDPGSLR>R"

<400> 1367
Lys Glu Asp Leu Gly Ser Leu Gly Lys Val Asp Pro Leu Cys Ser Ser
1 5 10 15

Lys Thr Tyr Thr Val Ser Pro Arg Lys Arg Val Asp Pro Val Ser Ser
20 25 30

Asp Lys Val Asp Pro Val Phe Pro Arg Lys Glu Glu Pro Arg Tyr Ser
35 40 45

Gly Lys Glu His Pro Val Ser Ser Glu Lys Val Ala Pro Thr Ser Ala
50 55 60

Glu Lys Val Asp Leu Val Leu Ser Gly Lys Arg
65 70 75

<210> 1368
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R446H"

<400> 1368
Ala Pro Ala Ser Glu Asp Ser Leu Ser Val Glu Gly Arg Arg Gly Pro
1 5 10 15

Leu Arg Ala Val Met Gln Ser Leu Arg His His Pro Ser Cys Cys Gly
20 25 30

Cys Ser Gly Ala Ala Pro Glu
35

<210> 1369
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T100P"

<400> 1369
Ala Arg Ala Ser Gly Pro Lys Ala Arg Pro Ser Ala Gly Gly His Trp
1 5 10 15

Trp Ser Ser Thr Val Gly Asn Val Ser Pro Pro Met Gly Gly Ser Asp
20 25 30

Leu Cys Arg Leu Arg Ala Pro Ser Ala Ala Ala Met Gln Arg Ser His
35 40 45

Ser Asp Leu Val
    50

<210> 1370
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V241M"

<400> 1370
Lys Ala Ala Glu Gln Leu Ala Thr Thr Thr Cys His Ala Leu Pro Pro
1   5   10   15

Ala Ala Leu Leu Cys Gly Met Arg Glu Met Met Arg Ala Gly Gly Cys
            20   25   30

Cys His Ala Leu Pro Ala Thr Gly Ile Leu Ala Phe Pro Lys Leu Val
        35   40   45

Ala Ser Val Ser
    50

<210> 1371
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R633fs"

<400> 1371
Pro Ser Asp Pro Met Gly Asp Ser Ser Pro Gly Ser Gly Lys Lys Thr
1   5   10   15

Pro Ser Arg Ser Val Lys Ala Ser Pro Pro Gly Pro Ala Ala Ser Ala
            20   25   30

Ser Ser Ser Arg Ser Lys Ser

35

<210> 1372
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R10P"

<400> 1372
Met Gln Arg Ala Ala Ala Leu Val Arg Pro Pro Gly Cys Gly Pro Arg
1 5 10 15

Thr Pro Ser Ser Trp Gly Arg Ser Gln Ser Ser Ala Ala Ala Glu Ala
20 25 30

Ser Ala Val Leu
35

<210> 1373
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I123M"

<400> 1373
Asp Phe Leu Leu Gln Gly Arg Leu Tyr Ile Ser Pro Asn Trp Leu Cys
1 5 10 15

Phe His Ala Ser Leu Phe Gly Lys Asp Met Met Lys Val Val Ile Pro
20 25 30

Val Val Ser Val Gln Met Ile Lys Lys His Lys Met Ala Arg Leu Leu
35 40 45

Pro Asn Gly Leu
50

<210> 1374
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E69D"

<400> 1374
Gly Tyr Val Pro Lys Asn Phe Ile Asp Ile Gln Phe Pro Lys Trp Phe
1 5 10 15

His Glu Gly Leu Ser Arg His Gln Ala Asp Asp Asn Leu Leu Met Gly
20 25 30

Lys Glu Val Gly Phe Phe Ile Ile Arg Ala Ser Gln Ser Ser Pro Gly
35 40 45

Asp Phe Ser Ile
50

<210> 1375
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A300T"

<400> 1375
Arg His Leu Gln Phe Phe Ser Glu Phe Gly Asn Ser Asp Ile Tyr Val
1 5 10 15

Ser Leu Ala Gly Lys Lys Lys His Gly Thr Thr Pro Thr Asn Tyr Gly
20 25 30

Phe Cys Phe Lys Pro Asn Lys Ala Gly Gly Pro Arg Asp Leu Lys Met
35 40 45

Leu Cys Ala Glu
50

<210> 1376
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R239L"

<400> 1376
Ile Ser His Glu Asp Leu Ile Gln Asn Phe Leu Asn Ala Gly Ser Phe
1 5 10 15

Pro Glu Ile Gln Gly Phe Leu Gln Leu Leu Leu Gly Ser Gly Arg Lys
20 25 30

Leu Trp Lys Arg Phe Phe Cys Phe Leu Arg Arg Ser Gly Leu Tyr Tyr
35 40 45

Ser Thr Lys Gly
50

<210> 1377
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S344Y"

<400> 1377
Glu Ser Pro Ser Ala Pro Asp Gly Gly Cys Pro Gln Gly Gly Gly Asn
1 5 10 15

Arg Ala Lys Tyr Glu Ser Ala Gly Met Tyr Tyr Cys Val Pro Gln Val
20 25 30

Gly Leu Val Gly Pro Ala Ser Val Thr Phe Pro Val Val Ala Ser Gly
35 40 45

Glu Pro Val Ser
50

<210> 1378
<211> 37
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<400> 1378
Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn Glu Asp
1 5 10 15

Thr Phe Gln Leu Gln Ile Glu Glu Ala Trp Trp Gly Ser Tyr Lys Leu
20 25 30

Thr Leu Thr Glu Ile
35

<210> 1379
<211> 52
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<400> 1379
Glu Gly Tyr Arg Met Leu Phe Gln Asp Leu Glu Lys Lys Lys Glu Arg
1 5 10 15

Leu Val Val Val Asp Cys Glu Ser Glu Cys Cys Leu Asn Ala Ile Leu
20 25 30

Gly Gln Ile Ile Lys Leu Glu Lys Asn Gly Ile Gly Tyr His Tyr Ile

35 40 45

Leu Ala Asn Leu
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<210> 1380
<211> 52
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<400> 1380
Leu Val Gly Gly Leu Gly Leu Ala Met Leu Val Ala Leu Ile Glu Phe
1 5 10 15

Cys Tyr Lys Ser Arg Ala Glu Ala Lys Gln Gln Met Lys Val Ala Lys
20 25 30

Asn Ala Gln Asn Ile Asn Pro Ser Ser Ser Gln Asn Ser Gln Asn Phe
35 40 45

Ala Thr Tyr Lys
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<210> 1381
<211> 52
<212> PRT
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<400> 1381
Pro Arg Pro Ser Ala Ser Ala Thr Leu His Ser Ala Ile Trp Ile Val
1 5 10 15

Tyr Gly Ala Phe Val Gln Gln Gly Gly Lys Lys Ser Ser Val Asn Ser
20 25 30

Met Ala Met Arg Ile Val Met Gly Ser Trp Trp Leu Phe Thr Leu Ile
35 40 45

Val Cys Ser Ser
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<210> 1382
<211> 52
<212> PRT
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<400> 1382
Val Ser Arg Met Asp Asn Pro Ile Arg Thr Phe Gln Asp Leu Ser Lys
1 5 10 15

Gln Val Glu Met Ser Tyr Gly Thr Val Leu Leu Asp Ser Ala Val Tyr
20 25 30

Glu Tyr Phe Arg Ala Lys Gly Thr Asn Pro Leu Glu Gln Asp Ser Thr
35 40 45

Phe Ala Glu Leu
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<210> 1383
<211> 58
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<400> 1383
Tyr Thr Thr Leu Ala Thr Arg Met Met Met Gly Ala Trp Trp Leu Phe
1 5 10 15

Ala Leu Ile Val Ile Ser Ser Tyr Thr Gln Thr Ser Leu Leu Ser Ser
20 25 30

Leu Leu His Ala Leu Lys Val Pro Ser Ser Leu Ser Arg Thr Phe Pro
35 40 45

Ser Lys Gln Lys Ser Leu Met Ala Gln Ser
50 55

<210> 1384
<211> 52
<212> PRT
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<220>
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<223> /note="p.R368Q"

<400> 1384
Val Ser Ser Leu Gln Cys His Arg His Lys Pro Trp Arg Leu Gly Pro
1 5 10 15

Arg Phe Met Asn Leu Ile Lys Glu Ala Gln Gln Trp Asp Gly Leu Thr
20 25 30

Gly His Ile Thr Phe Asn Lys Thr Asn Gly Leu Arg Lys Asp Phe Asp
35 40 45

Leu Asp Ile Ile
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<210> 1385
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="p.R519Q"

<400> 1385

Trp Asn Gly Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala
1 5 10 15

Val Gly Ser Leu Thr Ile Asn Glu Glu Gln Gln Ser Glu Val Val Asp
20 25 30

Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg
35 40 45

Ser Asn Gly Thr
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<210> 1386
<211> 26
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<400> 1386
Met Glu Leu Glu Asn Ile Val Ala Asn Ser Leu Leu Leu Lys Ala Arg
1 5 10 15

Gln Gly Gly Tyr Gly Lys Lys Lys Trp Ser
20 25

<210> 1387
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F682L"

<400> 1387
Ser Ala Leu Leu Thr Lys Thr Asn Cys Ile Ala Arg Ile Phe Asp Gly
1 5 10 15

Val Lys Asn Gly Ala Gln Arg Pro Lys Leu Leu Ile Ser Pro Ser Ser

20 25 30

Gln Val Phe Ile Cys Leu Gly Leu Ile Leu Val Gln Ile Val Met Val
35 40 45

Ser Val Trp Leu
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<210> 1388
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R183C"

<400> 1388
Ala Asn Leu Leu Arg Leu Phe Gln Ile Pro Gln Ile Ser Tyr Ala Ser
1 5 10 15

Thr Ser Ala Lys Leu Ser Asp Lys Ser Cys Cys Tyr Asp Tyr Phe Ala
20 25 30

Arg Thr Val Pro Pro Asp Phe Tyr Gln Ala Lys Ala Met Ala Glu Ile
35 40 45

Leu Arg Phe Phe
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<210> 1389
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<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.P895fs"

<400> 1389
Ser Ser Gly Glu Thr Leu Arg Tyr Lys Asp Arg Arg Leu Ala Gln His
1 5 10 15

Lys Ser Glu Ile Glu Cys Phe Thr Pro Gln Arg Glu Tyr Gly Glu Trp
20 25 30

Trp Glu Ser Asn Asn Glu Gln Phe Gln Trp Lys Ile Arg His Val Gly
35 40 45

Pro Glu
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<210> 1390
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E363D"

<400> 1390
Gly Phe Asp Gln Tyr Phe Met Thr Arg Ser Leu Glu Asn Asn Arg Arg
1 5 10 15

Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp Asp Asn Phe Asn Cys Lys
20 25 30

Leu Thr Ser Ser Gly Thr Gln Ser Asp Asp Ser Thr Arg Lys Cys Thr
35 40 45

Gly Glu Glu Arg
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<210> 1391
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 1391
Ser Pro Thr Ser Gln Leu Val Ile Thr Phe Ser Leu Thr Ser Leu Gln
1 5 10 15

Val Val Gly Met Ile Ala Trp Leu Gly Gly Pro Ala Pro Thr Gln Arg
20 25 30

Asp

<210> 1392
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R679Q"

<400> 1392
Val Cys Ser Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser
1 5 10 15

Tyr Ala Ala Leu Leu Thr Lys Thr Asn Gln Gln Ile Tyr Arg Ile Phe
20 25 30

Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr
35 40 45

Ser Gln Leu Ala
50

<210> 1393
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R852C"

<400> 1393

Ser Val Ser Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile Ile
1 5 10 15

Phe His Pro Glu Gln Asn Val Gln Lys Cys Cys Lys Arg Ser Phe Lys
20 25 30

Ala Val Val Thr Ala Ala Thr Met Gln Ser Lys Leu Ile Gln Lys Gly
35 40 45

Asn Asp Arg Pro
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<210> 1394
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R192L"

<400> 1394
Ala Met Pro Lys Lys Asp Ala Arg Thr Leu Leu Ala Arg Phe Asn Glu
1 5 10 15

Gln Ile Glu Pro Ile Tyr Ala Leu Leu Leu Leu Glu Thr Glu Asp Val
20 25 30

Asn Leu Ala Tyr Glu Ile Leu Glu Pro Glu Pro Thr Glu Ile Pro Ala
35 40 45

Leu Lys Gln Ser
50

<210> 1395
<211> 52
<212> PRT
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<220>
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<223> /note="p.K306N"

<400> 1395
His Ala Gly Cys Gly Lys Thr Phe Ala Met Lys Gln Ser Leu Thr Arg
1 5 10 15

His Ala Val Val His Asp Pro Asp Lys Asn Asn Lys Met Lys Leu Lys
20 25 30

Val Lys Lys Ser Arg Glu Lys Arg Ser Leu Ala Ser His Leu Ser Gly
35 40 45

Tyr Ile Pro Pro
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<210> 1396
<211> 31
<212> PRT
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<220>
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<221> source
<223> /note="p.S767fs"

<400> 1396
Lys Glu Gly Pro Ser Gly Ser Gly Asp Ser Gln Leu Ser Ala Ser Ser
1 5 10 15

Arg Ser Glu Ser Gly Arg Met Lys Lys Val Ile Ile Lys Trp Ala
20 25 30

<210> 1397
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E562fs"

<400> 1397
Leu Ile Asp Leu Val Arg Trp Lys Ile Leu Lys Asp Lys His Ile Pro
1 5 10 15

Gln Phe Leu Gln Glu Ala Leu Glu Lys Arg Leu Lys Ala Val Glu Ser
20 25 30

Pro Ile Phe Gly Val Leu Ser Phe Ser Ser
35 40

<210> 1398
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<221> source
<223> /note="p.G549C"

<400> 1398
Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Ile
1 5 10 15

Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Cys Cys Thr Val Lys Leu Asp
20 25 30

Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Leu Arg
35 40 45

Glu Val Leu Asn
50

<210> 1399
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.C500R"

<400> 1399
Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn Tyr Ala Ala Asp
1 5 10 15

Lys Gly Ala Pro Tyr Val Asp Val Ile Arg Arg Leu Asn Ser Tyr Tyr
20 25 30

Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu Ile Gln Leu Gln Leu
35 40 45

Ala Thr Gln Phe
50

<210> 1400
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L501V"

<400> 1400
Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn Tyr Ala Ala Asp Lys
1 5 10 15

Gly Ala Pro Tyr Val Asp Val Ile Cys Val Val Asn Ser Tyr Tyr Ser
20 25 30

Trp Tyr His Asp Tyr Gly His Leu Glu Leu Ile Gln Leu Gln Leu Ala
35 40 45

Thr Gln Phe Glu
50

<210> 1401
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.L223fs"

<400> 1401

Ser Gln Arg Leu Phe Leu Pro Leu Ile Leu Lys Glu Val Asp Ser Leu
1 5 10 15

Leu Tyr Val Asp Thr Asp Ile Leu Phe Phe Thr Thr Ser
20 25

<210> 1402
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A214fs"

<400> 1402
Pro Gly Ala Ala Thr Glu Lys Ala Arg Lys Gln Gly Gly Ala Ala Lys
1 5 10 15

Asp Thr Arg Ala Gln Ser Gly Glu Ala Lys Glu Gly Ala Pro Gln Ala
20 25 30

Arg Gln Gly His Ala Gly Thr Phe Gln Cys Trp Trp Ala Gln Gln Glu
35 40 45

Gly Lys Gly Gln Arg Gln Gln Glu Gln Pro Arg Arg Cys
50 55 60

<210> 1403
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q125R"

<400> 1403
Leu Ile Lys Ala Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His
1 5 10 15

Lys Ser Leu Ile Gly Lys Lys Gly Gln Arg Arg Lys Thr Ala

20 25 30

<210> 1404
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K144fs"

<400> 1404
Gly Lys Ser Glu Thr Ile Leu Ser Pro Pro Pro Glu Lys Arg Gly Arg
1 5 10 15

Lys Ala Thr Ser Gly Lys Lys Gly Gly Arg Asn Pro Arg Leu Pro Asn
20 25 30

His Gly Arg Pro Lys Ser Pro Asn Gln Arg Thr Ala Ile Lys Lys Glu
35 40 45

Leu Gln Ile Pro Pro Leu Lys Met Gly Gln Gly Met Asp Ser Pro Phe
50 55 60

Cys Leu Leu Arg Ala Leu Phe Trp Asp Arg Ser Cys Pro
65 70 75

<210> 1405
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.R131L"

<400> 1405
Asp Thr Asn Leu Cys Ala Ile His Ala Lys Arg Val Thr Ile Met Pro
1 5 10 15

Lys Asp Ile Gln Leu Ala Arg Arg Ile Leu Leu Gly Glu Arg Ala
20 25 30

<210> 1406
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R172C"

<400> 1406
Ala Glu Lys Met Gly Tyr Lys Ala Ile Phe Val Thr Val Asp Thr Pro
1 5 10 15

Tyr Leu Gly Asn Arg Leu Asp Asp Val Cys Cys Asn Arg Phe Lys Leu
20 25 30

Pro Pro Gln Leu Arg Met Lys Asn Phe Glu Thr Ser Thr Leu Ser Phe
35 40 45

Ser Pro Glu Glu
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<210> 1407
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.H12N"

<400> 1407
Met Ser Leu Val Cys Leu Thr Asp Phe Gln Ala Asn Asn Ala Arg Glu
1 5 10 15

Gln Leu Ser Lys Ser Thr Arg Asp Phe Ile Glu Gly Gly Ala Asp Asp
20 25 30

Ser Ile Thr Arg Asp Asp
35

<210> 1408
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R168H"

<400> 1408
Asn Lys Val Lys Lys Met Lys Arg Tyr His Val Gly Lys Val Trp Arg
1 5 10 15

Arg Glu Ser Pro Thr Ile Val Gln Gly His His Tyr Arg Glu Phe Cys
20 25 30

Gln Cys Asp Phe Asp Ile Ala Gly Gln Phe Asp Pro Met Ile Pro Asp
35 40 45

Ala Glu Cys Leu
50

<210> 1409
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S530fs"

<400> 1409
Glu Asn Ser Pro Leu Ser Asp Val Ala Lys Asn Thr Glu Ser Ser Ala
1 5 10 15

Phe Gly Gly Ser Leu Pro Ala Lys Lys Val Ile His Phe Lys Lys Ser
20 25 30

Lys Ile Ile Trp
35

<210> 1410
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F42L"

<400> 1410
Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu
1 5 10 15

Leu Val Val Tyr Pro Trp Thr Gln Arg Leu Leu Phe Glu Ser Phe Gly
20 25 30

Asp Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala
35 40 45

His Gly Lys Lys
50

<210> 1411
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F86C"

<400> 1411
Val Lys Ala His Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu
1 5 10 15

Ala His Leu Asp Asn Leu Lys Gly Thr Cys Cys Ala Thr Leu Ser Glu
20 25 30

Leu His Cys Asp Lys Leu His Val Asp Pro Glu Asn Phe Arg Leu Leu
35 40 45

Gly Asn Val Leu

50

<210> 1412
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G499V"

<400> 1412
Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Ser
1 5 10 15

Lys Leu Arg Phe Glu Val Phe Gln Pro Val Val Asp Tyr Ile Ile Arg
20 25 30

Glu Gly Ala Val Gly Lys Lys Met Tyr Phe Ile Gln His Gly Val Ala
35 40 45

Gly Val Ile Thr
50

<210> 1413
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R659L"

<400> 1413
Gln Ala Ile Ala Pro Ile Asn Tyr Pro Gln Met Thr Thr Leu Asn Ser
1 5 10 15

Thr Ser Ser Thr Thr Thr Pro Thr Ser Leu Leu Met Arg Thr Gln Ser
20 25 30

Pro Pro Val Tyr Thr Ala Thr Ser Leu Ser His Ser Asn Leu His Ser
35 40 45

Pro Ser Pro Ser
50

<210> 1414
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A714S"

<400> 1414
Gln Pro Ser Ala Ile Leu Ser Pro Cys Ser Tyr Thr Thr Ala Val Cys
1 5 10 15

Ser Pro Pro Val Gln Ser Pro Leu Ala Ser Ser Arg Thr Phe His Tyr
20 25 30

Ala Ser Pro Thr Ala Ser Gln Leu Ser Leu Met Gln Gln Gln Pro Gln
35 40 45

Gln Gln Val Gln
50

<210> 1415
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P231Q"

<400> 1415
Ile Ile Leu Asp Pro Lys Val Ile Lys Met Asn Tyr Leu Lys Ser Trp
1 5 10 15

Phe Val Val Asp Phe Ile Ser Ser Ile Gln Gln Val Asp Tyr Ile Phe
20 25 30

Leu Ile Val Glu Lys Gly Met Asp Ser Glu Val Tyr Lys Thr Ala Arg
35 40 45

Ala Leu Arg Ile
50

<210> 1416
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P326T"

<400> 1416
Leu Ile Gly Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln
1 5 10 15

Phe Leu Val Pro Leu Leu Gln Asp Phe Thr Thr Pro Asp Cys Trp Val
20 25 30

Ser Leu Asn Glu Met Val Asn Asp Ser Trp Gly Lys Gln Tyr Ser Tyr
35 40 45

Ala Leu Phe Lys
50

<210> 1417
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R525H"

<400> 1417
Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala
1 5 10 15

Leu Ile Gln Ser Leu Asp Ser Ser Arg His His Gln Tyr Gln Glu Lys
20 25 30

Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Pro Asp
35 40 45

Thr Arg Gln Arg
50

<210> 1418
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S9fs"

<400> 1418
Met Ser Gly Thr Lys Leu Glu Asp Ser Pro Pro Leu Ser Gln Leu Val
1 5 10 15

Ile Cys Phe Gly Ala Glu
20

<210> 1419
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S9fs"

<400> 1419
Met Ser Gly Thr Lys Leu Glu Asp Ser Pro Leu Val Ala Thr Gly His
1 5 10 15

Leu Leu Arg Ser
20

<210> 1420

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D100Y"

<400> 1420
Val Cys Val Ala Val Trp Lys Asn His His Met Arg Thr Val Thr Asn
1 5 10 15

Tyr Phe Ile Val Asn Leu Ser Leu Ala Tyr Tyr Val Leu Val Thr Ile
20 25 30

Thr Cys Leu Pro Ala Thr Leu Val Val Asp Ile Thr Glu Thr Trp Phe
35 40 45

Phe Gly Gln Ser
50

<210> 1421
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P901fs"

<400> 1421
Pro Asp Glu Val Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met
1 5 10 15

Ala Phe Thr Gly Gly Leu Asp Pro Pro Trp Glu Thr Leu Ser Thr Trp
20 25 30

Arg Pro Ser Glu Arg Trp Ser Cys Arg Ser Pro Ala Ser Leu Pro Arg
35 40 45

Met Trp Cys Trp Cys His Gln Ala Ser Met Pro Trp Arg Ala Thr Pro
50 55 60

Pro Leu Leu Gly Ala Thr Thr Ser Pro Pro Asp Ala Ser Gly Thr
65 70 75

<210> 1422
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A1044T"

<400> 1422
Cys Val Ser Ala Leu Leu Ser Val Glu Leu Gln Pro Leu Asp Glu Ala
1 5 10 15

Val Leu Gln Gln Lys Pro Asn Ile Asn Thr Thr Val Ala Thr Leu Glu
20 25 30

Lys Val Ile Glu Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe
35 40 45

Ala Ala Gly Leu
50

<210> 1423
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R503C"

<400> 1423
Ser Asn Leu Ile Arg Ile Glu Gly Asp Pro Gln Gly Val Gln Gln Ala
1 5 10 15

Lys Arg Glu Leu Leu Glu Leu Ala Ser Cys Cys Met Glu Asn Glu Arg
20 25 30

Thr Lys Asp Leu Ile Ile Glu Gln Arg Phe His Arg Thr Ile Ile Gly
35 40 45

Gln Lys Gly Glu
50

<210> 1424
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.G747fs"

<400> 1424
Glu Lys Gln Thr Lys Ser Phe Thr Val Asp Ile Arg Ala Lys Pro Glu
1 5 10 15

Tyr His Lys Phe Leu Ile Gly Lys Gly Ala Ala Lys Phe Ala Arg Cys
20 25 30

Ala Thr Ala Leu Glu His Val Ser Ser Ser Leu Arg Leu Arg Thr Arg
35 40 45

Thr Arg Thr
50

<210> 1425
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E1109K"

<400> 1425
Thr Val Val Val Asn Leu Leu Gln Lys Pro Leu Pro Phe Asp Arg Asp
1 5 10 15

Thr Lys Thr Leu Trp Lys Ala Leu Ala Lys Lys Lys Pro Ala Ser Ser
20 25 30

Gly Lys Leu Leu Gln Ala Leu Ile Asp Lys Leu Glu Thr Glu Leu Glu
35 40 45

Asp Asp Ile Ala
50

<210> 1426
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R333fs"

<400> 1426
Met Ala Gly Gly His Val Phe Arg Asn Ala His Phe Asp Tyr Ser Pro
1 5 10 15

Ala Gly Leu Ala Val His Arg Gly Gly Thr Leu Arg His Pro Arg Ala
20 25 30

Val Pro Ser Ala Ala Gly Pro Leu Arg Thr Pro His Ser His Pro Gln
35 40 45

Ala

<210> 1427
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P19A"

<400> 1427
Met Ser Glu Ala Val Arg Val Pro Ser Pro Ala Thr Pro Leu Val Val

1 5 10 15

Ala Ala Ala Ala Ala Pro Glu Glu Arg Lys Gly Lys Glu Ser Glu Arg
20 25 30

Glu Lys Leu Pro Pro Ile Val Ser Ala Gly Ala Gly Ala
35 40 45

<210> 1428
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A183S"

<400> 1428
Ile Cys Phe Lys Tyr Tyr His Gly Val Ser Gly Ala Leu Arg Ala Thr
1 5 10 15

Thr Pro Ser Val Thr Val Lys Asn Ser Ser Ser Ala Pro Ile Phe Lys
20 25 30

Ser Ile Gly Ala Asp Glu Thr Val Gln Gly Gln Gly Ser Arg Arg Leu
35 40 45

Ile Ser Phe Ser
50

<210> 1429
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R2330H"

<400> 1429
Pro Val Leu Ala Val Ile Gly Gly Val Asp Ala Gly Leu Arg Val Gly
1 5 10 15

Gly Arg Cys Val His Lys Gln Thr Gly His His His Ala Thr Leu Leu
20 25 30

Gly Val Val Lys Glu Gly Ser Thr Ser Ala Lys Val Gln Trp Asp Glu
35 40 45

Ala Glu Ile Thr
50

<210> 1430
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S329F"

<400> 1430
Ser Gln Met Leu Ser Ala Ile Leu Leu Leu Gln Leu Trp Asp Ser
1 5 10 15

Gly Ala Gln Glu Thr Asp Asn Glu Arg Phe Phe Ala Gln Gly Thr Ser
20 25 30

Ala Pro Leu Leu Pro Leu Leu Gln Arg Phe Gln Ser Ile Ile Cys Arg
35 40 45

Lys Asp Ala Pro
50

<210> 1431
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P96T"

<400> 1431
Ser Cys Leu Pro Gly Val Ser Gln Leu Leu Arg Arg Gly Asp Glu Val
1 5 10 15

Gly Ser Gly Leu Arg Cys Pro Leu Val Thr Thr Glu Ser Ala Ala Gly
20 25 30

Ser Thr Met Asp Ser Ala Gly Leu Gly Gln Glu Ala Pro Ala Leu Phe
35 40 45

Arg Pro Cys Thr
50

<210> 1432
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T482P"

<400> 1432
Cys Arg Ser Trp Arg Leu Pro Cys Ser Trp Leu Ser Thr Arg Met Pro
1 5 10 15

Trp Arg Ser Gly Trp Arg Lys Thr Cys Pro Pro Pro Ala Cys Ser Gly
20 25 30

Cys Lys Leu Cys Cys Arg Thr Ser Ala Arg Cys Leu Pro Pro Arg Cys
35 40 45

His Pro Pro Ala
50

<210> 1433
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.S467Y"

<400> 1433
Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro
1   5   10   15

Leu Ile Pro Trp Asp Tyr Cys Pro Ile Tyr Tyr Arg Cys Glu Gly Asp
            20   25   30

Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile Ser Cys Ala
        35   40   45

Lys Thr Lys Gln
    50

<210> 1434
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.M686T"

<400> 1434
Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro
1   5   10   15

Leu Val Cys Glu Gln His Lys Met Arg Thr Thr Val Leu Gly Val Ile
            20   25   30

Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val
        35   40   45

Arg Val Ala Tyr
    50

<210> 1435
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G229A"

<400> 1435
Pro Gln Cys Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr
1 5 10 15

Arg Gly Leu Met Asp His Thr Glu Ser Ala Ala Lys Ile Cys Gln Arg
            20 25 30

Trp Asp His Gln Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr
        35 40 45

Pro Asp Lys Gly
    50

<210> 1436
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V692A"

<400> 1436
Ala Phe Arg Asp Gly Glu Val Arg Leu Val Arg Pro Ala Gly Leu Ser
1 5 10 15

Ser Gly Ser Gly Arg Val Glu Val Phe Ala Ala Gly Gly Arg Trp Gly
            20 25 30

Thr Val Cys Asp Asp Ser Trp Asn Ile Ser Gly Ala Ala Val Val Cys
        35 40 45

Arg Gln Leu Gly
    50

<210> 1437
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A72T"

<400> 1437
Val Ser Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser
1 5 10 15

Tyr Leu Arg Met His Arg Leu Cys Ala Thr Thr Gly Glu Trp Asn Gln
20 25 30

Val Gly Ala Gly Gly Glu Pro Leu Asp Ala Cys Tyr Leu Lys Ala Leu
35 40 45

Glu Gly Phe Val
50

<210> 1438
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R940L"

<400> 1438
Ala Gln Leu Val Ala Ala Ser Lys Val Lys Ala Asp Lys Asp Ser Pro
1 5 10 15

Asn Leu Ala Gln Leu Gln Gln Ala Ser Leu Leu Gly Val Asn Gln Ala
20 25 30

Thr Ala Gly Val Val Ala Ser Thr Ile Ser Gly Lys Ser Gln Ile Glu
35 40 45

Glu Thr Asp Asn
50

<210> 1439
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R280H"

<400> 1439
Pro Asp Ala Ala Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu
1 5 10 15

Ala Glu Thr Lys Val Arg Pro Leu Glu His His Arg Lys Tyr Met Leu
20 25 30

Lys Ser Leu Asp Gln Ile Glu Thr Val Asn Gly Gly Ser Val Ala Ser
35 40 45

Arg Leu Thr Phe
50

<210> 1440
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K188N"

<400> 1440
Ala Ala Ala Gly Val Lys Lys Val Ala Lys Ser Pro Lys Lys Ala Lys
1 5 10 15

Ala Ala Ala Lys Pro Lys Lys Ala Thr Asn Asn Ser Pro Ala Lys Pro
20 25 30

Lys Ala Val Lys Pro Lys Ala Ala Lys Pro Lys Ala Ala Lys Pro Lys
35 40 45

Ala Ala Lys Pro
50

<210> 1441
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A65V"

<400> 1441
Val Ser Glu Leu Ile Thr Lys Ala Val Ala Ala Ser Lys Glu Arg Ser
1 5 10 15

Gly Val Ser Leu Ala Ala Leu Lys Lys Val Val Leu Ala Ala Ala Gly
20 25 30

Tyr Asp Val Glu Lys Asn Asn Ser Arg Ile Lys Leu Gly Leu Lys Ser
35 40 45

Leu Val Ser Lys
50

<210> 1442
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I81M"

<400> 1442
Ser Gly Val Ser Leu Ala Ala Leu Lys Lys Ala Leu Ala Ala Ala Gly
1 5 10 15

Tyr Asp Val Glu Lys Asn Asn Ser Arg Met Met Lys Leu Gly Leu Lys
20 25 30

Ser Leu Val Ser Lys Gly Thr Leu Val Gln Thr Lys Gly Thr Gly Ala
35 40 45

Ser Gly Ser Phe

50

<210> 1443
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G133A"

<400> 1443
Asn Lys Lys Ala Ala Ser Gly Glu Ala Lys Pro Lys Ala Lys Lys Ala
1 5 10 15

Gly Ala Ala Lys Ala Lys Lys Pro Ala Ala Ala Ala Ala Lys Lys Pro
20 25 30

Lys Lys Ala Thr Gly Ala Ala Thr Pro Lys Lys Ser Ala Lys Lys Thr
35 40 45

Pro Lys Lys Ala
50

<210> 1444
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R25P"

<400> 1444
Met Ser Glu Thr Ala Pro Ala Ala Pro Ala Ala Pro Ala Pro Ala Glu
1 5 10 15

Lys Thr Pro Val Lys Lys Lys Ala Pro Pro Lys Ser Ala Gly Ala Ala
20 25 30

Lys Arg Lys Ala Ser Gly Pro Pro Val Ser Glu Leu Ile Thr Lys Ala
35 40 45

Val Ala Ala
    50

<210> 1445
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R30P"

<400> 1445
Gly Lys Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys Thr Arg Ser Ser
1   5   10   15

Arg Ala Gly Leu Gln Phe Pro Val Gly Pro Pro Val His Arg Leu Leu
            20   25   30

Arg Lys Gly Asn Tyr Ala Glu Arg Val Gly Ala Gly Ala Pro Val Tyr
        35   40   45

Leu Ala Ala Val
    50

<210> 1446
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.E77K"

<400> 1446
Asp Thr Gly Ile Ser Ser Lys Ala Met Gly Ile Met Asn Ser Phe Val
1   5   10   15

Asn Asp Ile Phe Glu Arg Ile Ala Gly Lys Lys Ala Ser Arg Leu Ala
            20   25   30

His Tyr Asn Lys Arg Ser Thr Ile Thr Ser Arg Glu Ile Gln Thr Ala
35 40 45

Val Arg Leu Leu
50

<210> 1447
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K13R"

<400> 1447
Met Pro Glu Pro Ala Lys Ser Ala Pro Ala Pro Lys Arg Arg Gly Ser
1 5 10 15

Lys Lys Ala Val Thr Lys Ala Gln Lys Lys Asp Gly Lys Lys Arg Lys
20 25 30

Arg Ser Arg Lys Glu Ser Tyr
35

<210> 1448
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A48S"

<400> 1448
Thr Lys Ala Ala Arg Lys Ser Ala Pro Ala Thr Gly Gly Val Lys Lys
1 5 10 15

Pro His Arg Tyr Arg Pro Gly Thr Val Ser Ser Leu Arg Glu Ile Arg
20 25 30

Arg Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg Lys Leu Pro Phe Gln
35 40 45

Arg Leu Val Arg
50

<210> 1449
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E74K"

<400> 1449
Leu Arg Glu Ile Arg Arg Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg
1 5 10 15

Lys Leu Pro Phe Gln Arg Leu Val Arg Lys Lys Ile Ala Gln Asp Phe
20 25 30

Lys Thr Asp Leu Arg Phe Gln Ser Ser Ala Val Met Ala Leu Gln Glu
35 40 45

Ala Cys Glu Ala
50

<210> 1450
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K37M"

<400> 1450
Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg
1 5 10 15

Lys Ser Ala Pro Ala Thr Gly Gly Val Met Met Lys Pro His Arg Tyr

20 25 30

Arg Pro Gly Thr Val Ala Leu Arg Glu Ile Arg Arg Tyr Gln Lys Ser
35 40 45

Thr Glu Leu Leu
50

<210> 1451
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R68P"

<400> 1451
Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val
1 5 10 15

Leu Lys Val Phe Leu Glu Asn Val Ile Pro Pro Asp Ala Val Thr Tyr
20 25 30

Thr Glu His Ala Lys Arg Lys Thr Val Thr Ala Met Asp Val Val Tyr
35 40 45

Ala Leu Lys Arg
50

<210> 1452
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R30P"

<400> 1452
Gly Lys Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys Ser Arg Ser Ser
1 5 10 15

Arg Ala Gly Leu Gln Phe Pro Val Gly Pro Pro Val His Arg Leu Leu
20 25 30

Arg Lys Gly Asn Tyr Ala Glu Arg Val Gly Ala Gly Ala Pro Val Tyr
35 40 45

Met Ala Ala Val
50

<210> 1453
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G54D"

<400> 1453
Lys Arg Lys Arg Ser Arg Lys Glu Ser Tyr Ser Ile Tyr Val Tyr Lys
1 5 10 15

Val Leu Lys Gln Val His Pro Asp Thr Asp Asp Ile Ser Ser Lys Ala
20 25 30

Met Gly Ile Met Asn Ser Phe Val Asn Asp Ile Phe Glu Arg Ile Ala
35 40 45

Gly Glu Ala Ser
50

<210> 1454
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P534fs"

<400> 1454
Leu Ser Ser His Ser Glu Lys Thr Lys Pro Glu Gln Ser Leu Leu Ser
1 5 10 15

Leu Gln His Pro Pro Ser Thr Ala Pro Leu Cys Leu Ser
20 25

<210> 1455
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H554fs"

<400> 1455
Pro Ser Thr Ala Pro Pro Val Pro Leu Leu Arg Ser His Ser Met Pro
1 5 10 15

Ser Ala Ala Cys Thr Ile Ser Thr Pro Thr Thr Pro Ser Glu Val Ala
20 25 30

Thr Pro Ser Met Thr Ile Ser Pro Thr Pro Lys Pro
35 40

<210> 1456
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q78R"

<400> 1456
Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg
1 5 10 15

Met Glu Pro Arg Ala Pro Trp Ile Glu Arg Arg Glu Gly Pro Glu Tyr
20 25 30

Trp Asp Gln Glu Thr Arg Asn Val Lys Ala Gln Ser Gln Thr Asp Arg
35 40 45

Val Asp Leu Gly
50

<210> 1457
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N104K"

<400> 1457
Glu Gly Pro Glu Tyr Trp Asp Arg Asn Thr Gln Ile Tyr Lys Ala Gln
1 5 10 15

Ala Gln Thr Asp Arg Glu Ser Leu Arg Lys Lys Leu Arg Gly Tyr Tyr
20 25 30

Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Ser Met Tyr Gly Cys
35 40 45

Asp Val Gly Pro
50

<210> 1458
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E84K"

<400> 1458
Leu Ser Glu Ala Tyr Asp Glu Asp Gln Leu Phe Phe Phe Asp Phe Ser
1 5 10 15

Gln Asn Thr Arg Val Pro Arg Leu Pro Lys Lys Phe Ala Asp Trp Ala

20 25 30

Gln Glu Gln Gly Asp Ala Pro Ala Ile Leu Phe Asp Lys Glu Phe Cys
35 40 45

Glu Trp Met Ile
50

<210> 1459
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A236fs"

<400> 1459
Tyr Thr Ala Ile Ala Tyr Trp Val Pro Arg Asn Ala Leu Pro Ser Asp
1 5 10 15

Leu Leu Glu Asn Val Leu Cys Gly Val Gly Leu Trp Pro Gly Cys Ala
20 25 30

Gly His His Arg Gly His Cys Ser His His Leu Leu Pro Glu Ala Leu
35 40 45

Leu Arg
50

<210> 1460
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G114fs"

<400> 1460
Asn Ser Gln Lys Asp Ile Leu Glu Glu Lys Arg Ala Val Pro Asp Arg
1 5 10 15

Met Cys Arg His Asn Tyr Glu Leu Gly Glu Ala His Asp Pro Ala Ala
20 25 30

Pro Ser Pro Ala
35

<210> 1461
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R247H"

<400> 1461
Ala Gln Ser Lys Met Leu Ser Gly Ile Gly Gly Phe Val Leu Gly Leu
1 5 10 15

Ile Phe Leu Gly Leu Gly Leu Ile Ile His His His Arg Gly Gln Lys
20 25 30

Gly Pro Arg Gly Pro Pro Pro Ala Gly Asn Ile Ser Ala Met Ile Gln
35 40 45

Ser Gly Glu Arg
50

<210> 1462
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G250S"

<400> 1462
Lys Met Leu Ser Gly Ile Gly Gly Phe Val Leu Gly Leu Ile Phe Leu
1 5 10 15

Gly Leu Gly Leu Ile Ile Arg His Arg Ser Ser Gln Lys Gly Pro Arg
20 25 30

Gly Pro Pro Pro Ala Gly Asn Ile Ser Ala Met Ile Gln Ser Gly Glu
35 40 45

Arg Ala Gln Ala
50

<210> 1463
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E362K"

<400> 1463
Leu Pro Pro Ser Ser Asn Ile Val Gln Thr Pro Glu Asp Phe Asn Leu
1 5 10 15

Leu Lys Ser Ser Asn Phe Arg Arg Tyr Lys Lys Val Leu Arg Glu Ile
20 25 30

Leu Thr Thr Leu Gly Leu Ser Cys Asp Met Lys Gln Val Pro Ala Leu
35 40 45

Thr Pro Leu Tyr
50

<210> 1464
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S12T"

<400> 1464

Met Phe Ala Ala Gly Leu Ala Pro Phe Tyr Ala Thr Thr Asn Phe Ser
1 5 10 15

Leu Trp Ser Ala Ala Tyr Cys Ser Ser Ala Gly Pro Gly Gly Cys Ser
20 25 30

Phe Pro Leu Asp Pro Ala
35

<210> 1465
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N231K"

<400> 1465
Gly Arg Pro Ala Gly Val His Leu Ser Gly Leu Gln Pro Ser Ala Gly
1 5 10 15

Gln Phe Phe Ala Ser Leu Asp Pro Ile Lys Lys Glu Ala Ser Ala Ile
20 25 30

Leu Ser Pro Leu Asn Ser Asn Pro Arg Asn Ser Val Gln His Gln Phe
35 40 45

Gln Asp Thr Phe
50

<210> 1466
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S133Y"

<400> 1466
Arg Glu Leu Tyr Val Gln Gly Gly Gly Asp Cys Pro Glu Met Ser Ile

1 5 10 15

Gly Ala Ile Lys Ile Ala Leu Glu Ile Tyr Tyr Leu Pro Gly Ser Phe
20 25 30

Ile Tyr Val Phe Thr Asp Ala Arg Ser Lys Asp Tyr Arg Leu Thr His
35 40 45

Glu Val Leu Gln
50

<210> 1467
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E248D"

<400> 1467
Glu Glu Phe Leu Asn His Ser Lys Ala Arg Glu Ala Glu Leu Arg Gln
1 5 10 15

Leu Arg Lys Ser Asn Met Glu Phe Glu Asp Asp Arg Asn Ala Ala Leu
20 25 30

Gln Lys His Val Glu Ser Met Arg Thr Ala Val Glu Lys Leu Glu Val
35 40 45

Asp Val Ile Gln
50

<210> 1468
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T417M"

<400> 1468
Gly His Asn Leu Leu Ser Pro Asp Gly Lys Met Ile Ser Val Ser Gly
1 5 10 15

Gly Gly Leu Pro Pro Val Ser Thr Leu Met Met Asn Ile His Ser Leu
20 25 30

Ser His His Asn Pro Gln Gln Ser Gln Asn Leu Ile Met Thr Pro Leu
35 40 45

Ser Gly Val Met
50

<210> 1469
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N302K"

<400> 1469
Gly Val Ser Pro Ser Lys Ala His Gly Leu Gly Ser Asn Leu Val Thr
1 5 10 15

Glu Val Arg Val Tyr Asn Trp Phe Ala Lys Lys Arg Arg Lys Glu Glu
20 25 30

Ala Phe Arg Gln Lys Leu Ala Met Asp Ala Tyr Ser Ser Asn Gln Thr
35 40 45

His Ser Leu Asn
50

<210> 1470
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L361fs"

<400> 1470
Gln Val Lys Thr Leu Gln Glu Thr Asn Met Met Tyr Met His Asn Thr
1 5 10 15

Val Ser Leu Glu Glu Glu Leu Lys Lys Gln Met Gln His Val His Asn
            20 25 30

<210> 1471
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G11C"

<400> 1471
Met Ser Ser Tyr Phe Val Asn Ser Phe Cys Cys Cys Arg Tyr Pro Asn
1 5 10 15

Gly Pro Asp Tyr Gln Leu His Asn Tyr Gly Asp His Ser Ser Val Ser
            20 25 30

Glu Gln Phe Arg Asp
        35

<210> 1472
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Y151C"

<400> 1472
Ala Glu Val Pro Ser Tyr Gln Arg Leu Val Pro Glu Ser Cys Pro Val
1 5 10 15

Glu Asn Pro Glu Val Pro Val Pro Gly Cys Cys Phe Arg Leu Ser Gln
            20   25   30

Thr Tyr Ala Thr Gly Lys Thr Gln Glu Tyr Asn Asn Ser Pro Glu Gly
        35   40   45

Ser Ser Thr Val
    50

<210> 1473
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Q67H"

<400> 1473
Gly Arg His Ala Ala Ala Ala Ala Ala Leu Gln Leu Tyr Gly Asn Ser
1   5   10   15

Ala Ala Gly Phe Pro His Ala Pro Pro His His Ala His Ala His Pro
            20   25   30

His Pro Ser Pro Pro Pro Ser Gly Thr Gly Cys Gly Gly Arg Glu Gly
        35   40   45

Arg Gly Gln Glu
    50

<210> 1474
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P122fs"

<400> 1474
Gly Ser Pro Ala Ala Ala Tyr Gln Ala Ala Pro Pro Pro Pro Pro His

1 5 10 15

Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala Gly Leu Pro Val Thr
20 25 30

Gly Ser Pro Arg Ser Phe Thr Asp Thr Ile Thr Tyr Arg Asp Ser Arg
35 40 45

Phe Leu Arg Pro Ser Lys Arg Pro Ser Trp Tyr Asn Ile Leu Thr Val
50 55 60

Asn Arg Pro Val Val Ile Leu Ala Arg Thr Gln Thr Thr
65 70 75

<210> 1475
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R284fs"

<400> 1475
Gly Gly Ala Gly Val Gln His Ile Ala Leu Lys Thr Glu Asp Ile Ile
1 5 10 15

Thr Ala Ile Arg His Leu Arg Glu Arg Pro Gly Val Leu Ile Cys Ser
20 25 30

Leu His Val Leu Gln Thr Thr Ala Gly Glu Ala Glu Asp Gly Gln Asp
35 40 45

Gln Gly Glu Gly Glu His
50

<210> 1476
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S468L"

<400> 1476
Asn His Ile Ile Leu Leu Thr Lys Ala Glu Pro Glu Ala Ile Pro Glu
1   5   10   15

Arg Arg Gln Ser Pro Lys Arg Leu Leu Leu Leu Arg Lys Asp Thr Ser
            20   25   30

Val Lys Ile Lys Ile Pro Pro Val Ala Glu Ala Gly Trp Asn Leu Tyr
        35   40   45

Ile Val Asn Thr
    50

<210> 1477
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.K812N"

<400> 1477
Val Ala Cys Leu Pro Asp Val Val Leu Gln Glu Leu Phe Phe Lys Leu
1   5   10   15

Thr Ser Gln Tyr Ile Trp Arg Leu Ser Asn Asn Arg Gln Pro Pro Asp
            20   25   30

Thr Thr Pro Leu Arg Thr Ser Glu Asp Leu Ile Asn Ala Cys Ser His
        35   40   45

Tyr Gly Leu Ile
    50

<210> 1478
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K58N"

<400> 1478
Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
1 5 10 15

Val Asp Arg Ala Ala Gly Leu Lys Glu Asn Asn Thr Leu Ile Leu Leu
20 25 30

Asp Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu
35 40 45

Ser Leu Gln Leu
50

<210> 1479
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61K"

<400> 1479
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Lys Lys Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 1480
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q61R"

<400> 1480
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Arg Arg Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 1481
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G12S"

<400> 1481
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Ser Ser Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1482
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G12D"

<400> 1482
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Asp Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1483
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G12A"

<400> 1483
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Ala Ala Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1484
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G13V"

<400> 1484
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Val Val Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
            20 25 30

Tyr Asp Pro Thr Ile Glu Asp
        35

<210> 1485
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P439fs"

<400> 1485
Pro His His His His His Arg Val Pro Arg Glu Glu Asp Glu Glu Val
1 5 10 15

Ser Ala Glu Leu Gly His Gln Ala Pro Gln Pro Gln Ala Lys Pro Pro
            20 25 30

Arg

<210> 1486
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.H92P"

<400> 1486
Leu Gly Ile Phe His His His Arg His Pro Gly His Val Ser His Val
1 5 10 15

Pro Asn Val Gly Leu His His His His Pro Pro Pro Arg His Thr Pro
20 25 30

His His Leu His His His His His Pro His Arg His His Pro Arg His
35 40 45

Ala Arg
50

<210> 1487
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.M1fs"

<400> 1487
Cys Leu Asn Ser Tyr Lys Ala Ser Ser Leu Ser Ser Met Phe Ser Thr
1 5 10 15

Asn Met Pro Pro Ser Met Gly Ser Met Ile Arg
20 25

<210> 1488
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G2539S"

<400> 1488
Gln His Gly Ser Gly Ser Ser Gln Ser Ser Gly Tyr Gly Arg Gln Gly
1 5 10 15

Ser Gly Ser Gly Gln Ser Pro Gly His Ser Ser Gln Arg Gly Ser Gly
20 25 30

Ser Arg Gln Ser Pro Ser Tyr Gly Arg His Gly Ser Gly Ser Gly Arg
35 40 45

Ser Ser Ser Ser
50

<210> 1489
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R120Q"

<400> 1489
Ile Tyr Lys Gln Tyr Phe Lys Ser Asn Phe Pro Ala Arg Ala Ala Tyr
1 5 10 15

Gln Val Ala Ala Leu Pro Lys Gly Ser Gln Gln Ile Glu Ile Glu Ala
20 25 30

Val Ala Ile Gln Gly Pro Leu Thr Thr Ala Ser Leu
35 40

<210> 1490
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E287K"

<400> 1490
Arg Asp Arg Cys Leu His Glu Ser Lys Gly Arg Ala His Pro Gln Val
1 5 10 15

Asp Pro Lys Leu Leu Asn Lys Leu His Lys Lys Tyr Phe His Glu Pro

20 25 30

Asn Lys Lys Phe Phe Glu Leu Val Gly Arg Thr Phe Asp Trp His
35 40 45

<210> 1491
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G399W"

<400> 1491
Glu Ile Asp Arg Glu Val Val Arg Arg Leu Arg Glu Phe Tyr Arg Pro
1 5 10 15

Phe Asn Leu Lys Phe Tyr Gln Met Thr Trp Trp His Asp Phe Gly Trp
20 25 30

Asp Gly

<210> 1492
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G313S"

<400> 1492
Val Pro Ala Lys Ala Glu Ala Gly Ala Glu Ala Gly Gly Gly Ala Gly
1 5 10 15

Pro Gly Ala Glu Asp Glu Ala Gly Arg Ser Ser Ala Val Gly Asp Pro
20 25 30

Glu Leu Gly Asp Pro Pro Ala Ala Pro Gln
35 40

<210> 1493
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F209L"

<400> 1493
Glu Ala Phe Ser Asp Ile Leu Arg Arg Glu Ile Gln His Phe Gly Val
1 5 10 15

Lys Ile Ser Ile Val Glu Pro Gly Tyr Leu Leu Arg Thr Gly Met Thr
20 25 30

Asn Met Thr Gln Ser Leu Glu Arg Met Lys Gln Ser Trp Lys Glu Ala
35 40 45

Pro Lys His Ile
50

<210> 1494
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R169W"

<400> 1494
Gln Ala Leu Arg Gly Val Gln Glu Ser Thr Glu Ala Arg Leu Arg Glu
1 5 10 15

Leu Arg Gln Gln Asn Glu Ile Leu Trp Trp Trp Glu Val Val Thr Leu
20 25 30

Arg Gln Ser His Gly Gln Gln His Arg Val Ile Gly Lys Leu Ile Gln
35 40 45

Cys Leu Phe Gly
    50

<210> 1495
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V85L"

<400> 1495
Asp Glu Asn Gly His Ile Ser Ile Pro Ser Met Val Ser Phe Thr Asp
1   5   10   15

Asn Asp Val Tyr Val Gly Tyr Glu Ser Leu Leu Glu Leu Ala Asp Ser
            20   25   30

Asn Pro Gln Asn Thr Ile Tyr Asp Ala Lys Arg Phe Ile Gly Lys Ile
        35   40   45

Phe Thr Ala Glu
    50

<210> 1496
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R483C"

<400> 1496
Arg Ile Gly Ser Phe Thr Ile Gln Asn Val Phe Pro Gln Ser Asp Gly
1   5   10   15

Asp Ser Ser Lys Val Lys Val Lys Val Cys Cys Val Asn Ile His Gly
            20   25   30

Ile Phe Ser Val Ala Ser Ala Ser Val Ile Glu Lys Gln Asn Leu Glu
35 40 45

Gly Asp His Ser
50

<210> 1497
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R282L"

<400> 1497
His Tyr Val Glu Ser Ile Asp Pro Val Thr Val Ser Ile Asn Ser Trp
1 5 10 15

Ile Glu Leu Glu Glu Asp His Leu Ala Leu Leu Val Glu Glu Ala Ile
20 25 30

Thr Arg Met Leu Val Cys Ala Leu Lys Thr Ala Glu Asn Pro Gln Asn
35 40 45

Thr Arg Ala Trp
50

<210> 1498
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S219L"

<400> 1498
Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met Pro
1 5 10 15

Ile Pro Val Phe Gly Leu Gln Asp Asp Leu Leu Lys Val Phe Lys Glu

20 25 30

Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
35 40 45

Val Ser Phe Phe
50

<210> 1499
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R236C"

<400> 1499
Ser Val Ser Ser Thr Tyr Ser Ile Leu Gln Ser Ser Ala Gly Gly Phe
1 5 10 15

Ala Gln Ile Gln Phe Asn Val Val Met Cys Cys Arg His Pro Leu Val
20 25 30

Tyr Val Val Ser Leu Leu Ile Pro Ser Ile Phe Leu Met Leu Val Asp
35 40 45

Leu Gly Ser Phe
50

<210> 1500
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R152C"

<400> 1500
Ala Ser Ile Trp Asn Val Thr Ala Ile Ala Leu Asp Arg Tyr Trp Ser
1 5 10 15

Ile Thr Arg His Met Glu Tyr Thr Leu Cys Cys Thr Arg Lys Cys Val
20 25 30

Ser Asn Val Met Ile Ala Leu Thr Trp Ala Leu Ser Ala Val Ile Ser
35 40 45

Leu Ala Pro Leu
50

<210> 1501
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W298C"

<400> 1501
Asp Thr Trp Arg Glu Gln Lys Glu Gln Arg Ala Ala Leu Met Val Gly
1 5 10 15

Ile Leu Ile Gly Val Phe Val Leu Cys Cys Cys Ile Pro Phe Phe Leu
20 25 30

Thr Glu Leu Ile Ser Pro Leu Cys Ser Cys Asp Ile Pro Ala Ile Trp
35 40 45

Lys Ser Ile Phe
50

<210> 1502
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q403R"

<400> 1502
Asp Phe Pro Glu Val Ser Ser Gly Ile Tyr Val Gln Glu Val Ala Pro
1 5 10 15

Asn Ser Pro Ser Gln Arg Gly Gly Ile Arg Arg Asp Gly Asp Ile Ile
20 25 30

Val Lys Val Asn Gly Arg Pro Leu Val Asp Ser Ser Glu Leu Gln Glu
35 40 45

Ala Val Leu Thr
50

<210> 1503
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D222N"

<400> 1503
Ala Phe Met Lys Glu Thr Ile Lys Leu Gly Ile Lys Ser Arg Pro Lys
1 5 10 15

Gly Leu Trp Gly Tyr Tyr Leu Tyr Pro Asn Asn Cys His Asn Tyr Asn
20 25 30

Val Tyr Ala Pro Asn Tyr Ser Gly Ser Cys Pro Glu Asp Glu Val Leu
35 40 45

Arg Asn Asn Glu
50

<210> 1504
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R451Q"

<400> 1504
Asn Pro Leu Glu Ala Lys Leu Tyr Gln Gln Thr Ile Tyr Cys Asp Ile
1 5 10 15

Leu Gly Arg Glu Ile Arg Leu Pro Leu Gln Gln Ile Lys Gly Glu Gly
20 25 30

Met Gly Pro Lys Ile His Phe Asn Phe Glu Leu Leu Asp Ile Gly Lys
35 40 45

Val Phe Thr Gly
50

<210> 1505
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R939Q"

<400> 1505
Pro Glu Leu Asn Leu Gly Ala His Phe Ser Leu Asp Thr His Tyr Tyr
1 5 10 15

His Phe Lys Leu Ile Asn Lys Gly Arg Gln Gln Ile Gln Gln Leu Phe
20 25 30

Trp Met Asn Asp Ser Phe Arg Pro Gln Ala Lys Leu Ser Lys Lys Gly
35 40 45

Arg Val Lys Lys
50

<210> 1506
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1187C"

<400> 1506
Val His Tyr Pro Asn Leu Ser Phe Glu Thr Lys Glu Leu Asp Phe Gly
1   5   10   15

Cys Ile Leu Asn Asp Thr Glu Leu Ile Cys Cys Tyr Val Thr Ile Thr
            20   25   30

Asn Cys Ser Pro Leu Val Val Lys Phe Arg Trp Phe Phe Leu Val Asn
        35   40   45

Asp Glu Glu Asn
    50

<210> 1507
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R158C"

<400> 1507
Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe Ser Pro Glu Glu
1   5   10   15

Val Leu Gly Met Val Leu Asn Tyr Ser Cys Cys Ser Leu Ala Glu Asp
            20   25   30

Phe Ala Glu Gln Pro Ile Lys Asp Ala Val Ile Thr Val Pro Val Phe
        35   40   45

Phe Asn Gln Ala
    50

<210> 1508
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R832C"

<400> 1508
Tyr Cys Glu Lys Glu Asn Asp Pro Lys Arg Arg Ser Cys Gln Thr Ala
1 5 10 15

Leu Val Glu Ile Leu Asp Val Ile Val Cys Cys Ser Phe Ala Pro Ile
20 25 30

Leu Pro His Leu Ala Glu Glu Val Phe Gln His Ile Pro Tyr Ile Lys
35 40 45

Glu Pro Lys Ser
50

<210> 1509
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S130R"

<400> 1509
Arg Thr Leu Tyr Asp Val Ile Leu Tyr Gly Leu Gln Glu His Ser Glu
1 5 10 15

Val Ser Gly Phe Leu Leu Glu Cys Asp Arg Arg Ser Val Gln Gly Ala
20 25 30

Leu Gln Lys His Leu Ala Leu Tyr Arg Ile Arg Arg Lys Val Thr Val
35 40 45

Glu Pro His Pro
50

<210> 1510
<211> 74
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K1213fs"

<400> 1510
Pro Val Asn Ala Trp Ala Ser Ser Leu His Ser Val Ser Ser Lys Ser
1 5 10 15

Phe Arg Asp Phe Leu Leu Glu Glu Lys Ser Leu Leu Leu Ala Ile Val
20 25 30

Gln Ala Ile Met Ser Lys Lys Phe Leu Leu Lys Glu Leu Lys Ile Leu
35 40 45

Arg His Gln Lys Leu Ser Asp Ala Leu Pro Met Val Pro Gln Asp Gln
50 55 60

Lys Ala Thr Ile Phe Gln Ile Tyr His Phe
65 70

<210> 1511
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K37fs"

<400> 1511
Ala Leu Pro Ser Thr Phe Arg Ser Val Leu Gly Ala Arg Leu Pro Pro
1 5 10 15

Pro Glu Arg Leu Cys Gly Phe Gln Lys Arg Leu Thr Ala Lys
20 25 30

<210> 1512
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R132G"

<400> 1512
Val Phe Arg Glu Ala Ile Ile Cys Lys Asn Ile Pro Arg Leu Val Ser
1 5 10 15

Gly Trp Val Lys Pro Ile Ile Ile Gly Gly Gly His Ala Tyr Gly Asp
20 25 30

Gln Tyr Arg Ala Thr Asp Phe Val Val Pro Gly Pro Gly Lys Val Glu
35 40 45

Ile Thr Tyr Thr
50

<210> 1513
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R132C"

<400> 1513
Val Phe Arg Glu Ala Ile Ile Cys Lys Asn Ile Pro Arg Leu Val Ser
1 5 10 15

Gly Trp Val Lys Pro Ile Ile Ile Gly Cys Cys His Ala Tyr Gly Asp
20 25 30

Gln Tyr Arg Ala Thr Asp Phe Val Val Pro Gly Pro Gly Lys Val Glu
35 40 45

Ile Thr Tyr Thr
50

<210> 1514

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R132H"

<400> 1514
Val Phe Arg Glu Ala Ile Ile Cys Lys Asn Ile Pro Arg Leu Val Ser
1 5 10 15

Gly Trp Val Lys Pro Ile Ile Ile Gly His His His Ala Tyr Gly Asp
20 25 30

Gln Tyr Arg Ala Thr Asp Phe Val Val Pro Gly Pro Gly Lys Val Glu
35 40 45

Ile Thr Tyr Thr
50

<210> 1515
<211> 52
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<400> 1515
Thr Ile Thr Pro Asp Glu Ala Arg Val Glu Glu Phe Lys Leu Lys Lys
1 5 10 15

Met Trp Lys Ser Pro Asn Gly Thr Ile Gln Gln Asn Ile Leu Gly Gly
20 25 30

Thr Val Phe Arg Glu Pro Ile Ile Cys Lys Asn Ile Pro Arg Leu Val
35 40 45

Pro Gly Trp Thr
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<210> 1516
<211> 52
<212> PRT
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<400> 1516
Val Phe Arg Glu Pro Ile Ile Cys Lys Asn Ile Pro Arg Leu Val Pro
1 5 10 15

Gly Trp Thr Lys Pro Ile Thr Ile Gly Lys Lys His Ala His Gly Asp
20 25 30

Gln Tyr Lys Ala Thr Asp Phe Val Ala Asp Arg Ala Gly Thr Phe Lys
35 40 45

Met Val Phe Thr
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<210> 1517
<211> 52
<212> PRT
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<400> 1517
Asp Asn Ala Phe Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr
1 5 10 15

Leu Thr Ala Arg Phe Gln Val Asn Asn Pro Pro Arg Pro Pro His Val
20 25 30

Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu
35 40 45

Leu Asp Glu Glu
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<210> 1518
<211> 52
<212> PRT
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<400> 1518
Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu Ala Ala Pro Pro Val
1   5   10   15

Ala Pro Ala Glu Ala Pro His Leu Val Gln Gln Val Asp Ala Ala Arg
            20   25   30

Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro
        35   40   45

Pro Leu Pro His
    50

<210> 1519
<211> 52
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<400> 1519
Ser Arg Ala Ala Arg Arg Pro Cys Gly Cys Pro Leu Gly Gly Glu Asp
1   5   10   15

Pro Pro Gly Thr Pro Ala Ala Thr Pro Gly Gly Ala Ala Cys Cys Cys
            20   25   30

Ala Pro Gln Pro Ala Glu Asp Glu Pro Pro Ala Pro Pro Ala Val Cys
35 40 45

Pro Arg Lys Arg
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<210> 1520
<211> 52
<212> PRT
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<400> 1520
Lys Asp Arg His Asp Phe Arg Ile Pro Gln Glu Glu Phe Asp Gly Asn
1 5 10 15

Gln Phe Gln Lys Ala Gln Ala Ile Ser Ala Ala Leu His Glu Met Ile
20 25 30

Gln Gln Thr Phe Asn Leu Phe Ser Thr Glu Asp Ser Ser Ala Ala Trp
35 40 45

Glu Gln Ser Leu
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<210> 1521
<211> 52
<212> PRT
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<400> 1521
Asp Arg His Asp Phe Arg Ile Pro Gln Glu Glu Phe Asp Gly Asn Gln
1 5 10 15

Phe Gln Lys Ala Gln Ala Ile Ser Val Phe Phe His Glu Met Ile Gln

20 25 30

Gln Thr Phe Asn Leu Phe Ser Thr Glu Asp Ser Ser Ala Ala Trp Glu
35 40 45

Gln Ser Leu Leu
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<210> 1522
<211> 52
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<400> 1522
Val Asp Glu Gly Leu Lys Asn Tyr Val Pro Val Asn His Phe Trp Asp
1 5 10 15

Gln Ser Glu Pro Arg Leu Phe Val Cys Lys Lys Ala Val Gln Glu Thr
20 25 30

Pro Arg Ser Gln Pro Gln Ser Ala Asn Gly Gln Pro Gln Asp Gly Arg
35 40 45

Ala Gly Pro Ala
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<210> 1523
<211> 52
<212> PRT
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<400> 1523
Tyr Glu Arg Ala Gly Asp Leu Phe Glu Lys Ile His Asn Pro Gln Lys
1 5 10 15

Ala Leu Glu Cys Tyr Arg Lys Gly Asn Thr Thr Phe Met Lys Ala Val
20 25 30

Glu Leu Ala Arg Leu Ala Phe Pro Val Glu Val Val Lys Leu Glu Glu
35 40 45

Ala Trp Gly Asp
50

<210> 1524
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 1524
Ala Gln His Tyr Ala Ser Leu Gln Glu Tyr Glu Ile Ala Glu Glu Leu
1 5 10 15

Tyr Thr Lys Gly Asp Arg Thr Lys Asp Val Val Ile Asp Met Tyr Thr
20 25 30

Gln Ala Gly Arg Trp Glu Gln Ala His Lys Leu Ala Met Lys Cys Met
35 40 45

Arg Pro Glu Asp
50

<210> 1525
<211> 52
<212> PRT
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<400> 1525
Ser Ser Pro Ser Pro Pro Gln Arg Ala Gln Arg Gly Asp His Ser Ser
1 5 10 15

Arg Glu Gln Gly His Ala Pro Gly Gly Ser Ser Ser Gln Ala Arg Gln
20 25 30

Ile Asp Phe Pro Leu Arg Ile Leu Val Pro Thr Gln Phe Val Gly Ala
35 40 45

Ile Ile Gly Lys
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<210> 1526
<211> 29
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<400> 1526
His Lys Val Ala Gly Leu Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly
1 5 10 15

Leu Leu Lys Met Asn Phe Thr Gly Gly Gly His Leu Pro
20 25

<210> 1527
<211> 52
<212> PRT
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<223> /note="p.R615S"

<400> 1527
Phe Leu Ala Glu Asp Arg Arg Ile Asn Val Ala Val Thr Arg Ala Arg
1 5 10 15

Arg His Val Ala Val Ile Cys Asp Ser Ser Ser Thr Val Asn Asn His
20 25 30

Ala Phe Leu Lys Thr Leu Val Glu Tyr Phe Thr Gln His Gly Glu Val
35 40 45

Arg Thr Ala Phe
50

<210> 1528
<211> 52
<212> PRT
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<220>
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<400> 1528
Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro
1 5 10 15

Asn Glu Asp Ile Val Glu Arg Asn Ile Gln Gln Ile Ile Val Pro Leu
20 25 30

Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg
35 40 45

Phe Val Tyr His
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<210> 1529
<211> 45
<212> PRT
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<223> /note="p.E90fs"

<400> 1529
Asp Pro Ala Ala Arg Arg Arg Lys Lys Lys Ser Tyr Tyr Ala Lys Leu

1 5 10 15

Arg Gln Gln Glu Ile Glu Arg Glu Arg Ala Ser Arg Glu Val Pro Gly
20 25 30

Ser Cys Gln Gly Thr Glu Arg Trp Ser Glu Gln Arg Leu
35 40 45

<210> 1530
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="p.L162R"

<400> 1530
Lys Arg Ser His Thr Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly
1 5 10 15

Ala Ser Phe Thr Gln Lys Gly Asn Leu Arg Arg Arg His Ile Lys Leu
20 25 30

His Thr Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys
35 40 45

Gln Arg Arg Asp
50

<210> 1531
<211> 52
<212> PRT
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<400> 1531
Phe Leu Leu Thr Ile Ser Ile Phe Leu Gly Leu Gly Gln Pro Arg Ser
1 5 10 15

Pro Lys Ser Lys Arg Lys Gly Gln Gly Trp Trp Pro Gly Pro Leu Ala
20 25 30

Pro Gly Pro His Gln Val Pro Leu Asp Leu Val Ser Arg Met Lys Pro
35 40 45

Tyr Ala Arg Met
50

<210> 1532
<211> 99
<212> PRT
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<400> 1532
Pro Tyr Glu Glu Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr
1 5 10 15

Ile Ser Arg Ser Ser Pro Gln Pro Pro Arg Gly Thr His Gly Asn Gly
20 25 30

Gly Arg Gly Gly Arg Gly Ala Gly Pro Arg Glu Ala Gly Pro Ala Thr
35 40 45

Leu Ser Arg Gly Pro Gly Glu Pro Glu Glu Pro Pro Ala Ala Ala Ala
50 55 60

Phe Pro Pro Ala Ala Glu Glu Leu Gly Leu Gly His Asp Gly Val Arg
65 70 75 80

Val Arg Gly Ala Gln Cys Met Arg Ala Ala Pro Gln Gly Pro Pro Arg
85 90 95

Ser Gln Leu

<210> 1533
<211> 59
<212> PRT

<213> Artificial Sequence

<220>
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polypeptide"

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<223> /note="p.L364fs"

<400> 1533
Lys Glu Ala Ser Ser Thr Phe Ser Trp Gly Ile Val Leu Ala Pro Leu
1 5 10 15

Ser Leu Ala Phe Leu Val Leu Gly Gly Asn Met Asp Ala Gln Thr Val
20 25 30

Gln Thr Gln Asn Trp Lys Ser Arg Trp Ser Asp Cys Ala Met Ala Ser
35 40 45

Ser Ser Arg Leu Ser Ile Leu Ser Gln Val Lys
50 55

<210> 1534
<211> 52
<212> PRT
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<223> /note="p.F50C"

<400> 1534
Asp Asp Trp Gly Leu Asp Thr Met Arg Gln Ile Gln Val Phe Glu Asp
1 5 10 15

Glu Pro Ala Arg Ile Lys Cys Pro Leu Cys Cys Glu His Phe Leu Lys
20 25 30

Phe Asn Tyr Ser Thr Ala His Ser Ala Gly Leu Thr Leu Ile Trp Tyr
35 40 45

Trp Thr Arg Gln
50

<210> 1535
<211> 52
<212> PRT
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<220>
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<223> /note="p.T647M"

<400> 1535
Lys His Glu Ile Pro Ala Thr Thr Leu Pro Val Pro Ser Leu Gly Asn
1 5 10 15

His His Thr Tyr Cys Asn Leu Pro Leu Met Met Leu Leu Asn Gly Gln
20 25 30

Leu Pro Leu Asn Asn Thr Leu Lys Asp Thr Gln Glu Phe His Arg Asn
35 40 45

Ser Ser Leu Leu
50

<210> 1536
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R103M"

<400> 1536
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
1 5 10 15

Gln Ser Lys Asn Phe His Leu Arg Pro Met Met Asp Leu Ile Ser Asn
20 25 30

Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
35 40 45

Cys Glu Tyr Ala

50

<210> 1537
<211> 65
<212> PRT
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<400> 1537
His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu
1 5 10 15

Tyr Arg Val Ser Leu Ala Cys Val Cys Ala Ala Pro Cys Asp Gly Leu
20 25 30

Ala Gly Pro Ala Gly Gly Trp Ser Leu Phe Gly Lys Pro Gly Ala Arg
35 40 45

Cys Thr Thr Thr Cys His Glu Gly Pro Gly Cys Pro Asp Ala Trp Pro
50 55 60

Leu
65

<210> 1538
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.A90T"

<400> 1538
Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
1 5 10 15

Asn Arg Ala Val Lys Ser Leu Gln Asn Thr Thr Ser Ala Ile Glu Ser
20 25 30

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
35 40 45

Thr Arg His Pro
50

<210> 1539
<211> 46
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.P215T"

<400> 1539
Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe
1 5 10 15

Met Ser Ser Phe Gln Ser Tyr Gly Ala Thr Thr Arg Gly Asp Lys Glu
20 25 30

Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
35 40 45

<210> 1540
<211> 36
<212> PRT
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<223> /note="p.D218fs"

<400> 1540
Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser
1 5 10 15

Phe Gln Ser Tyr Gly Ala Pro Arg Gly Glu Gln Gly Gly Ala Asp Thr
20 25 30

Pro Glu Val Leu
        35

<210> 1541
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.L47I"

<400> 1541
Leu Leu Pro Asp Glu Lys Ile Ser Leu Leu Pro Pro Val Asn Phe Thr
1   5   10   15

Ile Lys Val Thr Gly Leu Ala Gln Val Ile Ile Leu Gln Trp Lys Pro
            20   25   30

Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu Tyr Gln Val Lys
        35   40   45

Ile Asn Ala Pro
    50

<210> 1542
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.P216H"

<400> 1542
Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys
1   5   10   15

Val Thr Ser Asp His Ile Asn Phe Asp His His Val Tyr Lys Val Lys
            20   25   30

Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser
35 40 45

Ser Ile Leu Lys
50

<210> 1543
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S54L"

<400> 1543
Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser
1 5 10 15

Gln Leu Glu Val Asn Gly Ser Gln His Leu Leu Leu Thr Cys Ala Phe
20 25 30

Glu Asp Pro Asp Val Asn Ile Thr Asn Leu Glu Phe Glu Ile Cys Gly
35 40 45

Ala Leu Val Glu
50

<210> 1544
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E484K"

<400> 1544
Val Lys Val Leu Gln Asp Met Gly Leu Pro Thr Gly Ala Glu Gly Arg
1 5 10 15

Asp Ser Ser Lys Gly Glu Asp Ser Ala Lys Lys Glu Thr Glu Ala Lys

20 25 30

Pro Ala Val Val Ala Pro Ala Pro Val Val Glu Ala Val Ser Thr Pro
35 40 45

Ser Ala Ala Phe
50

<210> 1545
<211> 52
<212> PRT
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<220>
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<223> /note="p.P1340A"

<400> 1545
Lys Leu Val Phe Ile Arg Asn Glu Asp Ala Val Asn Gln Met Ala Val
1 5 10 15

Thr Pro Phe Pro Val Pro Ser Ser Ser Ala Ala Ser Ser Ile Glu Asp
20 25 30

Gln Ser Gly Thr Glu Pro Ile Ser Ser Glu Glu Asp Gly Ser Val Glu
35 40 45

Val Gly Ile Lys
50

<210> 1546
<211> 52
<212> PRT
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<220>
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<223> /note="p.S527fs"

<400> 1546
Pro Leu Leu Pro Gly Met Gly Trp Gly Pro Pro Pro Pro Pro Pro Pro
1 5 10 15

Leu Leu Pro Cys Thr Cys Ser Pro Pro Trp Arg Glu Ala Trp Arg Arg
20 25 30

Ser Ser Trp Pro Arg Trp Thr Met Ala Trp Ala Gln His Gly Ser Pro
35 40 45

Ala Ile Gly Gly
50

<210> 1547
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A220S"

<400> 1547
Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala Gln Lys
1 5 10 15

Arg Arg Met Leu His Cys Val Gln Arg Ser Ser Leu Ile Arg Ser Gln
20 25 30

Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu Leu
35 40 45

Val Glu Asn Arg
50

<210> 1548
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G56V"

<400> 1548
Pro Ser Pro Glu Ala Glu Met Leu Lys Phe Asn Leu Glu Cys Leu His
1 5 10 15

Lys Thr Phe Gly Pro Gly Gly Leu Gln Val Val Asp Thr Leu Ile Asp
20 25 30

Ile Gly Ser Gly Pro Thr Ile Tyr Gln Val Leu Ala Ala Cys Asp Ser
35 40 45

Phe Gln Asp Ile
50

<210> 1549
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S212F"

<400> 1549
Leu Lys Pro Gly Gly His Leu Val Thr Thr Val Thr Leu Arg Leu Pro
1 5 10 15

Ser Tyr Met Val Gly Lys Arg Glu Phe Phe Phe Cys Val Ala Leu Glu
20 25 30

Lys Glu Glu Val Glu Gln Ala Val Leu Asp Ala Gly Phe Asp Ile Glu
35 40 45

Gln Leu Leu His
50

<210> 1550
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R523Q"

<400> 1550
Ser Phe Met Phe Asn Gly Thr Ser Leu Gly Phe Val Asn Ser His Leu
1   5   10   15

Thr Ser Gly Ser Glu Lys Lys Leu Arg Gln Gln Asn Gln Asn Tyr Met
            20   25   30

Asn Ile Leu Arg Phe Leu Ala Leu Gly Asp Lys Lys Leu Ser Pro Phe
        35   40   45

Asn Ile Thr His
    50

<210> 1551
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R263C"

<400> 1551
Glu Gly Arg Leu Leu Phe Pro Pro Thr Tyr Lys Phe Asp Arg Asn Ser
1   5   10   15

Asn Asp Tyr Asp Thr Ser Glu Lys Lys Cys Cys Lys Pro Ala Trp Thr
            20   25   30

Asp Arg Ile Leu Trp Arg Leu Lys Arg Gln Pro Cys Ala Gly Pro Asp
        35   40   45

Thr Pro Ile Pro
    50

<210> 1552
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.T493M"

<400> 1552
Val Phe Gly Thr Gln Glu Asn Ser Val Gly Asp Arg Glu Trp Leu Asp
1   5   10   15

Leu Leu Arg Gly Gly Leu Lys Glu Leu Met Met Asp Leu Asp Tyr Arg
            20   25   30

Pro Ile Ala Met Gln Ser Leu Trp Asn Ile Lys Val Ala Val Leu Val
        35   40   45

Lys Pro Glu His
    50

<210> 1553
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A974fs"

<400> 1553
Ala Pro Arg Glu Glu Pro Leu Thr Pro Arg Leu Lys Pro Glu Gly Ala
1   5   10   15

Pro Glu Pro Glu Gly Val Ala Ala Pro His Pro Arg Thr Ala Ser Ile
            20   25   30

Thr Leu Pro Thr Thr Ser Leu Lys Gly Ser Arg Thr Ser Cys Cys Pro
        35   40   45

Arg Ser His Pro Arg Leu Pro Gly Pro Leu Ser His Leu Pro Pro Arg
    50   55   60

Thr Lys Trp Pro Leu Gln Cys Leu Leu His Ser Leu Gly Thr Thr Gly
65   70   75   80

Thr Leu Val Trp Glu Arg Gly Val Leu Gln Met Arg Ser Leu Glu Ala
                85   90   95

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His Cys Pro Leu Gln Thr Phe His Leu His His Cys Arg Thr Gln Pro
            100                 105                 110

Ser Ser Cys Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln Trp Ser Gly
        115                 120                 125

Ala Val Val Gly Leu Arg Pro Val Ala His His Leu Pro Arg Pro Ile
    130                 135                 140

Gln Gly Leu His Cys Pro Gln Ala Pro His Gln Pro Ala Leu Ser Trp
145                 150                 155                 160

Gly Lys Trp Pro Val Gly Met Thr Gly Pro Ala Arg Cys Cys Arg Trp
                165                 170                 175

Pro Arg Arg
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<210> 1554
<211> 70
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.P1154fs"

<400> 1554

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Ser Glu Val Asp Tyr Ala Pro Ala Gly Pro Ala Arg Ser Ala Leu Leu
1               5                   10                  15

Pro Gly Pro Leu Glu Leu Gln Pro Pro Gly Asp Cys Pro Arg Thr Met
            20                  25                  30

Ala Gly Pro Ser Ala Ser Leu His Pro Ala Ser Gly Arg Ala Ser Arg
        35                  40                  45

Lys Thr Trp Gln Arg Arg Leu Arg Ala Cys Arg Ala Gly Gly Pro Ala
    50                  55                  60

Gly Trp Ala Arg Gln Ala
65                  70
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<210> 1555
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.M1V"

<400> 1555
Val Val Ala Ala Thr Val Asn Leu Glu Leu Asp Pro Ile Phe Leu Lys
1 5 10 15

Ala Leu Gly Phe Leu His Ser Lys Ser Lys Asp
20 25

<210> 1556
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S460A"

<400> 1556
Met Arg Lys Ile Ser Asn Asn Ile Thr Leu Arg Glu Asp Gln Leu Asp
1 5 10 15

Thr Val Leu Ala Val Leu Glu Asp Ser Ala Ala Arg Asp Ile Arg Glu
20 25 30

Ala Leu His Glu Leu Leu Cys Cys Thr Asn Val Ser Thr Lys Glu Gly
35 40 45

Ile His Leu Ala
50

<210> 1557
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R940C"

<400> 1557
Gly Ile Val Trp Lys Thr Gly Pro Arg Thr Thr Ile Phe Val Lys Ser
1 5 10 15

Leu Glu Asp Pro Tyr Ser Gln Gln Ile Cys Cys Leu Gln Gln Gln Gln
20 25 30

Ala Gln Gln Pro Leu Gln Gln Gln Gln Gln Arg Asn Ala Tyr Thr Arg
35 40 45

Phe

<210> 1558
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R106I"

<400> 1558
Leu Cys Val Leu Lys Val Thr Gln Gln Ser Glu Lys His Leu Glu Lys
1 5 10 15

Ile Leu Asn Val Asp Glu Phe Val Lys Ile Ile Ile Phe Ser Val Ile
20 25 30

His Ser Asn Asp Pro Val Ala Arg Ala Ile Thr Leu Arg Met Leu Gly
35 40 45

Ser Leu Ala Ser
50

<210> 1559

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R799K"

<400> 1559
Trp Lys Pro Ser Arg Arg His Asp Thr Glu Pro Lys Ala Lys Cys Ala
1 5 10 15

Pro Gln Lys Arg Arg Thr Gln Glu Leu Lys Lys Gly Gly Arg Cys Ser
20 25 30

Pro Ala Gly Ser Ser Arg Pro Gly Ser Ala Arg Gly Glu Ala Val His
35 40 45

Ala Gly Gln Asn
50

<210> 1560
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R815fs"

<400> 1560
Lys Arg Arg Thr Gln Glu Leu Arg Gly Gly Arg Cys Ser Pro Ala Gly
1 5 10 15

Ser Ser Arg Pro Gly Ser Ala Arg Gly Arg Arg Ser Met Leu Gly Arg
20 25 30

Ile Leu Pro Thr Ile Val His Gln Glu Thr Lys
35 40

<210> 1561
<211> 46

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S844fs"

<400> 1561
Glu Arg Tyr Pro Val Val Met Ser Thr Tyr Leu Gly Val Met Gly Arg
1 5 10 15

Val Leu Leu Gln Asn Thr Ser Phe Phe Leu His Tyr Leu Met Arg Trp
20 25 30

Pro Ile Asn Leu Ile Arg Arg Trp Thr Ser Phe Trp Glu Ile
35 40 45

<210> 1562
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R267Q"

<400> 1562
Pro Tyr Met Arg Asn Gly Thr Leu Phe Asp Arg Leu Gln Cys Val Gly
1 5 10 15

Asp Thr Ala Pro Leu Pro Trp His Ile Gln Gln Ile Gly Ile Leu Ile
20 25 30

Gly Ile Ser Lys Ala Ile His Tyr Leu His Asn Val Gln Pro Cys Ser
35 40 45

Val Ile Cys Gly
50

<210> 1563
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R419Q"

<400> 1563
His Leu Glu His Thr Gly Phe Ser Lys Ala Lys Leu Glu Ser Met Glu
1 5 10 15

Thr Tyr Leu Lys Ala Val Lys Leu Phe Gln Gln Asn Asp Gln Asn Ser
20 25 30

Ser Gly Glu Pro Glu Tyr Ser Gln Val Ile Gln Ile Asn Leu Asn Ser
35 40 45

Ile Val Pro Ser
50

<210> 1564
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K123R"

<400> 1564
Arg Cys Ala Leu Asn Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg
1 5 10 15

Ser Gln Leu Asp Ile Ser Asp Pro Tyr Arg Arg Val Tyr Arg Ile Val
20 25 30

Pro Glu Gly Ala Lys Lys Gly Ala Lys Gln Leu Thr Leu Glu Asp Pro
35 40 45

Gln Met Ser Met
50

<210> 1565
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G591fs"

<400> 1565
Gly His Gly Ser Gly Gly Gly Gln Gly Pro Gly Asp Gly His Gly Ser
1 5 10 15

Gly Gly Gly Lys Asn Ser Gly Gly Gly Gln Arg Leu Arg Lys Trp Glu
20 25 30

Arg Ile Arg Trp
35

<210> 1566
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.21_22AA>A"

<400> 1566
Met Ala Ser Cys Ser Phe Thr Arg Asp Gln Ala Thr Arg Arg Leu Arg
1 5 10 15

Gly Ala Ala Ala Ala Ala Ala Ala Ala Leu Ala Ala Val Val Thr Thr
20 25 30

Pro Leu Leu Ser Ser Gly Thr Pro Thr Ala Leu Ile Gly Thr Gly Ser
35 40 45

Ser Cys Pro Gly Ala
50

<210> 1567

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L422P"

<400> 1567
Leu Val Ser Ala Pro Leu Gly Lys Phe Pro Ala Trp Thr Asn Arg Pro
1 5 10 15

Phe Pro Gly Pro Pro Pro Gly Pro Arg Pro Pro His Pro Leu Ser Leu
20 25 30

Leu Gly Ser Ala Pro Pro His Leu Leu Gly Leu Pro Gly Ala Ala Gly
35 40 45

His Pro Ala Ala
50

<210> 1568
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A425V"

<400> 1568
Cys Asp Glu Ser Ser Cys Ile Pro Lys Ala Phe Gly Asn Pro Lys Phe
1 5 10 15

Ala Leu Gln Gly Leu Pro Leu Asn Cys Val Val Pro Cys Pro Arg Arg
20 25 30

Ser Glu Pro Val Val Gln Cys Gln Tyr Pro Ser Gly Ala Glu Ala Gly
35 40 45

<210> 1569
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R86C"

<400> 1569
Ala Ala Ser Gly Ser Gly Leu Glu Lys Pro Pro Lys Asp Gln Pro Gln
1 5 10 15

Glu Gly Arg Lys Ser Lys Arg Arg Val Cys Cys Thr Thr Phe Thr Thr
20 25 30

Glu Gln Leu His Glu Leu Glu Lys Ile Phe His Phe Thr His Tyr Pro
35 40 45

Asp Val His Ile
50

<210> 1570
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.C2F"

<400> 1570
Met Phe Phe Ala Glu Val Gly Pro Ala Leu Cys Arg Gly Met Glu Arg
1 5 10 15

Asn Ser Leu Gly Cys Cys Glu Ala Pro Lys Lys Leu
20 25

<210> 1571
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R669Q"

<400> 1571
Pro Ile Val His Leu Thr Pro Ser Leu Glu Val Thr Pro Gln Ala Ile
1 5 10 15

Ser Val Val Gln Arg Asp Cys Arg Arg Gln Gln Gly Gln Glu Ala Val
20 25 30

Cys Leu Thr Ala Ala Leu Cys Phe Gln Val Thr Ser Arg Thr Pro Gly
35 40 45

Arg Trp Asp His
50

<210> 1572
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T673M"

<400> 1572
Tyr Leu Ala Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu
1 5 10 15

Phe Asn Ala Gly Asp Asp Ala Tyr Glu Met Met Thr Leu His Val Lys
20 25 30

Leu Pro Val Gly Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Glu Lys
35 40 45

Gln Ile Asn Cys
50

<210> 1573
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F900L"

<400> 1573
Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
1 5 10 15

Ile Lys Ala Asp Pro His Cys Leu Asn Leu Leu Leu Cys Asn Phe Gly
20 25 30

Lys Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly
35 40 45

Arg Pro Ser Ile
50

<210> 1574
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A48D"

<400> 1574
Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu Leu Pro Pro Pro Pro Arg
1 5 10 15

Val Gly Gly Phe Asn Leu Asp Ala Glu Asp Asp Pro Ala Val Leu Ser
20 25 30

Gly Pro Pro Gly Ser Phe Phe Gly Phe Ser Val Glu Phe Tyr Arg Pro
35 40 45

Gly Thr Asp Gly
50

<210> 1575

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G616C"

<400> 1575
Thr Glu Phe Arg Asp Lys Leu Ser Pro Ile Asn Ile Ser Leu Asn Tyr
1 5 10 15

Ser Leu Asp Glu Ser Thr Phe Lys Glu Cys Cys Leu Glu Val Lys Pro
20 25 30

Ile Leu Asn Tyr Tyr Arg Glu Asn Ile Val Ser Glu Gln Ala His Ile
35 40 45

Leu Val Asp Cys
50

<210> 1576
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R685H"

<400> 1576
Lys Arg Ser Lys Asn Leu Leu Gly Ser Arg Asp Leu Gln Ser Ser Val
1 5 10 15

Thr Leu Asp Leu Ala Leu Asp Pro Gly His His Leu Ser Pro Arg Ala
20 25 30

Thr Phe Gln Glu Thr Lys Asn Arg Ser Leu Ser Arg Val Arg Val Leu
35 40 45

Gly Leu Lys Ala
50

<210> 1577
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R283H"

<400> 1577
Thr Asp Gly Lys Lys Glu Gly Asp Ser Leu Asp Tyr Lys Asp Val Ile
1 5 10 15

Pro Met Ala Asp Ala Ala Gly Ile Ile His His Tyr Ala Ile Gly Val
20 25 30

Gly Leu Ala Phe Gln Asn Arg Asn Ser Trp Lys Glu Leu Asn Asp Ile
35 40 45

Ala Ser Lys Pro
50

<210> 1578
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L378I"

<400> 1578
Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile
1 5 10 15

Gln Leu Ile Ile Asp Ala Tyr Asn Ser Ile Ile Ser Ser Glu Val Ile
20 25 30

Leu Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser
35 40 45

Tyr Cys Lys Asn
    50

<210> 1579
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.D158N"

<400> 1579
Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu
1   5   10   15

Met Asp Leu Ser Tyr Ser Met Lys Asp Asn Asn Leu Glu Asn Val Lys
            20   25   30

Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile Thr Ser Asp
        35   40   45

Phe Arg Ile Gly
    50

<210> 1580
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A7fs"

<400> 1580
Met Cys Gly Ser Ala Leu Ala Phe Phe Tyr Arg Cys Ile Cys Leu Pro
1   5   10   15

Ala Lys Arg Pro Ala Arg Ser Arg Leu Val Pro Leu Gly Ser Leu Gly
            20   25   30

Val Phe Thr Cys Ser Trp Thr Gly Pro Arg
35 40

<210> 1581
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G254W"

<400> 1581
Lys Gly His Val Leu Phe Arg Pro Thr Val Ser Gln Gln Gln Ser Cys
1 5 10 15

Pro Thr Cys Ser Thr Ser Leu Leu Asn Trp Trp His Phe Lys Val Thr
20 25 30

Tyr Asp Val Ser Arg Asp Lys Ile Cys Asp Leu Leu Val Ala Asn Asn
35 40 45

His Phe Ala His
50

<210> 1582
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L842V"

<400> 1582
Thr Leu Asp Lys Glu Met Ser Phe Ser Val Leu Leu His Arg Val Trp
1 5 10 15

Lys Lys His Pro Val Asn Val Asp Phe Val Val Gly Ile Tyr Ile Pro
20 25 30

Pro Thr Asn Lys Phe Ser Pro Lys Ala His Gly Leu Ile Gly Gln Phe

35 40 45

Met Gln Glu Pro
50

<210> 1583
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E196K"

<400> 1583
Pro Glu Glu Thr Val Val Ile Ala Leu Tyr Asp Tyr Gln Thr Asn Asp
1 5 10 15

Pro Gln Glu Leu Ala Leu Arg Arg Asn Lys Lys Glu Tyr Cys Leu Leu
20 25 30

Asp Ser Ser Glu Ile His Trp Trp Arg Val Gln Asp Arg Asn Gly His
35 40 45

Glu Gly Tyr Val
50

<210> 1584
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R29L"

<400> 1584
Phe Ile Leu Leu Glu Glu Gln Leu Ile Lys Lys Ser Gln Gln Lys Arg
1 5 10 15

Arg Thr Ser Pro Ser Asn Phe Lys Val Leu Leu Phe Phe Val Leu Thr
20 25 30

Lys Ala Ser Leu Ala Tyr Phe Glu Asp Arg His Gly Lys Lys Arg Thr
35 40 45

Leu Lys Gly Ser
50

<210> 1585
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E167K"

<400> 1585
Ala Asp Ile Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp
1 5 10 15

Ile Ser Leu Asp Lys Cys Tyr Val Ile Lys Lys Leu Asn Thr Thr Ile
20 25 30

Val Leu Pro Pro Arg Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg
35 40 45

Gly Thr Tyr Leu
50

<210> 1586
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M1569I"

<400> 1586
Cys Gly Leu Glu Arg Asp Lys Phe Asp Asn Lys Thr Val Thr Phe Glu
1 5 10 15

Glu His Ile Lys Glu Glu His Asn Met Ile Cys His Tyr Leu Cys Phe
20 25 30

Ile Val Leu Val Lys Val Lys Asp Ser Thr Glu Tyr Thr Gly Pro Glu
35 40 45

Ser Tyr Val Ala
50

<210> 1587
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P358Q"

<400> 1587
Arg Asp Gly Val Pro Pro Thr Ser Lys Lys Lys Arg Gln Ala Gly Glu
1 5 10 15

Lys Ile Met Tyr Thr Leu Val Ser Val Gln Gln His Gly Asn Asp Ile
20 25 30

Ala Ser Leu Phe Glu Leu Asp Ala Thr Thr Leu Gln Arg Ala Asp Cys
35 40 45

Leu Val Pro Arg
50

<210> 1588
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S802fs"

<400> 1588

Phe Gln Ala Thr Ser Lys Lys Gly Ile Ser Arg Leu Asp Lys Gln Met
1 5 10 15

Arg Lys Phe Thr Asp Ile Arg Lys Lys Ala Asp Leu His Thr Gln
20 25 30

<210> 1589
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A462T"

<400> 1589
Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp Ile Asn Ile Asn
1 5 10 15

Asp Cys Leu Gly Gln Cys Gln Asn Asp Thr Thr Ser Cys Arg Asp Leu
20 25 30

Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala Gly Asp His
35 40 45

Cys Glu Arg Asp
50

<210> 1590
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V310I"

<400> 1590
Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn
1 5 10 15

Trp Phe His Ser Asn Asp Gly Gly Asn Ile Ile Leu Tyr Tyr Glu Val

20 25 30

Met Val Thr Gly Asn Leu Gly Ile Gln Trp Arg His Lys Pro Asn Val
35 40 45

Val Ser Val Glu
50

<210> 1591
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R283I"

<400> 1591
Met Ser Ser Pro Lys Arg Glu Ile Pro Gly Arg Ala Gly Asp Gly Ser
1 5 10 15

Glu His Cys Ser Ser Pro Asp Leu Arg Ile Ile Asn Gln Lys Arg Ile
20 25 30

Ala Glu Leu Asn Ala Thr Ile Arg Lys Leu Glu Asp Arg Asn Thr Leu
35 40 45

Leu Gly Asp Glu
50

<210> 1592
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G394fs"

<400> 1592
Val Asn His Thr Ile Ser Gly Lys Thr Glu Ser Ser Asn Ala Lys Thr
1 5 10 15

Arg Lys Gln Val Leu Ser Leu Gly Gly Gly Val Gln Val His Trp Ala
20 25 30

Arg Arg Gln Trp Pro Gln Gly Gln Trp Gln Val Glu Pro Lys Val Met
35 40 45

His

<210> 1593
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V422fs"

<400> 1593
Thr Gly Pro Ala Val Asn Gly Leu Lys Val Ser Gly Arg Leu Asn Pro
1 5 10 15

Lys Ser Cys Thr Lys Glu Val Gly Gly Gly Ser Cys Gly Arg Ala Cys
20 25 30

Ser Cys Gly Arg Gly Cys Gly Thr Pro Arg Gly Asp Trp Lys Arg His
35 40 45

Thr Arg Arg Arg Ser Arg Ser Arg Pro Pro Arg Arg
50 55 60

<210> 1594
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R97fs"

<400> 1594
His His Ala Val Asp Ile Asp Leu Tyr His Cys Pro Asn Cys Ala Val
1 5 10 15

Leu His Gly Ser Ser Leu Met Lys Lys Gly Gly Thr Gly Thr Asp Met
20 25 30

Thr Thr Gln Lys Leu Met Met Val Pro Asn Gln Cys Lys Leu Glu Leu
35 40 45

Glu Leu Ser Leu Arg Asn Tyr Ala Leu Glu Ser Ser Gln Val Pro Met
50 55 60

Lys
65

<210> 1595
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R313H"

<400> 1595
Thr Ser Val Trp Tyr His Val Leu Trp Gly Glu Lys Ile Phe Tyr Leu
1 5 10 15

Ile Lys Pro Thr Asp Glu Asn Leu Ala His His Tyr Glu Ser Trp Ser
20 25 30

Ser Ser Val Thr Gln Ser Glu Val Phe Phe Gly Asp Lys Val Asp Lys
35 40 45

Cys Tyr Lys Cys
50

<210> 1596
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R1198S"

<400> 1596
Ser His Ser Val Thr Thr Phe Arg Asn Asp Cys Arg Ser Pro Thr His
1 5 10 15

Leu Thr Val Ser Ser Thr Asn Thr Leu Ser Ser Ser Met Pro Ala Leu
20 25 30

His Arg Ala Pro Val Phe His Pro Pro Ile His His Ser Leu Glu Arg
35 40 45

Lys Glu Gly Ser
50

<210> 1597
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A11V"

<400> 1597
Met Arg Ala Gly Pro Glu Pro Gln Ala Leu Val Val Gly Gln Lys Arg
1 5 10 15

Gly Ala Leu Arg Leu Leu Val Pro Arg Leu Val Leu Thr Val Ser Ala
20 25 30

Pro Ala Glu Val Arg
35

<210> 1598
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.PPPPPPPPPPPP811del"

<400> 1598
Leu Asn Asn Asn Leu Glu Pro Cys Ser Val Thr Ile Asn Pro Leu Pro
1   5   10   15

Ser Pro Leu Pro Pro Thr Pro Pro Pro Leu Pro Val Ala Lys Asp Ser
            20   25   30

Gly Pro Glu Thr Leu Glu Lys Asp Leu Pro Arg Lys Glu Gly Asn Glu
        35   40   45

Lys Arg Ile Pro Lys Ser Ala Ser Ala Pro Ser Ala His Leu Phe Asp
    50   55   60

Ser Ser Gln Leu Val Ser Ala Arg Lys Lys Leu Arg Lys Thr Ala Glu
65   70   75   80

Gly Leu Gln Arg Arg Arg
                85

<210> 1599
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A395T"

<400> 1599
Ala Arg Thr Lys Val Glu Ile Ala Asn Ser Arg Thr Ala His Ala Arg
1   5   10   15

Ala Lys Ala Asp Ala Ala Asp Gln Ala Thr Thr Leu Ala Ala Arg Gln
            20   25   30

Glu Cys Asp Ile Ala Arg Ala Val Ala Arg Glu Leu Ser Pro Asp Phe
        35   40   45

Tyr Gln Pro Gly
    50

<210> 1600
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q433H"

<400> 1600
Glu Ala Arg Ile Ala Arg Ile Thr Ala Lys Glu Phe Ser Pro Ser Phe
1 5 10 15

Gln His Arg Glu Asn Gly Leu Glu Tyr His His Arg Pro Lys Arg Gln
20 25 30

Thr Ser Cys Asp Asp Ile Glu Val Leu Ser Thr Gly Thr Pro Leu Gln
35 40 45

Gln Glu Ser Pro
50

<210> 1601
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V92A"

<400> 1601
Glu Lys Glu Pro Ala Ala Arg Gly Thr Pro Gly Thr Gly Lys Glu Arg
1 5 10 15

Leu Lys Ala Gly Ala Ser Pro Arg Ser Ala Ala Pro Ala Arg Lys Lys
20 25 30

Ala Gln Thr Ala Pro Pro Leu Gln Pro Pro Pro Pro Pro Pro Ala Leu
35 40 45

Ser Glu Glu Leu
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<210> 1602
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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      polypeptide"

<220>
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<223> /note="p.S627L"

<400> 1602
Arg Val Ala Ala Gly Val Leu Cys Glu Leu Ala Gln Asp Lys Glu Ala
1   5   10   15

Ala Asp Ala Ile Asp Ala Glu Gly Ala Leu Leu Ala Pro Leu Met Glu
            20   25   30

Leu Leu His Ser Arg Asn Glu Gly Thr Ala Thr Tyr Ala Ala Ala Val
        35   40   45

Leu Phe Arg Ile
    50

<210> 1603
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V303I"

<400> 1603
Ser Lys His Phe Arg Ser Ser Lys Asp Pro Ser Ala Pro Pro Ala Pro
1   5   10   15

Ala Asn Leu Arg Leu Ala Asn Ser Thr Ile Ile Asn Ser Asp Gly Ser
            20   25   30

Val Thr Val Thr Ile Val Trp Asp Leu Pro Glu Glu Pro Asp Ile Pro
35 40 45

Val His His Tyr
50

<210> 1604
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R359H"

<400> 1604
Val Glu Ala Asp Ala Trp Val Thr Glu Ala Leu Leu Gly Leu Pro Ala
1 5 10 15

Ala Ala Glu Arg Glu Leu Glu Leu Leu His His Ala Ser Leu Glu His
20 25 30

Gln Arg Gly Val Ser Glu Leu Leu Arg Gly Arg Leu Arg Glu Leu Glu
35 40 45

Glu Ala Arg Glu
50

<210> 1605
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S253P"

<400> 1605
Val Gln Glu Gly Ala Glu Pro Pro Glu Gly Val Val Lys Val Pro Asn
1 5 10 15

His Leu Pro Leu Pro Gly Pro Pro Phe Pro Pro Phe Gln Asn Val Leu

20 25 30

Val Val Leu Glu Asp Lys Glu Asp Glu His Asn Ala Arg Glu Ala Glu
35 40 45

Val Leu Phe Thr
50

<210> 1606
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G376E"

<400> 1606
Ile Gly Trp Asn Thr Gly Ala Leu Val Ala Cys His Val Ser Val Met
1 5 10 15

Glu Tyr Val Thr Ala Val Val Cys Leu Glu Glu Phe Pro Leu Leu Thr
20 25 30

Val Asp Gly Pro Arg Gly Asp Val Asp Asp Pro Leu Leu Asp Met Lys
35 40 45

Thr Pro Val Leu
50

<210> 1607
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A81V"

<400> 1607
Gly Gly Phe Arg Ala Thr Leu Gln Val Leu Arg Gly Asp Arg Pro Ala
1 5 10 15

Leu Ala Ala Glu Asp Glu Leu Leu Gln Val Val Val Glu Cys Ala Ala
20 25 30

Phe Leu Gln Ala Pro Ala Leu Ala Arg Phe Leu Glu His Asn Leu Thr
35 40 45

Ser Asp Asn Cys
50

<210> 1608
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G442fs"

<400> 1608
Leu Ala Asp Arg Leu Leu Cys Arg Glu Gly Met Asp Val Ala Tyr Leu
1 5 10 15

Asn Gly Tyr Ile Tyr Ile Leu Gly Gly Ala Arg Pro Tyr Tyr Trp Ser
20 25 30

<210> 1609
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V549I"

<400> 1609
Tyr Leu Lys Leu Val Leu Phe Gln Asn Lys Leu His Leu Phe Val Arg
1 5 10 15

Ala Thr Gln Val Thr Val Glu Glu His Ile Ile Phe Arg Thr Ser Arg
20 25 30

Lys Asn Ser Leu Tyr Gln Tyr Asp Asp Ile Ala Asp Gln Trp Met Lys
35 40 45

Val Tyr Glu Thr
50

<210> 1610
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G376C"

<400> 1610
Glu Ala Glu Ser His Phe Ser Ser Ile Pro Asp Ala Phe Trp Trp Ala
1 5 10 15

Val Val Ser Met Thr Thr Val Gly Tyr Cys Cys Asp Met Tyr Pro Val
20 25 30

Thr Ile Gly Gly Lys Ile Val Gly Ser Leu Cys Ala Ile Ala Gly Val
35 40 45

Leu Thr Ile Ala
50

<210> 1611
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A415V"

<400> 1611
Thr Leu Lys Ala Ser Met Arg Glu Leu Gly Leu Leu Ile Phe Phe Leu
1 5 10 15

Phe Ile Gly Val Ile Leu Phe Ser Ser Val Val Val Tyr Phe Ala Glu
20 25 30

Ala Asp Asp Pro Thr Ser Gly Phe Ser Ser Ile Pro Asp Ala Phe Trp
35 40 45

Trp Ala Val Val
50

<210> 1612
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R231H"

<400> 1612
Ser Thr Ile Ala Leu Ser Leu Asn Thr Leu Pro Glu Leu Gln Glu Thr
1 5 10 15

Asp Glu Phe Gly Gln Leu Asn Asp Asn His His Gln Leu Ala His Val
20 25 30

Glu Ala Val Cys Ile Ala Trp Phe Thr Met Glu Tyr Leu Leu Arg Phe
35 40 45

Leu Ser Ser Pro
50

<210> 1613
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K455fs"

<400> 1613
Val Pro Val Ile Val Asn Asn Phe Gly Met Tyr Tyr Ser Leu Ala Met

1 5 10 15

Ala Lys Gln Lys Leu Pro Lys Lys Lys Arg Ser Ile Phe Arg Gly His
20 25 30

Arg Ser Trp Asp Leu Pro Ile Ile Val Asn Leu Ser
35 40

<210> 1614
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S438L"

<400> 1614
Asn Gln Arg Ala Asp Lys Arg Arg Ala Gln Lys Lys Ala Arg Leu Ala
1 5 10 15

Arg Ile Arg Val Ala Lys Thr Gly Ser Leu Leu Asn Ala Tyr Leu His
20 25 30

Ser Lys Arg Asn Gly Leu Leu Asn Glu Ala Leu Glu Leu Thr Gly Thr
35 40 45

Pro Glu Glu Glu
50

<210> 1615
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G149A"

<400> 1615
Met Phe Ile Leu Asn Phe Glu Val Val Met Glu Lys Asp Met Val Gly
1 5 10 15

Ser Pro Ala His Asp Thr Asn His Arg Ala Ala Pro Pro Thr Ser Trp
20 25 30

Leu Ala Pro Gly Arg Ala Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu
35 40 45

Leu Ala Leu Thr
50

<210> 1616
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M455I"

<400> 1616
Ser Ser Leu Thr Ser Val Gly Phe Gly Asn Val Ser Ala Asn Thr Asp
1 5 10 15

Ala Glu Lys Ile Phe Ser Ile Cys Thr Ile Ile Leu Ile Gly Ala Leu
20 25 30

Met His Ala Leu Val Phe Gly Asn Val Thr Ala Ile Ile Gln Arg Met
35 40 45

Tyr Ser Arg Trp
50

<210> 1617
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P102fs"

<400> 1617
Gly Thr Trp Phe Leu Phe Gly Val Val Trp Tyr Leu Val Ala Val Ala
1 5 10 15

His Gly Asp Leu Leu Glu Leu Asp Pro Arg Pro Thr Thr Pro Pro Val
20 25 30

Trp Tyr Arg Cys Thr His Ser Leu Glu Pro Ser Ser Ser Pro Leu Asn
35 40 45

Pro Lys Pro Pro Leu Ala Met Ala Ser Ala Thr Ser Val Arg Asn Val
50 55 60

His Trp Pro Leu Cys Phe Leu Leu Pro Ser Trp Cys Ser Pro Pro Ser
65 70 75 80

Trp Lys Ser Ser Ser Gln Val Pro Ser Trp Arg Arg Leu Pro Gly Pro
85 90 95

Arg Ser Gly Leu Arg Pro Phe Val Ser Ala Ser Met Gln Leu Trp Pro
100 105 110

Pro Thr Met Ala Ser Pro Ala Ser
115 120

<210> 1618
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L430F"

<400> 1618
Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser
1 5 10 15

Ser Thr Thr Ser Glu Lys Ala Tyr Ser Phe Phe Gly Asp Leu Pro Met
20 25 30

Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu
35 40 45

Val Ser Lys Thr
    50

<210> 1619
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S21G"

<400> 1619
Met Tyr Arg Pro Arg Ala Arg Ala Ala Pro Glu Gly Arg Val Arg Gly
1   5   10   15

Cys Ala Val Pro Gly Gly Thr Val Leu Leu Leu Leu Ala Tyr Leu Ala
            20   25   30

Tyr Leu Ala Leu Gly Thr Gly Val Phe Trp Thr Leu Glu Gly Arg
        35   40   45

<210> 1620
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G23V"

<400> 1620
Met Glu Val Ser Gly His Pro Gln Ala Arg Arg Cys Cys Pro Glu Ala
1   5   10   15

Leu Gly Lys Leu Phe Pro Val Val Leu Cys Phe Leu Cys Phe Leu Val
            20   25   30

Thr Tyr Ala Leu Val Gly Ala Val Val Phe Ser Ala Ile Glu Asp Gly
        35   40   45

Gln

<210> 1621
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S6W"

<400> 1621
Met Leu Pro Ser Ala Trp Trp Arg Glu Arg Pro Gly Tyr Arg Ala Gly
1 5 10 15

Val Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser
20 25 30

<210> 1622
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R166L"

<400> 1622
His Trp Asp Leu Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr
1 5 10 15

Thr Ile Gly Phe Gly Asn Ile Ser Pro Leu Leu Thr Glu Gly Gly Lys
20 25 30

Ile Phe Cys Ile Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe
35 40 45

Leu Leu Ala Gly
50

<210> 1623
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N151K"

<400> 1623
Lys Leu Leu Leu Tyr His Thr Glu Glu Thr Ile Lys Ile Asn Gln Lys
1 5 10 15

Cys Ser Tyr Ile Pro Lys Cys Gly Lys Lys Lys Phe Glu Glu Ser Met
20 25 30

Ser Leu Val Asn Val Val Met Glu Asn Phe Arg Lys Tyr Gln His Phe
35 40 45

Ser Cys Tyr Ser
50

<210> 1624
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D211N"

<400> 1624
Ser Arg Val Phe Ser Ile Leu Ser Ile Leu Val Val Met Gly Ser Ile
1 5 10 15

Ile Thr Met Cys Leu Asn Ser Leu Pro Asn Asn Phe Gln Ile Pro Asp
20 25 30

Ser Gln Gly Asn Pro Gly Glu Asp Pro Arg Phe Glu Ile Val Glu His
35 40 45

Phe Gly Ile Ala
50

<210> 1625
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L314fs"

<400> 1625
Lys Leu Tyr Arg Phe Phe Lys Tyr Ile Glu Asn Arg Asp Val Ala Lys
1 5 10 15

Thr Val Leu Lys Glu Arg Gly Leu Lys Thr Phe Ala Leu Glu Leu Lys
20 25 30

Val Thr Leu Pro Val Lys Lys Lys Leu Arg Glu Gly Leu Ala Ala Gly
35 40 45

Leu Lys Ser Ser Ile Ile Met Tyr Asn Ala Pro Ser Ser Arg Cys His
50 55 60

Gly Lys Arg Lys Lys Gly Arg Val Ala Met Trp Ile Ser Ser Val Phe
65 70 75 80

Glu Ala Asn Pro Ser Arg Ile Trp
85

<210> 1626
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T6M"

<400> 1626
Met Ser Asp Pro Ile Met Met Leu Asn Val Gly Gly Lys Leu Tyr Thr
1 5 10 15

Thr Ser Leu Ala Thr Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala
20 25 30

<210> 1627
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L447I"

<400> 1627
Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile Ala Lys
1 5 10 15

Ala Gly Gln Glu Phe Ala Arg Asn Asn Ile Ile Met Gly Asp Asp Ile
20 25 30

Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn Leu Gln Val
35 40 45

Ser Glu Pro Gln
50

<210> 1628
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F361L"

<400> 1628
His Leu Ser Asn Leu Glu Tyr Ala Cys Gly Ser Asn Leu His Gln Val
1 5 10 15

Ser Ala Arg Ser Trp Asp His Asn Glu Leu Leu Phe Ala Gln Phe Ala
20 25 30

Gly Asp His Thr Leu Leu Thr Pro Gly Tyr Ser Val Ile Ile Glu Lys

35 40 45

Leu Ala Glu Gly
50

<210> 1629
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1316fs"

<400> 1629
Ser Leu Arg Asp Leu Leu His Ser Gly Pro Gly Lys Leu Pro Gln Thr
1 5 10 15

Pro Leu Asp Thr Gly Ile Pro Phe Pro Arg Ser Ser Leu His Pro Gln
20 25 30

Gln Glu

<210> 1630
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P423S"

<400> 1630
Val Ser Ser Ile Glu Glu Asp Val Ile Val Glu Tyr Gly Ala Asp Ile
1 5 10 15

Ser Ser Lys Asp Phe Gly Ser Gly Phe Ser Ser Val Lys Asp Gly Arg
20 25 30

Arg Lys Ile Leu Pro Glu Glu Glu Glu Tyr Ala Leu Ser Gly Trp Asn
35 40 45

Leu Asn Asn Met
    50

<210> 1631
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R470C"

<400> 1631
Pro Glu Arg Asp Glu Trp His Leu Val Ala Pro Met Leu Thr Arg Arg
1   5   10   15

Ile Gly Val Gly Val Ala Val Leu Asn Cys Cys Leu Leu Tyr Ala Val
            20   25   30

Gly Gly Phe Asp Gly Thr Asn Arg Leu Asn Ser Ala Glu Cys Tyr Tyr
        35   40   45

Pro Glu Arg Asn
    50

<210> 1632
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G480W"

<400> 1632
Pro Met Leu Thr Arg Arg Ile Gly Val Gly Val Ala Val Leu Asn Arg
1   5   10   15

Leu Leu Tyr Ala Val Gly Gly Phe Asp Trp Trp Thr Asn Arg Leu Asn
            20   25   30

Ser Ala Glu Cys Tyr Tyr Pro Glu Arg Asn Glu Trp Arg Met Ile Thr
35 40 45

Ala Met Asn Thr
50

<210> 1633
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G603W"

<400> 1633
Leu Asp Ser Val Glu Cys Tyr Asp Pro Asp Thr Asp Thr Trp Ser Glu
1 5 10 15

Val Thr Arg Met Thr Ser Gly Arg Ser Trp Trp Val Gly Val Ala Val
20 25 30

Thr Met Glu Pro Cys Arg Lys Gln Ile Asp Gln Gln Asn Cys Thr Cys
35 40 45

<210> 1634
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S144F"

<400> 1634
Gly Met Glu Val Val Ser Ile Glu Gly Ile His Pro Lys Val Met Glu
1 5 10 15

Arg Leu Ile Glu Phe Ala Tyr Thr Ala Phe Phe Ile Ser Met Gly Glu
20 25 30

Lys Cys Val Leu His Val Met Asn Gly Ala Val Met Tyr Gln Ile Asp
35 40 45

Ser Val Val Arg
50

<210> 1635
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V155F"

<400> 1635
Pro Lys Val Met Glu Arg Leu Ile Glu Phe Ala Tyr Thr Ala Ser Ile
1 5 10 15

Ser Met Gly Glu Lys Cys Val Leu His Phe Phe Met Asn Gly Ala Val
20 25 30

Met Tyr Gln Ile Asp Ser Val Val Arg Ala Cys Ser Asp Phe Leu Val
35 40 45

Gln Gln Leu Asp
50

<210> 1636
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R260L"

<400> 1636
Asp Asp Leu Asn Val Arg Cys Glu Ser Glu Val Phe His Ala Cys Ile
1 5 10 15

Asn Trp Val Lys Tyr Asp Cys Glu Gln Leu Leu Arg Phe Tyr Val Gln

20 25 30

Ala Leu Leu Arg Ala Val Arg Cys His Ser Leu Thr Pro Asn Phe Leu
35 40 45

Gln Met Gln Leu
50

<210> 1637
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V411M"

<400> 1637
Arg Lys Leu Ser Gln Lys Leu Arg Glu Leu Thr Glu Gln Pro Pro Met
1 5 10 15

Pro Ala Arg Pro Arg Trp Met Lys Cys Met Met Glu Glu Thr Gly Thr
20 25 30

Phe Phe Glu Pro Thr Leu Ala Ala Leu Phe Val Arg Glu Ala Phe Gly
35 40 45

Pro Ser Thr Arg
50

<210> 1638
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S203L"

<400> 1638
Leu Asn Gly Ser Glu Asp Ser Gly Arg Gly Arg Gly Ile Arg Gly Arg
1 5 10 15

Gly Ile Arg Ile Ala Pro Thr Ala Pro Leu Leu Arg Gly Arg Gly Gly
20 25 30

Ala Ile Pro Pro Pro Pro Pro Gly Arg Gly Val Leu Thr Pro Arg
35 40 45

Gly Ser Thr Val
50

<210> 1639
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K63R"

<400> 1639
Arg Lys Val Ala Lys Glu Gly Gly Pro Lys Val Thr Ser Arg Asn Phe
1 5 10 15

Glu Lys Ser Ile Thr Lys Leu Gly Lys Arg Arg Gly Val Lys Gln Phe
20 25 30

Lys Asn Lys Gln Gln Gly Asp Lys Ser Pro Lys Asn Lys Phe Gln Pro
35 40 45

Ala Asn Lys Phe
50

<210> 1640
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T120fs"

<400> 1640
Ser Thr Pro Lys Arg Val Pro Met Gly Pro Ile Ile Val Pro Pro Gly
1 5 10 15

Gly His Ser Val Pro Ser Thr Pro Pro Arg Gly Asp His Arg Ser Asn
20 25 30

Gln Asn Arg Glu Trp Cys Leu Glu Glu
35 40

<210> 1641
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I902fs"

<400> 1641
Gly Leu Glu Thr Gly Trp Asn Cys His Ile Ser Leu Thr Pro Asn Gly
1 5 10 15

Asp Met Pro Gly Ser Glu Ile Pro Pro Pro Ala Pro Ala Thr Gln Ala
20 25 30

Pro Cys Met Met Thr
35

<210> 1642
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K895fs"

<400> 1642
Pro Met Asn His Asp Gln Phe His Leu Val Pro Asn His Ile Val Val
1 5 10 15

Ser Ala Glu Gly Asn Ile Ser Lys Lys Gln Asn Ala Leu Ala Glu His
20 25 30

<210> 1643
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R181Q"

<400> 1643
Tyr Arg Ala Val Ile Ile His Gly Phe Val Glu Glu Leu Val Val Asn
1 5 10 15

Glu Asp Pro Glu Tyr Gln Trp Ile Asp Gln Gln Ile Arg Thr Pro Arg
20 25 30

Ala Ser Asn Glu Ala Arg Gln Arg Leu Ile Ser Leu Met Ser Gly Glu
35 40 45

Leu Gln Arg Lys
50

<210> 1644
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1082W"

<400> 1644
Ser His Ser Ile Thr Ile Asp Phe Thr His Pro Cys His Val Ala Leu
1 5 10 15

Ile Arg Ile Trp Asn Tyr Asn Lys Ser Trp Trp Ile His Ser Phe Arg
20 25 30

Gly Val Lys Asp Ile Thr Met Leu Leu Asp Thr Gln Cys Ile Phe Glu

35 40 45

Gly Glu Ile Ala
50

<210> 1645
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L330I"

<400> 1645
Phe Pro Asp Gln Glu Arg Met Cys Ser Arg Pro Gly Ser Arg Arg Glu
1 5 10 15

Arg Pro Leu Ser Ala Thr Arg Lys Thr Ile Ile Cys Glu Ala Glu Tyr
20 25 30

Pro Glu Glu Asp Ala Ser Ala Val Leu Gln Ala Ile Gln Val Glu Asn
35 40 45

Ala Ala Leu Gln
50

<210> 1646
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A1592fs"

<400> 1646
Pro Arg Trp Glu Ser Ser Ala Thr Leu Arg Phe Thr Asp Ala Pro Cys
1 5 10 15

Gln Asp Val Ser Asp Ala Ala Val Ser Asp Leu Glu Asp Cys Ser Gln
20 25 30

Ser Leu Ser Leu Ser Thr Met Gln Glu Asp Met Glu Ser Ser Gly Ala
35 40 45

Asp Thr Phe
50

<210> 1647
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q446P"

<400> 1647
Gly Gln Ser Pro Met Gly Gly Pro Phe Ile Pro Ala Ala Pro Val Lys
1 5 10 15

Thr Ala Leu Pro Ala Gly Pro Gln Pro Pro Pro Pro Gln Pro Gln Pro
20 25 30

Pro Leu Pro Ser Gln Pro Gln Ala Gln Lys Arg Arg Phe Thr Glu Glu
35 40 45

Leu Pro Asp Glu
50

<210> 1648
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R516fs"

<400> 1648
Thr Gly Phe Ser Ser Gln Asn Glu Ile Glu Gly Ala Gly Ser Lys Pro
1 5 10 15

Ala Ser Ser Ser Gly Lys Glu Arg Glu Gly Gln Ala Val Asp Ala Ser
20 25 30

Thr Ser Leu Ser Ser Asp Trp Asn Lys Asn Arg Val Arg
35 40 45

<210> 1649
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L4680P"

<400> 1649
Ser Met Ser Leu His Gly Asn His Met Thr Leu Ala Cys Phe His Gly
1 5 10 15

Pro Asn Phe Arg Ser Lys Ser Trp Ala Pro Pro Phe His Leu Glu Glu
20 25 30

Pro Asn Ile Ala Phe Trp Thr Glu Ala Gln Lys Ile Trp Glu Asp Gly
35 40 45

Ser Ser Asp His
50

<210> 1650
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S4937Y"

<400> 1650
Ile Thr Tyr Thr Thr Val Asp Trp Arg Asp Phe Met Cys Asn Thr Trp
1 5 10 15

His Leu Glu Pro Thr Leu Arg Leu Ile Tyr Tyr Trp Thr Gly Arg Lys
20 25 30

Ile Asp Pro Val Gly Val Asp Tyr Ile Leu Gln Lys Leu Gly Phe His
35 40 45

His Ala Arg Thr
50

<210> 1651
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1588fs"

<400> 1651
Ala Asn Ser Leu Leu Asp Arg Gly Met Gln Leu Ser Gly Ser Thr Ser
1 5 10 15

Asn Thr Pro Tyr Thr Pro Leu Glu Lys Asn Ser Leu Ile Thr Gln Met
20 25 30

Met Lys His
35

<210> 1652
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A149V"

<400> 1652
Tyr Phe Arg Lys Gly Pro Phe Phe Gly Leu Ala Cys Phe Ala Asn Met
1 5 10 15

Pro Val Glu Ser Glu Leu Glu Arg Gly Val Val Arg Met Lys Ser Val

20 25 30

Gly Ile Leu Ser Pro Ser Tyr Thr Leu Leu Tyr Arg Tyr Met His Phe
35 40 45

Leu Glu Asn Gln
50

<210> 1653
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1203Q"

<400> 1653
Ser Val Thr Val Glu Ile Ser Asp Ser Ala Pro Pro Ala Pro Leu Val
1 5 10 15

Lys Glu Val Thr Lys Arg Phe Ser Thr Gln Gln Asp Ala Ala Pro Val
20 25 30

Ser Thr Glu Pro Ala Trp Leu Ala Leu Ala Lys Arg Lys Ala Lys Ala
35 40 45

Trp Ser Asp Cys
50

<210> 1654
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R308fs"

<400> 1654
Glu Arg Ala Pro Arg Glu Glu Gln Gln Arg Ser Leu Glu Ala Pro Gly
1 5 10 15

Trp Glu Asp Ala Glu Arg Arg Glu Arg Arg Ser Ala Ser Ala Trp Arg
20 25 30

Arg Arg Arg Ser Glu Gly Val Cys Arg Pro Arg Pro Lys Arg Arg Arg
35 40 45

Gly Gly Gly Trp Arg Arg Thr Pro Gly Trp Arg Ser Gly Gly Gly Arg
50 55 60

Arg Arg Arg Lys Glu Asp Ala Arg Arg Ser Ser Lys Gly Arg Arg Arg
65 70 75 80

Arg Arg Leu Arg Asp Gly Lys Ser Trp Asn Ser Arg Arg Arg Arg Cys
85 90 95

Arg Gly Arg Pro Arg Arg Trp Arg Arg Leu Gly Arg Ala Gly Gly Ala
100 105 110

Arg Arg Arg Arg Ile Trp Gly Lys Arg Arg Arg Arg Ala Arg Arg Thr
115 120 125

Trp Arg Thr Gly Gly Gly Ser Ser Val Ser Phe
130 135

<210> 1655
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E309fs"

<400> 1655
Arg Ala Pro Arg Glu Glu Gln Gln Arg Ser Leu Glu Ala Pro Gly Trp
1 5 10 15

Glu Asp Ala Glu Arg Arg Glu Arg Glu Gly Ala Arg Ala Pro Gly Gly
20 25 30

Gly Gly Gly Ala Lys Ala Ser Ala Gly Pro Gly Pro Ser Gly Gly Glu
35 40 45

Ala Ala Ala Gly Gly Gly Arg Gln Ala Gly Gly Ala Glu Ala Ala Gly
50 55 60

Gly Gly Gly Arg Lys Met Arg Gly Gly Ala Gln Lys Ala Gly Gly Gly
65 70 75 80

Gly Gly

<210> 1656
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S138F"

<400> 1656
Leu Arg Gly Trp Tyr Asn Cys Leu Thr Leu Ala Ile Tyr Gly Ser Val
1 5 10 15

Asp Arg Val Ile Ser His Asp Arg Asp Phe Phe Pro Pro Pro Pro Pro
20 25 30

Pro Pro Pro Pro Pro Pro Gln Pro Gln Pro Ser Leu Lys Arg Asn Pro
35 40 45

Lys His Ala Asp
50

<210> 1657
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1526N"

<400> 1657

Val Leu Ser Ala Pro Glu Ser Leu Gln Asn Leu Phe Asn Asn Arg Thr
1 5 10 15

Ala Tyr Val Leu Ala Asp Val Met Asp Asn Asn Gln Leu Lys Ser Met
20 25 30

Trp Phe Thr Pro Phe Gln Ala Glu Glu Ile Asp Thr Asp Leu Asp Leu
35 40 45

Val Lys Val Asp
50

<210> 1658
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1272F"

<400> 1658
Asp Gly Glu Arg Leu Ser Ala Val Lys Ser Ser Asp Leu Ile Asn Lys
1 5 10 15

Met Asp Leu Gln Arg Ala Ala Ile Ile Phe Phe Gly Tyr Arg Ile Gln
20 25 30

Gly Val Ile Ala Gln Pro Val Asp Arg Val Lys Arg Pro Ser Pro Glu
35 40 45

Ser Gln Ser Asn
50

<210> 1659
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.L63F"

<400> 1659
Leu Gln Glu Ala Glu Asp Asp Val Asp Pro Gly His Ser Ser Ser Val
1 5 10 15

Lys Glu Leu Asp Thr Asp Ala Asp Lys Phe Phe Lys Lys Lys Thr Ala
20 25 30

Glu Asp Arg Thr Gln Ala Phe His Leu Arg Gln Asn Leu Ser Ala Leu
35 40 45

Asp Lys Met His
50

<210> 1660
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K97N"

<400> 1660
Thr Gln Ala Phe His Leu Arg Gln Asn Leu Ser Ala Leu Asp Lys Met
1 5 10 15

His Glu Glu Gln Glu Leu Phe Thr Glu Asn Asn Met Arg Gly Glu Leu
20 25 30

Arg Ala Cys Arg Gln Arg Arg Asp Leu Ile Asp Lys Gln Gln Glu Ala
35 40 45

Val Ala Ala Glu
50

<210> 1661
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q108H"

<400> 1661
Cys Leu Arg Asp Glu Val Val Val His Leu Ala Pro Leu Asn Pro Leu
1   5   10   15

Leu Leu Arg Gln Gly Asp Phe Tyr Leu His His Val Glu Pro Gln Glu
            20   25   30

Glu Gln Ser Val Cys Ile Met Ile Lys Cys Leu Ser Leu Asp Leu Cys
        35   40   45

Thr Val Asp Lys
    50

<210> 1662
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V474M"

<400> 1662
Ala Ala Leu Gln Gln Lys Ser Gln Glu Glu Leu Leu Lys Arg Arg Glu
1   5   10   15

Gln Gln Leu Ala Glu Arg Glu Ile Asp Met Met Leu Glu Arg Glu Leu
            20   25   30

Asn Ile Leu Ile Phe Gln Leu Asn Gln Glu Lys Pro Lys Val Lys Lys
        35   40   45

Arg Lys Gly Lys
    50

<210> 1663
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R477W"

<400> 1663
Gln Gln Lys Ser Gln Glu Glu Leu Leu Lys Arg Arg Glu Gln Gln Leu
1 5 10 15

Ala Glu Arg Glu Ile Asp Val Leu Glu Trp Trp Glu Leu Asn Ile Leu
20 25 30

Ile Phe Gln Leu Asn Gln Glu Lys Pro Lys Val Lys Lys Arg Lys Gly
35 40 45

Lys Phe Lys Arg
50

<210> 1664
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P415fs"

<400> 1664
Thr Gly Ile Asp Leu Ser Gly Cys Thr Lys Trp Trp Arg Phe Ala Glu
1 5 10 15

Phe Gln Tyr Leu Gln Pro Gly Pro Pro Gly Gly Phe Arg Gln Trp Trp
20 25 30

Cys Thr Cys Arg Met Ser Gly Pro Ser Cys Leu Leu Trp Arg Ser Gly
35 40 45

Arg Pro Cys Ala Ser Arg Lys Leu Gln Arg Gln Leu Pro Gln Pro Arg
50 55 60

Arg His Lys Gly Lys Arg Ser Leu Leu Asn Arg His Leu Met Pro Trp
65 70 75 80

Ser Lys Gln Gln Thr Leu Leu Asp Gly Thr Gln Lys Leu Gln Arg Pro
85 90 95

Pro His Ser Arg Lys Arg Thr Leu Ile Ser Gln Arg Pro Leu His Pro
100 105 110

Pro

<210> 1665
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C345F"

<400> 1665
Asn Val Arg Asp Lys Thr Thr Leu Leu Met Gln Glu Asp Ala Gln Phe
1 5 10 15

Asn Phe Phe Pro Ser Val Phe Thr Thr Phe Phe Pro Lys Arg Glu Ser
20 25 30

Lys Ser Gly Ala Leu Lys Gln Ser Ser Asp Phe Ser Gln Phe Lys Val
35 40 45

Pro Asp Val Ser
50

<210> 1666
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R574C"

<400> 1666
Pro Ala Lys Met Ile Leu Asp Asn His Asp Ile Ser Val Glu Met Gly

1 5 10 15

Val Lys Ser Asn Tyr Glu Ile Arg Ile Cys Cys Arg Pro Cys Glu Ile
20 25 30

Lys Lys Thr Asp Cys Cys Lys Glu Asn Leu Glu Lys Pro Arg Ser Pro
35 40 45

Gly Glu Val Thr
50

<210> 1667
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.K690fs"

<400> 1667
Leu Glu Gln Ser Leu Gln Ser His Lys Lys Leu Lys Leu Thr Lys Met
1 5 10 15

Arg Ala Lys Lys Lys Lys Lys Lys Lys Arg Asn
20 25

<210> 1668
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N851S"

<400> 1668
Ser Asn Ile Asn Gly His Asp Tyr Met Arg Asn Ile Val His Leu Pro
1 5 10 15

Val Phe Leu Asn Ser Arg Gly Leu Ser Ser Ser Ala Arg Lys Phe Leu
20 25 30

Val Thr Ser Ala Thr Asn Gly Asp Val Pro Cys Ser Asp Thr Thr Gly
35 40 45

Ile Gln Glu Asp
50

<210> 1669
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K1115fs"

<400> 1669
Leu Asn Cys Val Arg Glu Arg Trp Ser Asp Ala Leu Ile Lys Arg Arg
1 5 10 15

Glu Tyr Leu Asp Glu Gln Ile Lys Lys Ser Ala Ile Lys Gln Arg Lys
20 25 30

Gln Arg Thr Met Trp Ser Gly Lys Pro Ser Leu Trp Ser Ser Gly
35 40 45

<210> 1670
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R598Q"

<400> 1670
Val Phe Thr Leu Val Met Thr Gln Thr Lys Thr Glu Phe Val Glu Gly
1 5 10 15

Glu Glu His Asp His Arg Ile Thr Ser Gln Gln Ile Asn Leu Ile Asp
20 25 30

Leu Ala Gly Ser Glu Arg Cys Ser Thr Ala His Thr Asn Gly Asp Arg
35 40 45

Leu Lys Glu Gly
50

<210> 1671
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E252Q"

<400> 1671
Thr Ser Met Asn Arg Glu Ser Ser Arg Ser His Ala Val Phe Thr Ile
1 5 10 15

Thr Ile Glu Ser Met Glu Lys Ser Asn Gln Gln Ile Val Asn Ile Arg
20 25 30

Thr Ser Leu Leu Asn Leu Val Asp Leu Ala Gly Ser Glu Arg Gln Lys
35 40 45

Asp Thr His Ala
50

<210> 1672
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R145Q"

<400> 1672
Gly Leu Ile Pro Arg Ile Cys Glu Gly Leu Phe Ser Arg Ile Asn Glu
1 5 10 15

Thr Thr Arg Trp Asp Glu Ala Ser Phe Gln Gln Thr Glu Val Ser Tyr
20 25 30

Leu Glu Ile Tyr Asn Glu Arg Val Arg Asp Leu Leu Arg Arg Lys Ser
35 40 45

Ser Lys Thr Phe
50

<210> 1673
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R17C"

<400> 1673
Met Ser Val Thr Glu Glu Asp Leu Cys His His Met Lys Val Val Val
1 5 10 15

Cys Cys Val Arg Pro Glu Asn Thr Lys Glu Lys Ala Ala Gly Phe His
20 25 30

Lys Val Val His Val Val Asp Lys His Ile Leu
35 40

<210> 1674
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1320W"

<400> 1674
Thr Val Thr Ile Ile His Glu Lys Gly Ser Glu Leu His Trp Lys Asp
1 5 10 15

Val Arg Glu Leu Val Val Gly Arg Ile Trp Trp Asn Lys Pro Glu Val

20 25 30

Asp Glu Ala Ala Val Asp Ala Ile Leu Ser Leu Asn Ile Ile Ser Ala
35 40 45

Lys Tyr Leu Lys
50

<210> 1675
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E54K"

<400> 1675
Asn Phe Asp Gly Ile Lys Leu Asp Leu Ser His Glu Phe Ser Leu Val
1 5 10 15

Ala Pro Asn Thr Glu Ala Asn Ser Phe Lys Lys Ser Lys Asp Tyr Leu
20 25 30

Gln Val Cys Leu Arg Ile Arg Pro Phe Thr Gln Ser Glu Lys Glu Leu
35 40 45

Glu Ser Glu Gly
50

<210> 1676
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E991K"

<400> 1676
Asn Glu Ile Glu Thr Ala Thr Arg Ser Ile Thr Asn Asn Val Ser Gln
1 5 10 15

Ile Lys Leu Met His Thr Lys Ile Asp Lys Lys Leu Arg Thr Leu Asp
20 25 30

Ser Val Ser Gln Ile Ser Asn Ile Asp Leu Leu Asn Leu Arg Asp Leu
35 40 45

Ser Asn Gly Ser
50

<210> 1677
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E350K"

<400> 1677
Lys Glu Gln Ile Thr Ile Ser Gln Leu Ser Leu Val Asp Leu Ala Gly
1 5 10 15

Ser Glu Arg Thr Asn Arg Thr Arg Ala Lys Lys Gly Asn Arg Leu Arg
20 25 30

Glu Ala Gly Asn Ile Asn Gln Ser Leu Met Thr Leu Arg Thr Cys Met
35 40 45

Asp Val Leu Arg
50

<210> 1678
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R150Q"

<400> 1678
Ser Pro Gly Glu Gly Gly Leu Leu Pro Arg Cys Leu Asp Met Ile Phe
1 5 10 15

Asn Ser Ile Gly Ser Phe Gln Ala Lys Gln Gln Tyr Val Phe Lys Ser
20 25 30

Asn Asp Arg Asn Ser Met Asp Ile Gln Cys Glu Val Asp Ala Leu Leu
35 40 45

Glu Arg Gln Lys
50

<210> 1679
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.W3R"

<400> 1679
Met Thr Arg Arg Thr Ser Gly Gln Leu Gln Arg Glu Lys Gln Ala Arg
1 5 10 15

Pro Gly Ser Gly Ala Val Leu Ala Phe Pro Asp Asp Lys
20 25

<210> 1680
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S1065fs"

<400> 1680
Ser Leu Gln Ser Ser Arg Glu Ser Leu Asn Ser Cys Gly Phe Val Glu
1 5 10 15

Gly Lys Pro Arg Pro Met Gly Ser Pro Gly Trp Ala Ser Pro Ala Cys
20 25 30

Pro Arg Pro Arg Ser Thr Ser His Pro Ala Leu Leu Pro Arg Asp Ala
35 40 45

Lys Ser Thr Pro Arg Arg Gly Ser Cys Arg Leu Pro Pro His Cys Leu
50 55 60

Pro Arg Ala Arg Ile Pro Ala Trp Arg Leu Gly Ser Pro Cys Cys Ser
65 70 75 80

Pro Arg Cys Val Arg Pro Arg Leu Glu
85

<210> 1681
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V1113M"

<400> 1681
Arg Cys Lys Val Tyr Thr Gln Lys Gly Val Leu Pro Ser Pro Ala Pro
1 5 10 15

Leu Pro Pro Ser Ser Lys Asp Ser Gly Met Met Ala Ser Arg Glu Ser
20 25 30

Leu Leu Gln Pro Glu Val Arg Thr Pro Pro Val Gly Met Ser Pro Gln
35 40 45

Val Leu Lys Lys
50

<210> 1682
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A1114V"

<400> 1682
Cys Lys Val Tyr Thr Gln Lys Gly Val Leu Pro Ser Pro Ala Pro Leu
1 5 10 15

Pro Pro Ser Ser Lys Asp Ser Gly Val Val Val Ser Arg Glu Ser Leu
20 25 30

Leu Gln Pro Glu Val Arg Thr Pro Pro Val Gly Met Ser Pro Gln Val
35 40 45

Leu Lys Lys Ser
50

<210> 1683
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A2033T"

<400> 1683
Ser Lys Glu Ala Met Cys Phe Asn Ala Lys Leu Lys Ile Leu Glu His
1 5 10 15

Arg Gln Gln Arg Ile Ala Glu Val Arg Thr Thr Lys Tyr Glu Trp Leu
20 25 30

Met Lys Glu Leu Glu Ala Thr Lys Gln Tyr Leu Met Leu Asp Pro Asn
35 40 45

Lys Trp Leu Ser
50

<210> 1684
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K925N"

<400> 1684
Leu Asp Ala Cys Asn Leu Lys Arg Arg Lys Gly Ser Phe Gly Ser Ile
1 5 10 15

Asp His Leu Gln Lys Leu Asp Glu Gln Asn Asn Lys Trp Leu Asp Glu
20 25 30

Glu Val Glu Lys Val Leu Asn Gln Arg Gln Glu Leu Glu Glu Leu Glu
35 40 45

Ala Asp Leu Lys
50

<210> 1685
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G480R"

<400> 1685
Ile Ser Ala Ile Gln Lys Ala Gly Leu Val Asp Val Asp Gly His Leu
1 5 10 15

Val Gly Glu Pro Glu Gly Gln Asn Phe Arg Arg Leu Gly Val Ala Pro
20 25 30

Phe Ser Thr Lys Pro Gly Lys Lys Ala Lys Ser Lys Lys Thr Phe Lys
35 40 45

Glu Pro Leu Ser
50

<210> 1686
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R594Q"

<400> 1686
Ile Arg Pro Asp Thr Pro Pro Ser Lys Pro Val Ala Phe Glu Glu Phe
1 5 10 15

Lys Asn Glu Gln Gly Ser Glu Ile Asn Gln Gln Ile Phe Lys Glu Asn
20 25 30

Lys Ser Ile Leu Asn Glu Arg Arg Lys Arg Ala Ser Glu Thr Thr Gln
35 40 45

His Ile Asn Ala
50

<210> 1687
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P335fs"

<400> 1687
Val Asp Pro Lys Pro Thr Thr Thr Asp Ile Gly Ser Asp Val Thr Leu
1 5 10 15

Thr Cys Val Trp Val Gly Asn Pro Pro Ser Leu Ser Pro Gly Pro Lys
20 25 30

Arg Thr Gln Ile Trp Ser
35

<210> 1688
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G604C"

<400> 1688
Val Asp Leu Lys Gln Asp Leu Arg Cys Asp Thr Ile Asp Thr Arg Glu
1 5 10 15

Glu Tyr Glu Met Lys Asp Pro Thr Asn Cys Cys Tyr Tyr Asn Val Arg
20 25 30

Ala His Glu Asp Arg Pro Ser Ser Arg Ala Val Leu Tyr Ala Asp Tyr
35 40 45

Arg Ala Pro Gly
50

<210> 1689
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V649fs"

<400> 1689
Pro Pro Ser Pro Leu Gly Pro Pro Gly Thr Pro Thr Phe Tyr Asp Phe
1 5 10 15

Asn Pro His Leu Gly Met Val Pro Pro Ala Asp Phe Thr Glu Pro Gly
20 25 30

Gln Ala Ile Ser Pro His Pro Thr Leu Glu Leu Ser Pro Ala Thr Ser
35 40 45

Asn Pro His Pro Leu Gly Pro Gln Ile Trp Pro Pro Gly Leu Pro Pro
50 55 60

Ser His Met Leu Pro Ser Pro His Leu Ala Thr Arg Val Ser Arg Leu

860

65 70 75 80

Thr Cys Asp Ile Phe Pro Met Glu Glu Ser Trp Asp Leu Gln Leu Ala
85 90 95

Ile Met Asp Cys Ser Asp Phe
100

<210> 1690
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W557G"

<400> 1690
Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr Tyr Lys Tyr
1 5 10 15

Leu Gln Lys Pro Met Tyr Glu Val Gln Gly Gly Lys Val Val Glu Glu
20 25 30

Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu Pro Tyr
35 40 45

Asp His Lys Trp
50

<210> 1691
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D816H"

<400> 1691
Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Thr His Gly Arg Ile Thr
1 5 10 15

Lys Ile Cys Asp Phe Gly Leu Ala Arg His His Ile Lys Asn Asp Ser
20 25 30

Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala
35 40 45

Pro Glu Ser Ile
50

<210> 1692
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D816Y"

<400> 1692
Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Thr His Gly Arg Ile Thr
1 5 10 15

Lys Ile Cys Asp Phe Gly Leu Ala Arg Tyr Tyr Ile Lys Asn Asp Ser
20 25 30

Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala
35 40 45

Pro Glu Ser Ile
50

<210> 1693
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D816V"

<400> 1693
Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Thr His Gly Arg Ile Thr
1 5 10 15

Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Val Ile Lys Asn Asp Ser
20 25 30

Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala
35 40 45

Pro Glu Ser Ile
50

<210> 1694
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N822Y"

<400> 1694
Asn Ile Leu Leu Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly
1 5 10 15

Leu Ala Arg Asp Ile Lys Asn Asp Ser Tyr Tyr Tyr Val Val Lys Gly
20 25 30

Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn
35 40 45

Cys Val Tyr Thr
50

<210> 1695
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.N822K"

<400> 1695
Asn Ile Leu Leu Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly
1 5 10 15

Leu Ala Arg Asp Ile Lys Asn Asp Ser Lys Lys Tyr Val Val Lys Gly
20 25 30

Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn
35 40 45

Cys Val Tyr Thr
50

<210> 1696
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T568fs"

<400> 1696
Ser Phe Gly Lys Leu Arg Asp Ala Leu Arg Arg Ser Ser Glu Met Leu
1 5 10 15

Val Lys Lys Leu Gln Gly Gly Thr Pro Arg Ser Pro Leu Thr Pro Gly
20 25 30

<210> 1697
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I104fs"

<400> 1697
Ser Leu Lys Phe Pro Ser Ser His Arg Arg Ala Ser Pro Gly Leu Ser

1 5 10 15

Met Pro Ser Ser Ser Pro Pro Ile Lys Asn Thr His Pro Leu Leu Gln
20 25 30

Ala Cys Ser Pro Ser Ala Cys Arg Cys Pro Cys His Gln
35 40 45

<210> 1698
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S224fs"

<400> 1698
Gly Ile Glu Pro Gln Arg Thr Asp Tyr Tyr Pro Glu Glu Met Ser Pro
1 5 10 15

Pro Leu Met Asn Ser Val Ser Pro Pro Ala Ser Ile Val Ala Arg Glu
20 25 30

Ser Pro Phe Gly His Arg Ala Ala Trp Glu Glu Thr Phe Thr Cys Gly
35 40 45

Ile Pro Gly Tyr Ser Lys Glu Ala Glu Asp Thr Gln Met
50 55 60

<210> 1699
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K434Q"

<400> 1699
Gly Arg Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr His Thr Cys Asp
1 5 10 15

Tyr Ala Gly Cys Gly Lys Thr Tyr Thr Gln Gln Ser Ser His Leu Lys
20 25 30

Ala His Leu Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Asp Trp
35 40 45

Asp Gly Cys Gly
50

<210> 1700
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E419Q"

<400> 1700
Leu Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Thr Trp Glu Gly
1 5 10 15

Cys Asp Trp Arg Phe Ala Arg Ser Asp Gln Gln Leu Thr Arg His Tyr
20 25 30

Arg Lys His Thr Gly Ala Lys Pro Phe Gln Cys Gly Val Cys Asn Arg
35 40 45

Ser Phe Ser Arg
50

<210> 1701
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S118L"

<400> 1701
Glu Lys Tyr Leu Thr Pro Gln Leu Pro Pro Val Pro Ile Ile Pro Glu
1 5 10 15

His Lys Lys Tyr Arg Arg Asp Ser Ala Leu Leu Val Val Asp Gln Phe
20 25 30

Phe Thr Asp Thr Glu Gly Leu Pro Tyr Ser Ile Asn Met Asn Val Phe
35 40 45

Leu Pro Asp Ile
50

<210> 1702
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W321S"

<400> 1702
Asp Ala Trp Thr Tyr Cys Ile Ser Lys Asn Glu Trp Ile Gln Phe Asn
1 5 10 15

His Pro Tyr Thr Glu Lys Pro Arg Leu Ser Ser His Thr Ala Cys Ala
20 25 30

Ser Asp Glu Gly Glu Val Ile Val Phe Gly Gly Cys Ala Asn Asn Leu
35 40 45

Leu Val His His
50

<210> 1703
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.E635K"

<400> 1703
Asp Arg Trp Asp Phe Ala Pro Pro Leu Pro Ser Asp Thr Phe Ala Leu
1 5 10 15

Ala His Thr Ala Thr Val Arg Ala Lys Lys Lys Ile Phe Val Thr Gly
20 25 30

Gly Ser Leu Arg Phe Leu Leu Phe Arg Phe Ser Ala Gln Glu Gln Arg
35 40 45

Trp Trp Ala Gly
50

<210> 1704
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E213K"

<400> 1704
Phe Leu Ile Ser Gly Val Thr Leu Asp Asn Cys Val Glu Val Gly Arg
1 5 10 15

Ile Ala Asn Thr Tyr Asn Leu Thr Glu Lys Met Asp Lys Tyr Val Asn
20 25 30

Ser Phe Val Leu Lys Asn Phe Pro Ala Leu Leu Ser Thr Gly Glu Phe
35 40 45

Leu Lys Leu Pro
50

<210> 1705
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P231fs"

<400> 1705
Lys Tyr Leu Val Glu Asp Val Leu Leu Leu Asn Phe Glu Glu Met Arg
1 5 10 15

Ala Leu Leu Asp Ser Leu Pro Pro Pro Trp Ser Arg Ser Trp Arg Ser
            20 25 30

Ser Arg Cys Pro Cys Cys Gly Trp Ser Thr Thr Ala Arg Pro Ala Cys
        35 40 45

Ser Met Arg Leu Thr Ser
    50

<210> 1706
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.D185G"

<400> 1706
Asp Asn Phe Val Pro Leu Met Ser Arg Pro Asp Phe Leu Ser Tyr Leu
1 5 10 15

Ser Phe Glu Lys Leu Met Ser Tyr Leu Gly Gly Asn Asp His Leu Ser
            20 25 30

Arg Phe Pro Glu Ile Glu Leu Tyr Glu Ala Val Gln Ser Trp Leu Arg
        35 40 45

His Asp Arg Arg
    50

<210> 1707
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E33K"

<400> 1707
Tyr Met Leu Ala Asn Leu Thr His Leu His Ser Glu Gln Leu Leu Gln
1 5 10 15

Gly Leu Asn Leu Leu Arg Gln His His Lys Lys Leu Cys Asp Ile Ile
20 25 30

Leu Arg Val Gly Asp Val Lys Ile His Ala His Lys Val Val Leu Ala
35 40 45

Ser Val Ser Pro
50

<210> 1708
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R326C"

<400> 1708
Gln Leu Ser Gln Val Val Glu Ala Cys Cys Lys Phe Leu Met Lys Gln
1 5 10 15

Leu His Pro Ser Asn Cys Leu Gly Ile Cys Cys Ser Phe Ala Asp Ala
20 25 30

Gln Gly Cys Thr Asp Leu His Lys Val Ala His Asn Tyr Thr Met Glu
35 40 45

His Phe Met Glu
50

<210> 1709
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P57T"

<400> 1709
Glu Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp
1 5 10 15

Ala His Cys Gly Gly Val Leu Val His Thr Thr Gln Trp Val Leu Thr
20 25 30

Ala Ala His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His
35 40 45

Asn Leu Phe Glu
50

<210> 1710
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E161K"

<400> 1710
Val Lys Val Leu Gly Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr
1 5 10 15

Cys Tyr Ala Ser Gly Trp Gly Ser Ile Lys Lys Pro Glu Glu Phe Leu
20 25 30

Arg Pro Arg Ser Leu Gln Cys Val Ser Leu His Leu Leu Ser Asn Asp
35 40 45

Met Cys Ala Arg
50

<210> 1711
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R120H"

<400> 1711
Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala Ala
1 5 10 15

Ser His Asp Gln Asp Ile Met Leu Leu His His Leu Ala Arg Pro Ala
20 25 30

Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp Cys Ser
35 40 45

Ala Asn Thr Thr
50

<210> 1712
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R29Q"

<400> 1712
Asn Glu Lys Leu Asp Asn Gln Arg Leu Lys Asn Phe Lys Asn Lys Gly
1 5 10 15

Arg Asp Leu Glu Thr Met Arg Arg Gln Gln Gln Asn Glu Val Val Val
20 25 30

Glu Leu Arg Lys Asn Lys Arg Asp Glu His Leu Leu Lys Arg Arg Asn
35 40 45

Val Pro His Glu

50

<210> 1713
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E553fs"

<400> 1713
Tyr Cys Gly Pro Ser Ser Tyr Asn Gln Gly Gln Glu Ser Gly Ala Gly
1 5 10 15

Cys Gly Pro Gly Asp Val Phe Pro Glu Pro Glu Gly Ser Gly Trp Pro
20 25 30

Trp Arg Pro Arg Gln Cys Leu Cys Trp Ser Glu Arg Gly Ser Lys Glu
35 40 45

Cys Leu Phe Leu Lys Glu Arg
50 55

<210> 1714
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A59G"

<400> 1714
Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu
1 5 10 15

Thr Cys Leu Leu Asp Ile Leu Asp Thr Gly Gly Gly Gln Glu Glu Tyr
20 25 30

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
35 40 45

Val Phe Ala Ile
50

<210> 1715
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61K"

<400> 1715
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Lys Lys Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn Thr
50

<210> 1716
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61R"

<400> 1716
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Arg Arg Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 1717
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61L"

<400> 1717
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Leu Leu Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 1718
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61H"

<400> 1718
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly His His Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 1719
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61H"

<400> 1719
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly His His Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 1720
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12S"

<400> 1720
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Ser Ser Gly Val Gly

1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1721
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12R"

<400> 1721
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Arg Arg Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1722
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12C"

<400> 1722
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Cys Cys Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1723
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12D"

<400> 1723
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Asp Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1724
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12A"

<400> 1724
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Ala Ala Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1725
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12V"

<400> 1725
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Val Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 1726
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G13C"

<400> 1726
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Cys Cys Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu Asp
35

<210> 1727
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G13D"

<400> 1727
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Asp Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu Asp
35

<210> 1728
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A146T"

<400> 1728
Pro Ser Arg Thr Val Asp Thr Lys Gln Ala Gln Asp Leu Ala Arg Ser
1 5 10 15

Tyr Gly Ile Pro Phe Ile Glu Thr Ser Thr Thr Lys Thr Arg Gln Arg
20 25 30

Val Glu Asp Ala Phe Tyr Thr Leu Val Arg Glu Ile Arg Gln Tyr Arg
35 40 45

Leu Lys Lys Ile
50

<210> 1729
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R839G"

<400> 1729
Asp Arg Leu Ala Thr Ala Leu Ala Gly Leu Ala Gln Glu Val Ala Thr
1 5 10 15

Met Arg Thr Gln Val Asn Arg Leu Gly Gly Gly Arg Pro Gln Gly Pro
20 25 30

Gly Pro Met Gly Gln Ala Ser Trp Met Trp Thr Leu Pro Arg Gly Pro
35 40 45

Arg Trp Ala His
50

<210> 1730
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L299W"

<400> 1730
Lys Arg Thr Ala Ala Glu Asn Asp Phe Val Thr Leu Lys Lys Asp Val
1 5 10 15

Asp Asn Ala Tyr Met Ile Lys Val Glu Trp Trp Gln Ser Lys Val Asp
20 25 30

Leu Leu Asn Gln Glu Ile Glu Phe Leu Lys Val Leu Tyr Asp Ala Glu
35 40 45

Ile Ser Gln Ile
50

<210> 1731
<211> 40

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F154fs"

<400> 1731
Arg Gly Asn Lys Ser Ile Ser Met Ser Val Ala Gly Ser Arg Gln Gly
1 5 10 15

Ala Cys Phe Gly Gly Ala Gly Gly Phe Arg His Trp Trp Leu Trp Trp
20 25 30

Trp Ile Trp Gly Leu Leu Gln Trp
35 40

<210> 1732
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L197P"

<400> 1732
Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu Glu Gln Gln
1 5 10 15

Asn Lys Val Leu Asp Thr Lys Trp Thr Pro Pro Leu Gln Glu Gln Gly
20 25 30

Thr Lys Thr Val Arg Gln Asn Leu Glu Pro Leu Phe Glu Gln Tyr Ile
35 40 45

Asn Asn Leu Arg
50

<210> 1733
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S59A"

<400> 1733
Thr Gln Lys Ser Tyr Lys Val Ser Thr Ser Gly Pro Arg Ala Phe Ser
1 5 10 15

Ser Arg Ser Tyr Thr Ser Gly Pro Gly Ala Ala Arg Ile Ser Ser Ser
20 25 30

Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly Gly Leu Gly Gly
35 40 45

Gly Tyr Gly Gly
50

<210> 1734
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I116V"

<400> 1734
Cys Gly Thr Gly Cys Gly Ile Gly Gly Gly Ile Gly Tyr Gly Gln Glu
1 5 10 15

Gly Ser Ser Gly Ala Val Ser Thr Arg Val Val Arg Trp Cys Arg Pro
20 25 30

Asp Cys Arg Val Glu Gly Thr Cys Leu Pro Pro Cys Cys Val Val Ser
35 40 45

Cys Thr Pro Pro
50

<210> 1735
<211> 52
<212> PRT
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<223> /note="p.M124I"

<400> 1735
Ala Cys Gln Ser Glu Ser Ser Ser Ala Gly Leu Ala Cys Val Ser Gln
1 5 10 15

Pro Cys Gln Ser Glu Ser Thr Gln Gln Ile Ile Gly Phe Val Ala Gln
20 25 30

Ser Cys Gln Pro Ala Ser Leu Lys Gly Asn Ser Cys Pro Pro Lys Thr
35 40 45

Ser Lys Ser Lys
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<210> 1736
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.S48R"

<400> 1736
Thr Cys Cys Arg Pro Ser Cys Cys Glu Thr Thr Cys Cys Arg Thr Thr
1 5 10 15

Tyr Cys Arg Pro Ser Cys Cys Val Ser Arg Arg Cys Cys Arg Pro Gln
20 25 30

Cys Cys Gln Ser Val Cys Cys Gln Pro Thr Cys Cys Arg Pro Arg Cys
35 40 45

Cys Ile Ser Ser

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<210> 1737
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.S74C"

<400> 1737
Val Cys Tyr Gln Pro Thr Cys Cys His Pro Ser Cys Cys Ile Ser Ser
1 5 10 15

Cys Cys Arg Pro Tyr Cys Cys Glu Ser Cys Cys Cys Cys Arg Pro Cys
20 25 30

Cys Cys Gln Thr Thr Cys Cys Arg Thr Thr Cys Cys Arg Thr Thr Cys
35 40 45

Cys Cys Pro Ser
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<210> 1738
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C91F"

<400> 1738
Cys Arg Pro Tyr Cys Cys Glu Ser Ser Cys Cys Arg Pro Cys Cys Cys
1 5 10 15

Gln Thr Thr Cys Cys Arg Thr Thr Cys Phe Phe Arg Thr Thr Cys Cys
20 25 30

Cys Pro Ser Cys Cys Val Ser Ser Cys Cys Arg Pro Gln Cys Cys Gln
35 40 45

Ser Val Cys Cys
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<210> 1739
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.T63S"

<400> 1739
Thr Cys Tyr Arg Pro Ser Tyr Ser Val Ser Cys Cys Cys Arg Pro Gln
1   5   10   15

Cys Cys Gln Ser Val Cys Cys Gln Pro Ser Ser Cys Cys Arg Pro Ser
            20   25   30

Cys Cys Val Ser Ser Cys Cys Lys Pro Gln Cys Cys Gln Ser Val Cys
        35   40   45

Cys Gln Pro Thr
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<210> 1740
<211> 44
<212> PRT
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      polypeptide"

<220>
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<223> /note="p.D18V"

<400> 1740
Met Val Ser Ser Cys Cys Gly Ser Val Cys Ser Asp Gln Gly Cys Gly
1   5   10   15

Gln Val Val Leu Cys Gln Glu Thr Cys Cys Arg Pro Ser Cys Cys Glu
            20   25   30

Thr Thr Cys Cys Arg Thr Thr Cys Cys Arg Pro Ser
35 40

<210> 1741
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 1741
Gly Ser Cys Gly Gly Ser Lys Gly Gly Cys Gly Ser Cys Gly Gly Cys
1 5 10 15

Lys Gly Gly Cys Gly Ser Cys Gly Gly Tyr Tyr Lys Gly Gly Cys Gly
20 25 30

Ser Gly Cys Gly Gly Cys Gly Ser Gly Cys Gly Val Pro Val Cys Cys
35 40 45

Cys Ser Cys Ser
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<210> 1742
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T555M"

<400> 1742
Phe Asn Leu Pro Ala Ser His Tyr Tyr Lys Tyr Lys Gln Gln Phe Ile
1 5 10 15

Phe Pro Asp Val Val Pro Val Pro Glu Met Met Pro Thr Arg Ala Pro
20 25 30

Gln Val Ile Leu His Pro Val Thr Ser Asn Pro Ile Leu Glu Gly Asn
35 40 45

Pro Leu Leu Gln
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<210> 1743
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R632S"

<400> 1743
Leu Val Val Gly Ser Pro Gly Pro Val Pro Arg Leu Val Leu Ser Asp
1 5 10 15

Leu His Leu Leu Thr Gln Ser Gln Val Ser Ser Val Ser Trp Ser Pro
20 25 30

Ala Glu Asp His Asn Ala Pro Ile Glu Lys Tyr Asp Ile Glu Phe Glu
35 40 45

Asp Lys Glu Met
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<210> 1744
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T186M"

<400> 1744
Pro Pro Ser Ala Glu Pro Leu Arg Ile Tyr Trp Met Asn Ser Lys Ile
1 5 10 15

Leu His Ile Lys Gln Asp Glu Arg Val Met Met Met Gly Gln Asn Gly

20 25 30

Asn Leu Tyr Phe Ala Asn Val Leu Thr Ser Asp Asn His Ser Asp Tyr
35 40 45

Ile Cys His Ala
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<210> 1745
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P441del"

<400> 1745
Val Glu Asp Phe Val Phe Asp Ala Gly Val Gly Asp Ile Gly Asn Arg
1 5 10 15

Ile Leu His Val Arg Asn Ala Pro Ser Ala Ala Thr Ser Ser Ile Ala
20 25 30

Ile Ser Gly Met Ile Ala Asp Glu Val Gln Gln Arg Phe Glu Leu
35 40 45

<210> 1746
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W162L"

<400> 1746
His Pro Val Gly Trp Cys Glu Lys Thr Lys His Glu Leu His Ile Pro
1 5 10 15

Lys Gly Tyr Arg Lys Asp Lys Phe Val Leu Leu Met Asp Tyr Leu Lys
20 25 30

Ala Cys Lys Leu Gln Asn Ala Pro Lys Lys Leu Phe Arg Asn Arg Ser
35 40 45

Pro Asn Gly Pro
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<210> 1747
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M5L"

<400> 1747
Met Tyr Arg Leu Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
1 5 10 15

Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
20 25 30

<210> 1748
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A41T"

<400> 1748
Ala Ile Leu Ala Lys Gln Phe Thr Lys Cys Glu Leu Ser Gln Leu Leu
1 5 10 15

Lys Asp Ile Asp Gly Tyr Gly Gly Ile Thr Thr Leu Pro Glu Leu Ile
20 25 30

Cys Thr Met Phe His Thr Ser Gly Tyr Asp Thr Gln Ala Ile Val Glu
35 40 45

Asn Asn Glu Ser
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<210> 1749
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1030Y"

<400> 1749
Asn Thr Cys Asp Pro Glu Thr Gly Glu Cys Val Cys Pro Pro His Thr
1 5 10 15

Gln Gly Val Lys Cys Glu Glu Cys Glu Tyr Tyr Gly His Trp Gly Tyr
20 25 30

Asp Ala Glu Val Gly Cys Gln Ala Cys Asn Cys Ser Leu Val Gly Ser
35 40 45

Thr His His Arg
50

<210> 1750
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A558V"

<400> 1750
Ser Leu Ser Thr Ser Ala Asp Ser Leu Thr Thr Pro Arg Leu Thr Leu
1 5 10 15

Ser Glu Leu Asp Asp Ile Ile Lys Asn Val Val Ser Gly Ile Tyr Ala
20 25 30

Glu Ile Asp Gly Ala Lys Ser Glu Leu Gln Val Lys Leu Ser Asn Leu
35 40 45

Ser Asn Leu Ser
50

<210> 1751
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E639K"

<400> 1751
Asn Gly Leu Val Gln Lys Ala Leu Asp Ala Ser Asn Val Tyr Glu Asn
1 5 10 15

Ile Val Asn Tyr Val Ser Glu Ala Asn Lys Lys Thr Ala Glu Phe Ala
20 25 30

Leu Asn Thr Thr Asp Arg Ile Tyr Asp Ala Val Ser Gly Ile Asp Thr
35 40 45

Gln Ile Ile Tyr
50

<210> 1752
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M1293I"

<400> 1752
Pro Asn Gly Leu Leu Phe Tyr Tyr Ala Ser Gly Ser Asp Val Phe Ser
1 5 10 15

Ile Ser Leu Asp Asn Gly Thr Val Ile Ile Ile Asp Val Lys Gly Ile

20 25 30

Lys Val Gln Ser Val Asp Lys Gln Tyr Asn Asp Gly Leu Ser His Phe
35 40 45

Val Ile Ser Ser
50

<210> 1753
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L2223R"

<400> 1753
Ser Ser Met Ala Trp Ala Arg Leu His Arg Leu Asn Ala Ser Ile Ala
1 5 10 15

Asp Leu Gln Ser Gln Leu Arg Ser Pro Arg Arg Gly Pro Arg His Glu
20 25 30

Thr Ala Gln Gln Leu Glu Val Leu Glu Gln Gln Ser Thr Ser Leu Gly
35 40 45

Gln Asp Ala Arg
50

<210> 1754
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G588W"

<400> 1754
Gly Leu Ala Pro Leu Gly Ser Glu Thr Phe Gly Gln Ser Pro Ala Val
1 5 10 15

His Val Val Leu Gly Glu Pro Val Pro Trp Trp Asn Pro Val Thr Trp
20 25 30

Thr Gly Pro Gly Phe Ala Arg Val Leu Pro Gly Ala Gly Leu Arg Phe
35 40 45

Ala Val Asn Asn
50

<210> 1755
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G1239W"

<400> 1755
Glu Ala Asp Phe Lys Asp Leu Arg Gly Asn Val Ser Glu Ile Glu Arg
1 5 10 15

Ile Leu Lys His Pro Val Phe Pro Ser Trp Trp Lys Phe Leu Lys Val
20 25 30

Lys Asp Tyr His Asp Ser Val Arg Arg Gln Ile Met Gln Leu Asn Glu
35 40 45

Gln Leu Lys Ala
50

<210> 1756
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P174Q"

<400> 1756
Lys Arg Ser Arg Ala Asp Gly Pro Trp Glu Pro Tyr Gln Phe Tyr Ser
1 5 10 15

Ala Ser Cys Gln Lys Thr Tyr Gly Arg Gln Gln Glu Gly Gln Tyr Leu
20 25 30

Arg Pro Gly Glu Asp Glu Arg Val Ala Phe Cys Thr Ser Glu Phe Ser
35 40 45

Asp Ile Ser Pro Leu
50

<210> 1757
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A223fs"

<400> 1757
Pro Arg His Ile Pro Ala Asn Arg Gly Glu Ile Lys Gly Ser Glu Ser
1 5 10 15

Ala Thr Tyr Val Pro Val Ala Pro Pro His Pro Ser Leu Ala Thr Arg
20 25 30

Asp Gln Thr Gly Ala Cys Leu Ala Arg Pro Gly
35 40

<210> 1758
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T163fs"

<400> 1758

Pro Glu Asn Ser Glu Thr Gly Gly Asn Glu Ser Gln Pro Asp Ser Gln
1 5 10 15

Glu Asp Pro Arg Glu Val Leu Lys Lys His Trp Asn Ser Ala Tyr Leu
20 25 30

Gly Arg Thr Leu Leu Val Thr Cys Ile Leu Tyr His Arg Trp Ile Val
35 40 45

Thr Ser Met Cys Gln Ser Gln Arg Trp Leu Thr Ser Thr Thr Ser Arg
50 55 60

Ser Ser Ala Leu Met Trp Thr
65 70

<210> 1759
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P185fs"

<400> 1759
Met Lys Ser Leu Gly Leu Ser Asp Glu Glu Ile Val Lys Phe Ser Glu
1 5 10 15

Ala Glu His Trp Leu Asp Tyr Phe Pro Ala Thr Gly Tyr Ser Gly Phe
20 25 30

Lys Lys Asn Gly Phe Glu Gly Arg Leu Ala Ser Phe Leu His His His
35 40 45

<210> 1760
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.L18W"

<400> 1760
Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val
1 5 10 15

Leu Trp Trp Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro
20 25 30

Gly Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg
35 40

<210> 1761
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R176W"

<400> 1761
Ser Pro Ala Asp Arg Asp Gln Ile Ala Gln Gln Leu Gly Leu Thr Asn
1 5 10 15

Ala Gln Val Ile Thr Trp Phe Gln Asn Trp Trp Arg Ala Lys Leu Lys
20 25 30

Arg Asp Leu Glu Glu Met Lys Ala Asp Val Glu Ser Ala Lys Lys Leu
35 40 45

Gly Pro Ser Gly
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<210> 1762
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P445fs"

<400> 1762
Ser Asp Ala Leu Val Ile Phe Gln Leu Tyr Glu Lys Ile Lys Val Pro
1 5 10 15

Val Asp Trp Asn Arg Val Asn Lys Pro Ala Ile Pro Gln Thr Gly Arg
20 25 30

Gln Tyr Glu Glu Ala
35

<210> 1763
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L16Q"

<400> 1763
Met Lys Gln Arg Phe Ser Ala Leu Gln Leu Leu Lys Leu Leu Leu Gln
1 5 10 15

Gln Leu Gln Pro Pro Leu Pro Arg Ala Leu Arg Glu Ala Leu Cys Pro
20 25 30

Glu Pro Cys Asn Cys Val Pro Asp Gly Ala
35 40

<210> 1764
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H410Y"

<400> 1764
Ser Pro Val Thr Ser Ala His Ser Gly Thr Tyr Arg Cys Tyr Gly Ser
1 5 10 15

Leu Ser Ser Asn Pro Tyr Leu Leu Ser Tyr Tyr Pro Ser Asp Ser Leu
20 25 30

Glu Leu Met Val Ser Gly Ala Ala Glu Thr Leu Ser Pro Pro Gln Asn
35 40 45

Lys Ser Asp Ser
50

<210> 1765
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L479del"

<400> 1765
Gly Leu Gly Arg His Leu Gly Val Val Ile Gly Ile Leu Val Ala Val
1 5 10 15

Ile Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg
20 25 30

Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln
35 40 45

His Pro Ala Gly Ala
50

<210> 1766
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S598P"

<400> 1766

Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Arg
1 5 10 15

Val Leu Ser Ser Pro Gly Pro Gln Ala Pro Pro Pro Pro Pro Pro Arg
20 25 30

Ser Leu Pro Leu Thr Leu Pro Arg Cys Arg Leu Leu His Leu Lys Pro
35 40 45

Pro Arg Met
50

<210> 1767
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S150T"

<400> 1767
Ile Met Ala Phe Ala His Gln Pro Thr Phe Ser Arg Ile Ser Arg Pro
1 5 10 15

Phe Ser Ala Gly Ile Met Phe Phe Ser Thr Thr Thr Leu Phe Val Val
20 25 30

Leu Ala Leu Ala Ile Tyr Thr Gly Val Thr Val Ser Phe Leu Gly Arg
35 40 45

Arg Phe Gly Asp
50

<210> 1768
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.R203H"

<400> 1768
Thr Thr Val Gln Val Lys Glu Val Asn Arg Met His Ile Ser Pro Asn
1 5 10 15

Asn Arg Asn Ala Ile His Pro Gly Asp His His Ile Leu Glu Ile Asn
20 25 30

Gly Thr Pro Val Arg Thr Leu Arg Val Glu Glu Val Glu Asp Ala Ile
35 40 45

Ser Gln Thr Ser
50

<210> 1769
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R183W"

<400> 1769
Phe Cys Val Cys Leu Lys Glu Ser Phe Pro Asn Leu Lys Thr Arg Lys
1 5 10 15

Leu Thr Arg Val Glu Trp Gly Lys Ile Trp Trp Arg Leu Met Gly Lys
20 25 30

Pro Arg Arg Cys Ser Ser Ala Phe Phe Glu Glu Glu Arg Ser Ala Leu
35 40 45

Lys Gln Lys Arg
50

<210> 1770
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E231K"

<400> 1770
Gln Lys Arg Gln Lys Ile Arg Leu Leu Gln Gln Arg Lys Val Ala Asp
1 5 10 15

Val Ser Gln Phe Lys Asp Leu Pro Asp Lys Lys Ile Pro Leu Pro Leu
20 25 30

Val Ile Gly Thr Lys Val Thr Ala Arg Leu Arg Gly Val His Asp Gly
35 40 45

Leu Phe Thr Gly
50

<210> 1771
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P410T"

<400> 1771
Pro Asp Thr Ile Arg Glu Arg Ser Phe Lys Asp Phe His Ser Thr Ala
1 5 10 15

Leu Ser Phe Tyr Phe Thr Cys Lys Lys Thr Thr Lys Ile Arg Glu Lys
20 25 30

Lys Leu Gln His Leu Leu Val Asp Glu Gly Gln Thr Val Gln Leu Glu
35 40 45

Cys Ser Ala Asp
50

<210> 1772
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P236Q"

<400> 1772
Gly Ser Lys Leu Cys Pro Leu Gln Ile Phe Asp Lys Ile Cys Leu Asn
1 5 10 15

Ile Leu Phe Met Met Phe Gly Tyr Asp Gln Gln Lys Asn Leu Asn Met
20 25 30

Ser Arg Leu Asp Val Tyr Phe Ser His Asn Pro Ala Gly Thr Ser Val
35 40 45

Gln Asn Met Leu
50

<210> 1773
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P955fs"

<400> 1773
Pro Arg Cys Leu Val Asp Ser Ala Glu Thr Lys Asn His Arg Pro Gly
1 5 10 15

Asn Gly Ala Gly Pro Lys Lys Ala Pro Glu Pro Ser Gln Glu Leu Arg
20 25 30

Asp Ser Glu
35

<210> 1774
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.G199C"

<400> 1774
Pro Val Ile Val Pro Glu Glu His Leu Gln Gln Cys Arg Val Tyr Arg
1 5 10 15

Gly Gly Lys Trp Pro His Gly Ala Val Cys Cys Val Pro Asp Gln Glu
20 25 30

Gly Ile Ser Asp Ala Asp Phe Val Leu Tyr Val Gly Ala Leu Ala Thr
35 40 45

Glu Arg Cys Ser
50

<210> 1775
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q285del"

<400> 1775
Arg His Gln Gln Gln Gln Glu Gln Gln Asn Ser Gln Arg Leu Gly Gln
1 5 10 15

Gly Glu Pro Gly Pro Gly Gln Gly Leu Gln Glu Val Leu Ser Ser Arg
20 25 30

Met Glu Gly Met Met Ala Ser Tyr Thr Pro Leu Ala Pro Pro Gln Gln
35 40 45

Gln Ile Val Ala Met
50

<210> 1776
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T532P"

<400> 1776
Ala Asp Asp Asn Leu Lys Thr Pro Ser Glu Arg Gln Leu Thr Ala Leu
1 5 10 15

Pro Pro Ser Ala Asp Asp Asn Ile Lys Pro Pro Pro Ala Glu Arg Leu
20 25 30

Arg Gly Pro Leu Pro Pro Ser Ala Asp Asp Asn Leu Lys Thr Pro Ser
35 40 45

Glu Arg Gln Leu
50

<210> 1777
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P90S"

<400> 1777
Ala Glu Gly Ile Ala Met Leu Leu Gly Thr Ala Gly Pro Ser Arg Leu
1 5 10 15

Pro Ala Ala Pro Asp Ala Ser Gln Ala Ser Ser Leu Arg Ser Pro Trp
20 25 30

Ala Leu Ser Val Ala Ala Ala Leu Cys Ser Pro Val Ser Cys His Pro
35 40 45

Cys Gly Arg His
50

<210> 1778
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L144M"

<400> 1778
Cys Val Leu Ala Pro Gly Ser Gly Ser Arg Pro Thr Pro His Ile Val
1 5 10 15

Tyr Ser Val Pro Ala Ala Arg Thr Cys Met Met Gly Ala Pro Gly Ser
20 25 30

Leu Ser Pro Cys His Leu Cys Val His Ile Cys Ala His Thr Tyr Ser
35 40 45

Gly Thr Pro Val
50

<210> 1779
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.RAPWMEQ147del"

<400> 1779
Leu Ser Val Gly Asp Val Asp Asp Thr Gln Cys Val Arg Leu Asp Ser
1 5 10 15

Asp Ala Thr Ser Pro Arg Met Glu Pro Glu Gly Pro Glu Tyr Trp Glu
20 25 30

Glu Glu Thr Gly Thr Ala Lys Ala Lys Ala Gln Phe Tyr Arg Val Asn
35 40 45

Leu Arg Thr Leu Ser Gly Tyr Tyr Asn Gln Ser Glu Ala
50 55 60

<210> 1780
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G93E"

<400> 1780
Ala Gly Glu Asp Gly Arg Met Ile Ala Ser Gln Val Val Asp Ile Asn
1 5 10 15

Leu Ala Ala Glu Pro Lys Val Asn Arg Glu Glu Asn Ala Gly Val Lys
20 25 30

Arg Ser Ala Ala Glu Met Tyr Gly Ser Ser Phe Asp Leu Asp Tyr Gly
35 40 45

Phe Gln Arg Asp
50

<210> 1781
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F906I"

<400> 1781
Glu Phe Ile Phe Leu Ile Gly Ile Asp Lys Thr Lys Tyr Ala Ile Ala
1 5 10 15

Cys Pro Ile Phe Ala Gly Leu Leu His Ile Ile Phe Phe Leu Ala Ala
20 25 30

Phe Ala Trp Met Cys Leu Glu Gly Val Gln Leu Tyr Leu Met Leu Val
35 40 45

Glu Val Phe Glu
    50

<210> 1782
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.E740D"

<400> 1782
Phe Pro Glu Asn Met Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn
1   5   10   15

Thr Leu Lys Gln Asn Gly Arg Asn Gly Asp Asp Ile Arg Val Ala Phe
            20   25   30

Val Leu Tyr Asn Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser
        35   40   45

Met Lys Leu Gly
    50

<210> 1783
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R826H"

<400> 1783
Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu Asn Phe Asn Pro
1   5   10   15

Asn Cys Ser Phe Trp Ser Tyr Ser Lys His His Thr Met Thr Gly Tyr
            20   25   30

Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr

35 40 45

Thr Cys Ser Cys
50

<210> 1784
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1183Q"

<400> 1784
Ser Gly Ser Arg Thr Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg
1 5 10 15

Ile Arg Arg Met Trp Asn Asp Thr Val Gln Gln Lys Gln Ser Glu Ser
20 25 30

Ser Phe Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu
35 40 45

Gly Leu Leu Asn
50

<210> 1785
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S974L"

<400> 1785
Ser Asp Thr Phe Ser Asn Phe Thr Phe Trp Arg Glu Pro Leu Pro Pro
1 5 10 15

Phe Glu Asn Gln Asp Ile His Ser Ala Leu Leu Ala
20 25

<210> 1786
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A186S"

<400> 1786
Thr Asp Gln Gly Ala Cys Ala Gly Ser Pro Ser Leu Val Ala Ala Ala
1 5 10 15

Arg Arg Ala Phe Pro Cys Lys Asp Ala Ser Ser Leu Cys Ala Tyr Ala
20 25 30

Val Thr Tyr Thr Ala Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly
35 40 45

Ser Arg Leu Val
50

<210> 1787
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R527S"

<400> 1787
Leu Lys Ile Gln Pro Gly Ala Val Pro Gly Cys Asn Asn Ser Met Pro
1 5 10 15

Gly Gly Pro Arg Val Ser Ile Gln Ser Ser Ser Pro Gly Ser Ser Gln
20 25 30

Leu Val His Ile Pro Glu Glu Thr Gln Glu Asn Ile Ser Thr Ser Pro
35 40 45

Lys Ser Ser Ser
50

<210> 1788
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E2103K"

<400> 1788
Val Ser Leu Ser Thr Pro Ala Gln Leu Val Ala Pro Ser Val Val Val
1 5 10 15

Lys Gly Thr Leu Ser Val Thr Ser Ser Lys Lys Leu Tyr Phe Glu Val
20 25 30

Asp Glu Glu Asp Pro Asn Phe Lys Lys Ile Asp Pro Lys Ile Leu Ala
35 40 45

Tyr Thr Glu Gly
50

<210> 1789
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D717G"

<400> 1789
Ser Ile His Val Pro Ser Pro Ala Val Pro Lys Leu Ser Met Ala Lys
1 5 10 15

Cys Arg Arg Asn Val Glu Asn Phe Leu Gly Gly Ala Cys Lys Lys Leu
20 25 30

Gly Val Ser Gln Glu Arg Leu Cys Leu Pro His His Ile Leu Glu Glu
35 40 45

Arg Gly Leu Val
50

<210> 1790
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N132K"

<400> 1790
Asn Ser Asn Arg Leu Thr Lys Ile Thr Asn Asp Met Phe Ser Gly Leu
1 5 10 15

Ser Asn Leu His His Leu Ile Leu Asn Lys Lys Asn Gln Leu Thr Leu
20 25 30

Ile Ser Ser Thr Ala Phe Asp Asp Val Phe Ala Leu Glu Glu Leu Asp
35 40 45

Leu Ser Tyr Asn
50

<210> 1791
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L24V"

<400> 1791
Met Ala Arg Pro Val Arg Gly Gly Leu Gly Ala Pro Arg Arg Ser Pro
1 5 10 15

Cys Leu Leu Leu Leu Trp Leu Val Val Leu Leu Arg Leu Glu Pro Val

20 25 30

Thr Ala Ala Ala Gly Pro Arg Ala Pro Cys Ala Ala Ala Cys Thr Cys
35 40 45

Ala Gly
50

<210> 1792
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L26V"

<400> 1792
Met Ala Arg Pro Val Arg Gly Gly Leu Gly Ala Pro Arg Arg Ser Pro
1 5 10 15

Cys Leu Leu Leu Leu Trp Leu Leu Leu Val Val Arg Leu Glu Pro Val
20 25 30

Thr Ala Ala Ala Gly Pro Arg Ala Pro Cys Ala Ala Ala Cys Thr Cys
35 40 45

Ala Gly Asp Ser
50

<210> 1793
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1058T"

<400> 1793
Thr Cys Asp Gly Asp Asn Asp Cys Gly Asp Tyr Ser Asp Glu Thr His
1 5 10 15

Ala Asn Cys Thr Asn Gln Ala Thr Arg Thr Thr Pro Gly Gly Cys His
20 25 30

Thr Asp Glu Phe Gln Cys Arg Leu Asp Gly Leu Cys Ile Pro Leu Arg
35 40 45

Trp Arg Cys Asp
50

<210> 1794
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G1488fs"

<400> 1794
Gly Ser Gly His Met Glu Val Leu Arg Gly His Glu Phe Leu Ser His
1 5 10 15

Pro Phe Ala Val Thr Leu Tyr Gly Gly Gly Gly Leu Leu Asp
20 25 30

<210> 1795
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G1488fs"

<400> 1795
Gly Ser Gly His Met Glu Val Leu Arg Gly His Glu Phe Leu Ser His
1 5 10 15

Pro Phe Ala Val Thr Leu Tyr Gly Gly Arg Ser Thr Gly Leu Thr Gly
20 25 30

Glu Gln Thr His Trp Leu Arg Pro Thr Ser Gly Pro Ala Thr Met Ser
35 40 45

Pro Trp Tyr Arg Gly Pro Thr Pro Ser Pro Leu Thr Cys Arg Cys Thr
50 55 60

Thr Pro Pro Ala Ser Pro Trp Leu Pro Ile Pro Val Arg Pro Met Gly
65 70 75 80

Ala Arg Ala Pro Ala Pro Thr Cys Val Ser Ser Thr Thr Thr Gly Pro
85 90 95

Cys Pro Ala Pro Ala Pro Thr Ser
100

<210> 1796
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L11del"

<400> 1796
Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Gly Gly Ala Leu Ala His
1 5 10 15

Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp Pro Pro Ala
20 25 30

Val Leu Leu Glu Val Gln
35

<210> 1797
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P92R"

<400> 1797
Gln Gln Glu Arg Pro Gln Glu Glu Leu Glu Leu Glu Leu Arg Ala Gly
1 5 10 15

Gly Gly Pro Gln Glu Asp Cys Pro Gly Arg Arg Gly Ser Gly Gly Tyr
20 25 30

Ser Ala Met Pro Asp Ala Ile Ile Arg Thr Lys Asp Ser Leu Ala Ala
35 40 45

Gly Ala Ser Phe
50

<210> 1798
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G310C"

<400> 1798
Cys Thr Trp Leu Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg
1 5 10 15

Phe Thr Asp Phe Lys Leu Asp Gly Thr Cys Cys Tyr Gly Asp Tyr Val
20 25 30

Lys Ile Tyr Asp Gly Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val
35 40 45

Leu Thr Ala Phe
50

<210> 1799
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G3563C"

<400> 1799
Phe Asp Cys Ala Asp Gly Ser Asp Glu Arg Asn Cys Glu Thr Ser Cys
1   5   10   15

Ser Lys Asp Gln Phe Arg Cys Ser Asn Cys Cys Gln Cys Ile Pro Ala
            20   25   30

Lys Trp Lys Cys Asp Gly His Glu Asp Cys Lys Tyr Gly Glu Asp Glu
        35   40   45

Lys Ser Cys Glu
    50

<210> 1800
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.L1392F"

<400> 1800
Ser Leu Arg Thr Thr Leu Ile Ala Gly Ala Met Glu His Pro Arg Ala
1   5   10   15

Ile Ala Leu Asp Pro Arg Tyr Gly Ile Phe Phe Phe Trp Thr Asp Trp
            20   25   30

Asp Ala Asn Phe Pro Arg Ile Glu Ser Ala Ser Met Ser Gly Ala Gly
        35   40   45

Arg Lys Thr Ile
    50

<210> 1801
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M4039I"

<400> 1801
Phe Gly Thr Cys Pro Gln His Cys Arg Asn Thr Lys Gly Ser Tyr Glu
1 5 10 15

Cys Val Cys Ala Asp Gly Phe Thr Ser Ile Ile Ser Asp Arg Pro Gly
20 25 30

Lys Arg Cys Ala Ala Glu Gly Ser Ser Pro Leu Leu Leu Leu Pro Asp
35 40 45

Asn Val Arg Ile
50

<210> 1802
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A516V"

<400> 1802
Ile Asp Met Val Asn Leu Asp Gly Ser Tyr Arg Val Thr Leu Ile Thr
1 5 10 15

Glu Asn Leu Gly His Pro Arg Gly Ile Val Val Val Asp Pro Thr Val
20 25 30

Gly Tyr Leu Phe Phe Ser Asp Trp Glu Ser Leu Ser Gly Glu Pro Lys
35 40 45

Leu Glu Arg Ala
50

<210> 1803
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S737L"

<400> 1803
Ile Phe Ser Ser Gln Val Ala Ile Arg Gly Ile Pro Phe Thr Leu Ser
1 5 10 15

Thr Gln Glu Asp Val Met Val Pro Val Leu Leu Gly Asn Pro Ser Phe
20 25 30

Phe Val Gly Ile Asp Phe Asp Ala Gln Asp Ser Thr Ile Phe Phe Ser
35 40 45

Asp Met Ser Lys
50

<210> 1804
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R2432I"

<400> 1804
Asn His Ser Pro Pro Phe Gln Thr Ile Asn Val Glu Arg Thr Val Met
1 5 10 15

Ser Leu Asp Tyr Asp Ser Val Ser Asp Ile Ile Ile Tyr Phe Thr Gln
20 25 30

Asn Leu Ala Ser Gly Val Gly Gln Ile Ser Tyr Ala Thr Leu Ser Ser
35 40 45

Gly Ile His Thr
50

<210> 1805
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R3043C"

<400> 1805
Cys Gly Asp Tyr Ser Asp Glu Arg Gly Cys Leu Tyr Gln Thr Cys Gln
1 5 10 15

Gln Asn Gln Phe Thr Cys Gln Asn Gly Cys Cys Cys Ile Ser Lys Thr
20 25 30

Phe Val Cys Asp Glu Asp Asn Asp Cys Gly Asp Gly Ser Asp Glu Leu
35 40 45

Met His Leu Cys
50

<210> 1806
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S1609P"

<400> 1806
Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu Arg Ser
1 5 10 15

Tyr Phe His Leu Phe Pro Pro Pro Pro Pro Pro Pro Cys Thr Asp Ser
20 25 30

Ser

<210> 1807

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R675Q"

<400> 1807
Asn Asn Asn Asn Val Ala Ile Pro Leu Thr Gly Val Lys Glu Ala Ser
1 5 10 15

Ala Leu Asp Phe Asp Val Thr Asp Asn Gln Gln Ile Tyr Trp Thr Asp
20 25 30

Ile Ser Leu Lys Thr Ile Ser Arg Ala Phe Met Asn Gly Ser Ala Leu
35 40 45

Glu His Val Val
50

<210> 1808
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D227N"

<400> 1808
Leu Asp His Arg Asp Leu Ile Pro Ile Ile Ala Ala Leu Glu Tyr Asn
1 5 10 15

Gln Trp Phe Thr Lys Leu Ser Ser Lys Asn Asn Leu Lys Leu Ser Thr
20 25 30

Asp Val Cys Glu Gln Ile Leu Arg Val Val Ser Arg Ser Asn Arg Leu
35 40 45

Glu Glu Leu Val
50

<210> 1809
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R787W"

<400> 1809
Ala Val Asp Lys Glu Leu Gln Val Ile Leu Glu Ser Met Val Ser Leu
1 5 10 15

Thr Gln Glu Leu Cys Pro Val Ala Met Trp Trp Val Ala Glu Gly His
20 25 30

Asn Lys Met Leu Ser Asn Val Ala Glu Arg Val Thr Val Pro Arg Asn
35 40 45

Phe Ile Arg Gly
50

<210> 1810
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R218W"

<400> 1810
Arg Arg Leu Glu Asn Leu Tyr Val Val Glu Glu Lys Asp Leu Cys Ala
1 5 10 15

Ala Cys Leu Arg Lys Cys Gln Asn Ala Trp Trp Asp Asn Leu Asn Arg
20 25 30

Ile Lys Asn Met Ala Thr Thr Thr Pro Arg Lys Thr Ile Phe Pro Asn
35 40 45

Leu Ile Ser Pro
    50

<210> 1811
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.K23T"

<400> 1811
Arg Lys Lys Thr Ser Ser Glu Gly Glu Thr Lys Pro Gln Thr Ser Thr
1   5   10   15

Val Asn Lys Phe Leu Arg Thr Ala Ser Asn Ala Glu Ser Arg Lys Glu
            20   25   30

Asp Asn Asp Leu Lys Thr Ser Asp Ser Gln Pro Ser Asp Trp Ile Gln
        35   40   45

Lys

<210> 1812
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.T102S"

<400> 1812
Glu Leu Glu Gln Pro His Thr Gln Gln Gly Pro Glu Lys Leu Ala Gly
1   5   10   15

Asn Ala Ile Tyr Thr Lys Pro Ser Phe Ser Ser Gln Glu His Lys Ala
            20   25   30

Ala Val Ser Val Leu Thr Pro Phe Ser Lys Gly Ala Pro Ser Thr Ser
35 40 45

Ser Pro Ala Lys
50

<210> 1813
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A406D"

<400> 1813
Glu Thr Pro Gly Gln Pro Pro Glu His His Glu Val Thr Val Ser Pro
1 5 10 15

Pro Gly His His Gln Thr His His Leu Asp Asp Ser Pro Ser Val Ser
20 25 30

Val Lys Pro Pro Asp Val Gln Leu Thr Ile Ala Ala Glu Pro Ser Ala
35 40 45

Glu Val Gly Thr
50

<210> 1814
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D558fs"

<400> 1814
Lys Glu Pro Ala Lys Glu Trp Lys Val Leu Lys Lys Lys Lys Glu Pro
1 5 10 15

Pro Lys Glu Leu Arg Gln Asp Pro Pro Ser Ser Arg Cys Trp Ala Gly

20 25 30

Ala Trp

<210> 1815
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1389H"

<400> 1815
Val Pro Pro Asp Thr Ile Thr Lys Lys Ala Gly Ser His Ile Gln Thr
1 5 10 15

Leu Met Gly Ser Gln Ser Leu Gln His His His Ser Arg Glu Gln Gln
20 25 30

Pro Tyr Glu Gly Asn Ile Asn Lys Val Thr Ile Gln Gln Phe Gln Ser
35 40 45

Pro Leu Pro Ile
50

<210> 1816
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A6V"

<400> 1816
Met Glu Ala Ala Ala Val Val Val Val Ala Ala Glu Ala Glu Val Glu
1 5 10 15

Asn Glu Asp Gly Asp Ser Ser Cys Gly Asp Val Cys Phe Met Asp Lys
20 25 30

<210> 1817
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.W792L"

<400> 1817
Arg Lys Arg Pro Val Lys Cys Pro Ala Asn Met Thr Pro Ala Leu Asp
1 5 10 15

Lys Leu Glu Ile Leu Arg Cys Gly Pro Leu Leu Asp Thr Leu Gln Gln
20 25 30

Val Thr Thr Val Thr Phe Gln Asp Leu Pro Gly Cys Val Leu Ser Thr
35 40 45

Leu Ala Glu Cys
50

<210> 1818
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K244fs"

<400> 1818
Leu Ile Val Gln Arg Trp Ile Arg Gly Phe Leu Val Arg Lys Asn Leu
1 5 10 15

Ser Pro Val Phe Phe His Lys Lys Lys Thr Ala Gly Lys Asn Tyr
20 25 30

<210> 1819
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S243Y"

<400> 1819
Ser Lys Ile Asn Phe Ala His Phe Pro Arg Leu Phe Asn Leu Arg Ser
1 5 10 15

Ile Tyr Leu Gln Trp Asn Arg Ile Arg Tyr Tyr Ile Ser Gln Gly Leu
20 25 30

Thr Trp Thr Trp Ser Ser Leu His Asn Leu Asp Leu Ser Gly Asn Asp
35 40 45

Ile Gln Gly Ile
50

<210> 1820
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S139L"

<400> 1820
Asp Leu Thr Asn Leu Thr Glu Leu Gln Leu Arg Asn Asn Ser Ile Arg
1 5 10 15

Thr Leu Asp Arg Asp Leu Leu Arg His Leu Leu Pro Leu Leu Arg His
20 25 30

Leu Asp Leu Ser Ile Asn Gly Leu Ala Gln Leu Pro Pro Gly Leu Phe
35 40 45

Asp Gly Leu Leu
50

<210> 1821
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L176V"

<400> 1821
Gly Leu Ala Gln Leu Pro Pro Gly Leu Phe Asp Gly Leu Leu Ala Leu
1 5 10 15

Arg Ser Leu Ser Leu Arg Ser Asn Arg Val Val Gln Asn Leu Asp Arg
20 25 30

Leu Thr Phe Glu Pro Leu Ala Asn Leu Gln Leu Leu Gln Val Gly Asp
35 40 45

Asn Pro Trp Glu
50

<210> 1822
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R517L"

<400> 1822
Ile Thr Pro Arg Glu Asp Glu Asp Pro His Arg Pro Pro Thr Ser Glu
1 5 10 15

Glu Leu Leu Thr Ala Tyr Gly Tyr Met Leu Leu Gly Phe Met Thr Ala
20 25 30

His Gly Gln Pro Asp Gln Pro Arg Ser Ala Arg Tyr Ile Leu Lys Asp
35 40 45

Tyr Val Ser Gly

50

<210> 1823
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F107L"

<400> 1823
Tyr Lys Gly Ser Pro Met Glu Ile Ser Leu Pro Ile Ala Leu Ser Lys
1 5 10 15

Asn Gln Glu Ile Val Ile Glu Ile Ser Leu Leu Glu Thr Ser Pro Lys
20 25 30

Ser Ser Ala Leu Gln Trp Leu Thr Pro Glu Gln Thr Ser Gly Lys Glu
35 40 45

His Pro Tyr Leu
50

<210> 1824
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F73L"

<400> 1824
Gln Lys Arg Ser Val Thr Ala Leu Met Val Leu Asn Leu Ala Leu Ala
1 5 10 15

Asp Leu Ala Val Leu Leu Thr Ala Pro Leu Leu Phe Leu His Phe Leu
20 25 30

Ala Gln Gly Thr Trp Ser Phe Gly Leu Ala Gly Cys Arg Leu Cys His
35 40 45

Tyr Val Cys Gly
50

<210> 1825
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.S148T"

<400> 1825
Gly Lys Asn Glu Glu Lys Ile Gln Val Leu Thr Asp Lys Ile Asp Val
1 5 10 15

Leu Leu Gln Gln Ile Glu Glu Leu Gly Thr Thr Glu Gly Lys Val Glu
20 25 30

Glu Ala Gln Gly Met Met Lys Leu Val Glu Gln Leu Lys Glu Glu Arg
35 40 45

Glu Leu Leu Arg
50

<210> 1826
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R310L"

<400> 1826
Gln Leu Glu Lys Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro
1 5 10 15

Leu Ser Tyr Ser Lys Ile Lys His Leu Leu Leu Leu Asp Gly Asn Arg
20 25 30

Ile Ser Glu Thr Ser Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val
35 40 45

Ala Asn Glu Val
50

<210> 1827
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R330C"

<400> 1827
Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
1 5 10 15

Leu Pro Pro Asp Met Tyr Glu Cys Leu Cys Cys Val Ala Asn Glu Val
20 25 30

Thr Leu Asn
35

<210> 1828
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I69L"

<400> 1828
Arg Ala Ser Gly Lys Asp Ser Ala Pro Thr Val Val Ser Gly Ile Leu
1 5 10 15

Gly Gly Ser Val Thr Leu Pro Leu Asn Leu Leu Ser Val Asp Thr Glu
20 25 30

Ile Glu Asn Val Ile Trp Ile Gly Pro Lys Asn Ala Leu Ala Phe Ala
35 40 45

Arg Pro Lys Glu
50

<210> 1829
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T64K"

<400> 1829
Ala Val Ala Phe His Asn Trp Lys Trp Leu Leu Met Arg Asn Met Val
1 5 10 15

Cys Lys Leu Gln Glu Gly Cys Glu Glu Lys Lys Leu Val Phe Ile Glu
20 25 30

Thr Gly Thr Ala Arg Gly Val Val Gly Phe Lys Gly Cys Ser Ser Ser
35 40 45

Ser Ser Tyr Pro
50

<210> 1830
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q710H"

<400> 1830
Asp Leu Leu Trp Lys Trp Asp Ala Leu Lys Ala Tyr Gln Asn Phe Val
1 5 10 15

Phe Glu Glu Asp Arg Leu His Ser Ile His His Ile Ala Asn His Ile

20 25 30

Cys Asn Leu Ile Gln Lys Gly Asn Ile Val Val Gln Trp Lys Leu Tyr
35 40 45

Asn Tyr Ile Phe
50

<210> 1831
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.RTQDLEGALRTKGLEL432del"

<400> 1831
Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys Ala Gln Leu Lys Asp Thr
1 5 10 15

Arg Gly Lys Leu Glu Gly Leu Glu Leu Glu Val Cys Glu Asn Glu Leu
20 25 30

Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu Arg Glu Lys Val Asn Leu
35 40 45

Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala Gln Ala Ala Leu Ala Arg
50 55 60

Asp Met Gly Pro Pro Thr Phe Pro Glu Asp Val Pro Ala Leu Gln Arg
65 70 75 80

Glu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu Glu Arg Gln Gly His
85 90 95

Asp Gln

<210> 1832
<211> 65
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P100fs"

<400> 1832
Val Pro Pro Arg Lys Ala Val Pro Val Thr Ser Phe Thr Tyr Ile Asn
1 5 10 15

Glu Asp Phe Arg Thr Glu Ser Pro Pro Ala Gln Ala Val Met Leu Arg
20 25 30

Met Pro Glu Ser Ser Gly His Thr Met Pro Thr Ser Ala Ala His His
35 40 45

Gln Ser Ser Ser Leu Ser Leu Glu Ser Trp Arg Arg Thr Trp Arg Arg
50 55 60

Ser
65

<210> 1833
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R345C"

<400> 1833
Glu Ala His Val Pro Leu Gln Asp Tyr Glu Ala Ser Asn Ser Val Thr
1 5 10 15

Pro Lys Met Val Val Leu Asp Ala Gly Cys Cys Tyr Gln Lys Leu Arg
20 25 30

Val Gly Ser Ser Gly Phe Ser His Phe Asn Ser Ser Asn Glu Glu Gln
35 40 45

Arg Ser Asn Thr
50

<210> 1834
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G53fs"

<400> 1834
Met Lys Phe Glu Val Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile
1 5 10 15

Ser Gln Cys Gly Arg Leu Ile Ala Gly Ala Arg Cys Pro Pro Pro Pro
20 25 30

<210> 1835
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L609H"

<400> 1835
Pro Gln Gly Glu Asp Ser Leu Ser Pro His Tyr Phe Pro Gln Ser Pro
1 5 10 15

Pro Gln Gly Glu Asp Ser Met Ser Pro His His Tyr Phe Pro Gln Ser
20 25 30

Pro Leu Gln Gly Glu Glu Phe Gln Ser Ser Leu Gln Ser Pro Val Ser
35 40 45

Ile Cys Ser Ser
50

<210> 1836
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P239del"

<400> 1836
Phe Gln Ser Ser Pro Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Ala
1 5 10 15

Gln Ser Pro Leu Gln Ile Pro Val Ser Ser Ser Ser Ser Thr Leu Leu
20 25 30

Ser Leu Phe Gln Ser Phe Ser Glu Arg Thr Gln Ser Thr Phe Glu Gly
35 40 45

Phe Ala Gln Ser Ser
50

<210> 1837
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V380M"

<400> 1837
Ser Val Leu Pro Ile Pro Gly Glu Gly Leu Ser Thr Ser Val Pro Pro
1 5 10 15

Thr Ala Ser Asp Gly Ser Asp Thr Ser Met Met Pro Pro Thr Pro Gly
20 25 30

Glu Gly Ala Ser Thr Leu Val Gln Pro Thr Ala Pro Asp Gly Pro Gly
35 40 45

Ser Ser Val Leu
50

<210> 1838

<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q45fs"

<400> 1838
Gly Asp Gly Arg Gly Glu Ile Gln Ala Thr Asn Ala Ser Gly Ser Pro
1 5 10 15

Thr Ser Met Leu Val Val Asp Ala Pro Ser Ala Leu Arg Arg Gln Ser
20 25 30

Thr Leu Ser Val Ser Thr Leu Pro Arg Pro Phe Arg Thr Arg Met Thr
35 40 45

Trp Arg Ser
50

<210> 1839
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G1156V"

<400> 1839
Lys Gly Phe Gly Phe Ser Leu Arg Gly Gly Arg Glu Tyr Asn Met Asp
1 5 10 15

Leu Tyr Val Leu Arg Leu Ala Glu Asp Val Val Pro Ala Glu Arg Cys
20 25 30

Gly Lys Met Arg Ile Gly Asp Glu Ile Leu Glu Ile Asn Gly Glu Thr
35 40 45

Thr Lys Asn Met
50

<210> 1840
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R1198C"

<400> 1840
Ile Asn Gly Glu Thr Thr Lys Asn Met Lys His Ser Arg Ala Ile Glu
1 5 10 15

Leu Ile Lys Asn Gly Gly Arg Arg Val Cys Cys Leu Phe Leu Lys Arg
20 25 30

Gly Asp Gly Ser Val Pro Glu Tyr Asp Pro Ser Ser Asp Arg His Gly
35 40 45

Pro Ala Thr Gly
50

<210> 1841
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L450M"

<400> 1841
Leu Ser Thr Thr Leu Lys Lys Ser Asn Met Gly Phe Gly Phe Thr Ile
1 5 10 15

Ile Gly Gly Asp Glu Pro Asp Glu Phe Met Met Gln Val Lys Ser Val
20 25 30

Ile Pro Asp Gly Pro Ala Ala Gln Asp Gly Lys Met Glu Thr Gly Asp
35 40 45

Val Ile Val Tyr
    50

<210> 1842
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P1044T"

<400> 1842
Pro Ser Ser Glu Lys Gln Ser Pro Met Ala Gln Gln Ser Pro Leu Ala
1   5   10   15

Gln Gln Ser Pro Leu Ala Gln Pro Ser Thr Thr Ala Thr Pro Asn Ser
            20   25   30

Pro Ile Ala Gln Pro Ala Pro Pro Gln Pro Leu Gln Leu Gln Gly His
        35   40   45

Glu Asn Ser Tyr
    50

<210> 1843
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Q591K"

<400> 1843
Gln Ala Asn Gln Gln Met Pro Ser Val Leu Pro Ser Gln Asn Lys Pro
1   5   10   15

Ser Leu Leu His Tyr Thr Gln Gln Gln Lys Lys Gln Gln Gln Gln Gln
            20   25   30

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
        35   40   45

Gln Gln Gln Gln
    50

<210> 1844
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Q572L"

<400> 1844
Tyr Leu Gln Gln Pro Thr Pro Thr Gln Ala Ser Ser Ala Thr Ala Ser
1   5   10   15

Ser Thr Ala Thr Ala Thr Leu Gln Leu Leu Leu Gln Gln Gln Gln Gln
            20   25   30

Gln Gln Gln Gln Pro Asp His Ser Ser Phe Leu Leu Gln Gln Met Met
        35   40   45

Gln Gln Pro Gln
    50

<210> 1845
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P162fs"

<400> 1845
Gln Pro His Pro Arg Met Lys Pro Ser Pro Leu Thr Pro Cys Pro Pro
1   5   10   15

Gly Val Pro Ser Pro Ser Pro Pro Pro Thr Gln Val Gly Thr Ser Asp

20 25 30

Pro

<210> 1846
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G431fs"

<400> 1846
Met Glu Ala Lys Asn Met Tyr Tyr Glu Ala Leu Glu Ala Ile Glu Thr
1 5 10 15

Tyr Leu Leu Asn Val Ser Pro Gly Gly Ala Asp Leu His Cys Arg Val
20 25 30

Ala Arg Gly Asp Ser Gly Pro Gln Asp Gly Ala Pro Gly Leu Phe Leu
35 40 45

Arg Gly His Asp Arg Pro Trp Arg Arg Gly Cys Gln Gly Arg Lys Glu
50 55 60

Gly Pro Leu Pro Arg Ala Arg Ser Pro Asp His Gln Asp Val Ser Arg
65 70 75 80

Val Ile Arg Pro Leu Arg His Gln Thr Trp Ala
85 90

<210> 1847
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P2063fs"

<400> 1847
Gly Pro Thr Val Pro Pro Arg Pro Glu Pro Gly Pro Ser Met Glu Pro
1 5 10 15

Ser Leu Thr Pro Pro Ala Val Pro Pro Val Leu Leu Ser
20 25

<210> 1848
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E2046D"

<400> 1848
Glu Gly Tyr Ser Tyr Glu Thr Ser Thr Lys Thr Thr Arg Thr Pro Asp
1 5 10 15

Thr Ser Thr Tyr Cys Tyr Glu Thr Ala Asp Asp Lys Ile Thr Arg Thr
20 25 30

Pro Gln Ala Ser Thr Tyr Ser Tyr Glu Thr Ser Asp Leu Cys Tyr Thr
35 40 45

Ala Glu Lys Lys
50

<210> 1849
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S411C"

<400> 1849
Glu Lys Met Gly Val Gly Arg Leu Asp Met Tyr Val Leu His Pro Pro
1 5 10 15

Ser Ala Gly Ala Glu Arg Thr Leu Ala Cys Cys Val Cys Ala Leu Leu
20 25 30

Val Trp His Pro Ala Gly Pro Gly Glu Lys Val Val Arg Val Leu Phe
35 40 45

Pro Gly Cys Thr
50

<210> 1850
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K530N"

<400> 1850
Gln Ala Val Thr Asp Ser Ala Met Thr Ser Lys Thr Leu Glu Lys Ala
1 5 10 15

Met Thr Glu Pro Ser Ala Leu Ile Glu Asn Asn Ser Ser Ile Gln Glu
20 25 30

Leu Phe Glu Met Arg Val Asp Asp Lys Asp Lys Ile Glu Gly Val Gly
35 40 45

Ala Ala Thr Ser
50

<210> 1851
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K1472fs"

<400> 1851

Glu Pro Ser Thr Val Ser Arg Asp Glu Val Arg Arg Lys Lys Ala Val
1 5 10 15

Tyr Lys Lys Ala Glu Leu Ala Lys Lys Asn Arg Ser Ser Gly Pro Leu
20 25 30

Ser Leu Gln Glu Ile His Phe Lys Thr Cys Tyr Gln Ile Tyr
35 40 45

<210> 1852
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K57N"

<400> 1852
Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg
1 5 10 15

Lys Arg Leu Glu Ala Phe Leu Thr Gln Asn Asn Gln Lys Val Gly Glu
20 25 30

Leu Lys Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn
35 40 45

Gly Gly Val Val
50

<210> 1853
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K57N"

<400> 1853
Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg

1 5 10 15

Lys Arg Leu Glu Ala Phe Leu Thr Gln Asn Asn Gln Lys Val Gly Glu
20 25 30

Leu Lys Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn
35 40 45

Gly Gly Val Val
50

<210> 1854
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P124S"

<400> 1854
Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile Arg Glu
1 5 10 15

Leu Gln Val Leu His Glu Cys Asn Ser Ser Ser Tyr Ile Val Gly Phe
20 25 30

Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu His
35 40 45

Met Asp Gly Gly
50

<210> 1855
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S184L"

<400> 1855
Pro Tyr Ile Val Gln Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Cys
1 5 10 15

Trp Ile Cys Met Glu Leu Met Ser Thr Leu Leu Phe Asp Lys Phe Tyr
20 25 30

Lys Tyr Val Tyr Ser Val Leu Asp Asp Val Ile Pro Glu Glu Ile Leu
35 40 45

Gly Lys Ile Thr
50

<210> 1856
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S251I"

<400> 1856
Ile His Arg Asp Ile Lys Pro Ser Asn Ile Leu Leu Asp Arg Ser Gly
1 5 10 15

Asn Ile Lys Leu Cys Asp Phe Gly Ile Ile Ile Gly Gln Leu Val Asp
20 25 30

Ser Ile Ala Lys Thr Arg Asp Ala Gly Cys Arg Pro Tyr Met Ala Pro
35 40 45

Glu Arg Ile Asp
50

<210> 1857
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.T261fs"

<400> 1857
Asp Arg Ser Gly Asn Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Gln
1 5 10 15

Leu Val Asp Ser Ile Ala Lys Thr Arg Cys Trp Leu
20 25

<210> 1858
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R287H"

<400> 1858
Arg Asp Ala Gly Cys Arg Pro Tyr Met Ala Pro Glu Arg Ile Asp Pro
1 5 10 15

Ser Ala Ser Arg Gln Gly Tyr Asp Val His His Ser Asp Val Trp Ser
20 25 30

Leu Gly Ile Thr Leu Tyr Glu Leu Ala Thr Gly Arg Phe Pro Tyr Pro
35 40 45

Lys Trp Asn Ser
50

<210> 1859
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q445R"

<400> 1859

Val Gln Phe Asn Asp Gly Asn Ala Ala Val Val Ser Met Trp Val Cys
1 5 10 15

Arg Ala Leu Glu Glu Arg Arg Ser Gln Arg Arg Gly Pro Pro
20 25 30

<210> 1860
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I761fs"

<400> 1860
Leu Asn Cys Ile Leu Gly Asn Gln Thr Glu Ser Asn Asn Trp Gln Glu
1 5 10 15

Leu Leu Gly Arg Leu Cys Leu Ile Asp Cys Cys Trp Asn Phe Leu Leu
20 25 30

Asn Phe Ile Leu Ile Leu Ser Val Leu Met Phe His Lys Leu Ser Leu
35 40 45

Leu Lys Ser Gly Ile Arg Ser Cys Cys Pro Ser
50 55

<210> 1861
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V1346del"

<400> 1861
Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser
1 5 10 15

Lys Tyr Gly Ala Phe Lys Glu Ser Val Ile Asn Tyr Thr Glu Gln Leu

20 25 30

Leu Arg Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp
35 40 45

Val Lys Gly Ala Asn
50

<210> 1862
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1384fs"

<400> 1862
Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu
1 5 10 15

Leu Ile Asp Ser Thr Gly Gln Arg Leu Lys Asn Cys Arg Phe Trp Ser
20 25 30

Cys Ser Gln Val Gly Ile Lys Arg Asn Trp Cys Arg Arg Val Ser Gly
35 40 45

Thr Ile Thr Gly Asp Asn Cys Ile Tyr Gly Thr
50 55

<210> 1863
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L318fs"

<400> 1863
Asp Gly Phe Ser Pro Tyr Ser Pro Glu Glu Thr Asn Arg Arg Val Asn
1 5 10 15

Lys Val Met Arg Ala Arg Leu Tyr Leu Thr Ala Ala Asp Arg Ala
20 25 30

<210> 1864
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P324L"

<400> 1864
Tyr Ser Pro Glu Glu Thr Asn Arg Arg Val Asn Lys Val Met Arg Ala
1 5 10 15

Arg Leu Tyr Leu Leu Gln Gln Ile Gly Leu Leu Asn Ser Phe Leu Ile
20 25 30

Gly Gly Asp Ser Pro Asp Asn Lys Tyr Arg Val Phe Ile Gly Pro Gln
35 40 45

Asn Cys Ser Cys
50

<210> 1865
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R449del"

<400> 1865
Lys Leu His Phe Glu Lys Ile Lys Ser Glu Gly Thr Cys Leu His Arg
1 5 10 15

Leu Glu Glu Glu Leu Val Met Arg Arg Glu Glu Leu Arg His Ala Leu
20 25 30

Asp Ile Arg Glu His Tyr Glu Arg Lys Leu Glu Arg Ala Asn Asn Leu
35 40 45

Tyr Met Glu Leu Asn
50

<210> 1866
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R275Q"

<400> 1866
Glu Asn Thr Ser Gly Phe Trp Leu Asn Arg Ser Asn Glu Leu Ile Trp
1 5 10 15

Leu Glu Leu Gln Ala Trp His Ala Gly Gln Gln Thr Ile Asn Asp Gln
20 25 30

Asp Phe Phe Leu Tyr Thr Ala Arg Gln Ala Ile Pro Asp Ile Ile Asn
35 40 45

Glu Ile Leu Thr
50

<210> 1867
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E524Q"

<400> 1867
Ala Tyr Leu Thr Leu Asp His Gln Leu Gln Pro Leu Ala Pro Cys Pro
1 5 10 15

Asn Ser Lys Glu Ser Met Ala Val Phe Gln Gln Gln His Cys Lys Met
            20   25   30

Ala Gln Glu Tyr Met Lys Val Gln Thr Glu Ile Ala Leu Leu Leu Gln
        35   40   45

Arg Lys Gln Glu
    50

<210> 1868
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R341G"

<400> 1868
Ser Arg Gly Gln His Gly Pro Ala Glu Arg Thr Pro Ser Glu Ile Gln
1   5   10   15

Phe His Gln Val Lys Phe Gly Ala Pro Gly Gly Arg Lys Glu Thr Asp
            20   25   30

Pro Leu Asn Glu Pro Trp Glu Glu Glu Trp Thr Leu Leu Gly Lys Glu
        35   40   45

Glu Leu Ser Gly
    50

<210> 1869
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P657fs"

<400> 1869
Leu Phe Asp Tyr Ala Arg Gln Met Gln Lys Leu Pro Val Ala Ile Pro

1 5 10 15

Ala His Lys Leu Pro Asp Arg Ile Leu Gln Gly Asn Phe Leu Tyr Gln
20 25 30

Gln Lys Ser Leu Lys Pro Asn Gly Ala Arg Ser Val Val Leu
35 40 45

<210> 1870
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A80fs"

<400> 1870
Ala Thr Ser Ser Lys Gln Leu Pro Leu Glu Pro Glu Ser Pro Ser Gly
1 5 10 15

Gln Val Gly Pro Arg Pro Ala Pro Pro Ala Gly Arg Val Pro Phe Leu
20 25 30

<210> 1871
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R487C"

<400> 1871
Glu Arg Leu Glu Lys Glu Glu Gln Asp Arg Leu Glu Arg Glu Glu Leu
1 5 10 15

Lys Arg Lys Ala Glu Glu Glu Arg Leu Cys Cys Leu Glu Glu Glu Ala
20 25 30

Arg Lys Gln Glu Glu Glu Arg Lys Arg Gln Glu Glu Glu Lys Lys Lys
35 40 45

Gln Glu Gly Glu
50

<210> 1872
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.Q308fs"

<400> 1872
Pro Gln Thr Lys Val Glu Glu Ser Pro Leu Glu Lys Val Glu Thr Pro
1 5 10 15

Pro Lys Ala Ser Val Asp Ala Pro Pro Arg
20 25

<210> 1873
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K485N"

<400> 1873
Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala
1 5 10 15

Trp Lys Ala Met Lys Glu Lys Glu Ala Asn Asn Lys Ile Ala Ala Lys
20 25 30

Lys Arg Leu Glu Glu Lys Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala
35 40 45

Ala Arg Lys Gly
50

<210> 1874
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E322K"

<400> 1874
Asn Pro His Lys Arg Ile Glu Val Glu Gln Ala Leu Ala His Pro Tyr
1 5 10 15

Leu Glu Gln Tyr Tyr Asp Pro Ser Asp Lys Lys Pro Ile Ala Glu Ala
20 25 30

Pro Phe Lys Phe Asp Met Glu Leu Asp Asp Leu Pro Lys Glu Lys Leu
35 40 45

Lys Glu Leu Ile
50

<210> 1875
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E315K"

<400> 1875
Glu Leu Asp Val Asp Lys Arg Leu Thr Ala Ala Gln Ala Leu Thr His
1 5 10 15

Pro Phe Phe Glu Pro Phe Arg Asp Pro Lys Lys Glu Glu Thr Glu Ala
20 25 30

Gln Gln Pro Phe Asp Asp Ser Leu Glu His Glu Lys Leu Thr Val Asp
35 40 45

Glu Trp Lys Gln
50

<210> 1876
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q511fs"

<400> 1876
Pro Pro Arg Leu Pro Pro Glu Ala Arg Pro Gly Arg Arg Met Phe Ser
1 5 10 15

Thr Ser Ala Leu Gln Gly Ala Gln Gly Val Pro Gly Leu Cys Leu Glu
20 25 30

Ala Thr Pro Lys Pro Thr Gly Leu Ser Ala Thr Arg His Trp Ala Thr
35 40 45

Cys Pro Cys Trp Arg Gly Thr Met Cys Glu Pro Pro Tyr Ser Leu His
50 55 60

Leu Ala Leu Cys Ser Cys Pro Ser Pro Phe Pro Arg Pro Leu Ser Ser
65 70 75 80

Leu Leu His Pro Leu Ala Leu Pro Ala Leu Pro Gly Pro Leu Lys Phe
85 90 95

Gln Gly Ala Cys Pro Gly Leu Leu Gly Gly Ala Asp Glu Gly Pro Ala
100 105 110

Pro Ala Pro Leu Thr Ser Ser Asn Lys Val Met Ser Ala Pro Asn
115 120 125

<210> 1877
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V100M"

<400> 1877
Asp Asn Ile Val Lys Val Tyr Glu Val Leu Gly Pro Lys Gly Thr Asp
1   5   10   15

Leu Gln Gly Glu Leu Phe Lys Phe Ser Met Met Ala Tyr Ile Val Gln
            20   25   30

Glu Tyr Met Glu Thr Asp Leu Ala Arg Leu Leu Glu Gln Gly Thr Leu
        35   40   45

Ala Glu Glu His
    50

<210> 1878
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A501D"

<400> 1878
Lys Ala Ala Leu Lys Ala Ala Leu Leu Lys Ser Leu Arg Ser Arg Leu
1   5   10   15

Arg Asp Gly Pro Ser Ala Pro Leu Glu Asp Asp Pro Glu Pro Arg Lys
            20   25   30

Pro Val Thr Ala Gln Glu Arg Gln Arg Glu Arg Glu Glu Lys Arg Arg
        35   40   45

Arg Arg Gln Glu
    50

<210> 1879
<211> 81
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L217fs"

<400> 1879
Ser Ser Ser Pro Leu Lys Thr Gly Glu Gln Thr Pro Pro His Glu His
1 5 10 15

Ile Cys Leu Ser Asp Glu Leu Pro Pro Pro Arg Ala Ala Pro Pro Pro
20 25 30

Pro Gln Ile Glu Ala Pro Pro Pro Thr Ala Leu Ala Ala Ala Ala Gln
35 40 45

Pro Pro Arg Trp His Leu Arg Val Val Pro Leu Leu Pro Arg Leu Gly
50 55 60

Val Gly Ala Thr Arg Ile Glu Thr Glu Ser Thr Thr Arg Pro Met Cys
65 70 75 80

Asp

<210> 1880
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T214fs"

<400> 1880
Glu Asn Leu Leu Tyr Thr Ser Lys Arg Pro Asn Ala Ile Leu Lys Leu
1 5 10 15

Thr Asp Phe Gly Phe Ala Lys Glu Thr His Gln Pro Gln Leu Phe Asp
20 25 30

His Ser Leu Leu Tyr Thr Val Leu Cys Gly Ser Arg Ser Ala Gly Ser
35 40 45

Arg Glu Val
    50

<210> 1881
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R193L"

<400> 1881
Pro Ile Cys Lys Ile Cys Phe Gln Gly Ala Glu Gln Gly Glu Leu Leu
1   5   10   15

Asn Pro Cys Arg Cys Asp Gly Ser Val Leu Leu Tyr Thr His Gln Leu
            20   25   30

Cys Leu Leu Lys Trp Ile Ser Glu Arg Gly Ser Trp Thr Cys Glu Leu
        35   40   45

Cys Cys Tyr Arg
    50

<210> 1882
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R170C"

<400> 1882
Gly Leu Pro Thr Ile Pro Val Met Leu Ile Leu Gly Lys Met Ile Arg
1   5   10   15

Trp Glu Asp Tyr Val Leu Arg Leu Trp Cys Cys Lys Tyr Ser Asn Lys
            20   25   30

Leu Gln Ile Leu Asn Ser Ile Phe Pro Gly Ile Gly Cys Pro Val Pro
35 40 45

Arg Ile Pro Ala
50

<210> 1883
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K152fs"

<400> 1883
Ala Ser Ser Thr Ser Ser Pro Lys Ala Glu Asp Gly Ala Thr Pro Ser
1 5 10 15

Pro Ser Asn Glu Thr Pro Lys Lys Lys Arg Ser Ala Phe Pro Ser Arg
20 25 30

Ser Leu Ser Ser
35

<210> 1884
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R481Q"

<400> 1884
Leu Pro Lys Gln Val Ala Asp His Tyr Asp Asn Phe Arg Ile Tyr Lys
1 5 10 15

Ala Leu Glu Ala Val Ser Ser Cys Val Gln Gln Gln Thr Asn Gly Phe
20 25 30

Val Gln Arg His Ala Pro Trp Lys Leu Asn Trp Glu Ser Pro Val Asp

35 40 45

Ala Pro Trp Leu
50

<210> 1885
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R324G"

<400> 1885
Ile Ser Leu Phe Leu Ile Ile Asn Ser Ser Ala Asn Pro Ile Ile Tyr
1 5 10 15

Phe Phe Val Gly Ser Leu Arg Lys Lys Gly Gly Leu Lys Glu Ser Leu
20 25 30

Arg Val Ile Leu Gln Arg Ala Leu Ala Asp Lys Pro Glu Val Gly Arg
35 40 45

Asn Lys Lys Ala
50

<210> 1886
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E166G"

<400> 1886
Tyr Ala Thr Asp Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Val Leu
1 5 10 15

Ala His Lys Leu Asn Ala Lys Leu Ala Gly Gly Leu Arg Arg Asn Gly
20 25 30

Thr Leu Pro Trp Leu Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln
35 40 45

Tyr Met Gln Asp
50

<210> 1887
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R36W"

<400> 1887
Ser Asp Glu Glu Gln Pro Arg Phe Gln Ser Ala Ala Asp Lys Arg Ala
1 5 10 15

His His Asn Ala Leu Glu Arg Lys Arg Trp Trp Asp His Ile Lys Asp
20 25 30

Ser Phe His Ser Leu Arg Asp Ser Val Pro Ser Leu Gln Gly Glu Lys
35 40 45

Ala Ser Arg Ala
50

<210> 1888
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H28R"

<400> 1888
Asp Asn Asp Asp Ile Glu Val Glu Ser Asp Glu Glu Gln Pro Arg Phe
1 5 10 15

Gln Ser Ala Ala Asp Lys Arg Ala His Arg Arg Asn Ala Leu Glu Arg
20 25 30

Lys Arg Arg Asp His Ile Lys Asp Ser Phe His Ser Leu Arg Asp Ser
35 40 45

Val Pro Ser Leu
50

<210> 1889
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q311E"

<400> 1889
Glu Trp Arg Leu Ser Phe Ala Arg Ser Glu Val Gln Leu Lys Lys Cys
1 5 10 15

Ile Ser Ser Ser Leu Met Gln Ala Tyr Glu Glu Ala Cys Lys Ala Ile
20 25 30

Ile Ile Lys Leu Leu Ser Arg Pro Lys Ala Ile Ser Pro Tyr His Leu
35 40 45

Arg Ser Met Met
50

<210> 1890
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P732fs"

<400> 1890

Ser Val Thr Thr Ala Thr Thr Asp Pro Gly Ala Ser Ser Leu Gly Lys
1 5 10 15

Ala Pro Ser Asn Ser Gly Arg Pro Pro Asn Ser Leu Ala Leu Cys Trp
20 25 30

Val Pro Ala Cys Trp Val Thr Cys Leu His
35 40

<210> 1891
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G780fs"

<400> 1891
Leu Pro Ser Leu Leu Gln Pro Pro Gly Pro Leu Leu Ser Gly Gln Leu
1 5 10 15

Gly Leu Gln Leu Leu Pro Gly Gly Gly Ser Ser Ser Thr Pro Leu Arg
20 25 30

Gly Phe

<210> 1892
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R43Q"

<400> 1892
Ala Val Gln Leu Pro Ile Asp Gln Val Asn Phe Val Val Cys Gln Leu
1 5 10 15

Phe Ala Leu Leu Ala Ala Ile Trp Phe Gln Gln Thr Tyr Leu His Ser

20 25 30

Ser Lys Thr Ser Ser Phe Ile Arg His Val Val Ala Thr Leu Leu Gly
35 40 45

Leu Tyr Leu Ala
50

<210> 1893
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R424W"

<400> 1893
His Trp Phe Leu Lys Met Arg Ala Tyr Asp Tyr Met Cys Met Gly Phe
1 5 10 15

Val Leu Leu Ser Leu Ala Asp Thr Leu Trp Trp Tyr Trp Ala Ser Ile
20 25 30

Tyr Phe Cys Ile His Phe Leu Ala Leu Ala Ala Leu Gly Leu Gly Leu
35 40 45

Ala Leu Gly Gly
50

<210> 1894
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A109T"

<400> 1894
Leu Val Ser Met Ser Ser Ala Trp Glu Thr Ile Thr Ile Tyr Leu Leu
1 5 10 15

Asn Asn Lys His Leu Val Ile Ala Asp Thr Thr Phe Val Arg His Ile
20 25 30

Asp Asn Val Phe Asp Ser Met Ile Cys Ile Ser Val Val Ala Ser Met
35 40 45

Cys Ser Leu Leu
50

<210> 1895
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R926Q"

<400> 1895
Lys Thr Met Lys Leu Met Thr Leu Ser Ile Arg Gln Leu Gly Arg Gly
1 5 10 15

Ser His Arg Lys Phe Glu Ile Ala Ser Gln Gln Asn Gly Leu Glu Lys
20 25 30

Tyr Ile Leu Gln Ala Ala Ser Lys Glu Ile Arg Asp Cys Trp Phe Ser
35 40 45

Glu Ile Ser Lys
50

<210> 1896
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S306F"

<400> 1896
Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile Thr Ala Ala
1 5 10 15

Tyr Val Arg Ile Leu Gln Arg Met Thr Phe Phe Ser Val Ala Pro Ala
20 25 30

Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg Thr Ala
35 40 45

Ile Ala Ile Cys
50

<210> 1897
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V141I"

<400> 1897
Val Tyr Thr Gln Ser Asp Val Tyr Asp Gln Leu Ile Phe Ala Val Asn
1 5 10 15

Gln Tyr Leu Gln Leu Tyr Asn Val Ser Ile Ile Gly Asn His Ala Tyr
20 25 30

Glu Asn Lys Gly Thr Lys Gln Ser Ala Met Ala Ile Cys Gln His Phe
35 40 45

Tyr Lys Arg Gly
50

<210> 1898
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R915Q"

<400> 1898
Ser Glu Leu Leu Gln Ser Val Pro Ser Met Phe Asn Phe Arg Ala Pro
1 5 10 15

Pro Asn Ala Leu Pro Glu Asn Leu Leu Gln Gln Lys Gly Lys Glu Arg
20 25 30

Tyr Thr Cys Arg Tyr Cys Gly Lys Ile Phe Pro Arg Ser Ala Asn Leu
35 40 45

Thr Arg His Leu
50

<210> 1899
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R969C"

<400> 1899
Thr Gly Glu Gln Pro Tyr Arg Cys Lys Tyr Cys Asp Arg Ser Phe Ser
1 5 10 15

Ile Ser Ser Asn Leu Gln Arg His Val Cys Cys Asn Ile His Asn Lys
20 25 30

Glu Lys Pro Phe Lys Cys His Leu Cys Asp Arg Cys Phe Gly Gln Gln
35 40 45

Thr Asn Leu Asp
50

<210> 1900
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L36R"

<400> 1900
His Arg Pro Leu Lys Arg Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro
1   5   10   15

Gln Asp Pro Lys Gln Lys Glu Asp Glu Arg Arg Thr Ala Leu Asn Val
            20   25   30

Lys Gln Gly Phe Asn Asn Gln Pro Ala Val Ser Gly Asp Glu His Gly
        35   40   45

Ser Ala Lys Asn
    50

<210> 1901
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G44S"

<400> 1901
Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro Lys Gln Lys Glu Asp
1   5   10   15

Glu Leu Thr Ala Leu Asn Val Lys Gln Ser Ser Phe Asn Asn Gln Pro
            20   25   30

Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn Val Ser Phe Asn
        35   40   45

Pro Ala Lys Ile
    50

<210> 1902
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L1224F"

<400> 1902
Ile Arg Ser Ser Cys Asp Arg His Leu Leu Ala Ala Ser Gln Asn Arg
1 5 10 15

Ile Val Asp Gly Ala Val Phe Ala Val Phe Phe Lys Ala Val Phe Val
20 25 30

Leu Gly Asp Ala Glu Leu Lys Gly Ser Gly Phe Thr Val Thr Gly Gly
35 40 45

Thr Glu Glu Leu
50

<210> 1903
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.C1292Y"

<400> 1903
Leu Cys Thr Asp Lys Glu Leu Ile Leu Asp Pro Val Leu Ser Asn Met
1 5 10 15

Gln Ala Gln Lys Leu Leu Gln Leu Ile Tyr Tyr Tyr Pro His Gly Ile
20 25 30

Lys Glu Cys Thr Glu Gly Asp Asn Leu Gln Arg Gln His Ile Lys Arg
35 40 45

Ile Leu Gln Asn
50

<210> 1904
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P2071S"

<400> 1904
Gln Asp Pro Met Arg Pro Arg Gln Pro Gln Val Arg Gln Gln Gln Arg
1 5 10 15

Leu Leu Gln Met Gln Gln Pro Gln Gln Ser Ser Gln Pro Gln Gln Pro
20 25 30

Pro Gln Pro Gln Gln Ser Ser Gln Ser Gln Ser Gln Thr Leu Gly Leu
35 40 45

Gln Ala Met Gln
50

<210> 1905
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q2115del"

<400> 1905
Leu Gly Leu Gln Ala Met Gln Pro Gln Gln Pro Leu Phe Pro Arg Gln
1 5 10 15

Gly Leu Gln Gln Thr Gln Gln Gln Gln Thr Ala Ala Leu Val Arg Gln
20 25 30

Leu Gln Lys Gln Leu Ser Ser Asn Gln Pro Gln Gln Gly Val Thr Pro
35 40 45

Tyr Gly His Pro Ser
50

<210> 1906
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S35I"

<400> 1906
Trp Arg Ser Thr Ala Phe Arg Gln Lys Leu Val Ser Gln Ile Glu Asp
1 5 10 15

Ala Met Arg Lys Ala Gly Val Ala His Ile Ile Lys Ser Ser Lys Asp
20 25 30

Met Glu Ser His Val Phe Leu Lys Ala Lys Thr Arg Asp Glu Tyr Leu
35 40 45

Ser Leu Val Ala
50

<210> 1907
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H449Q"

<400> 1907
Thr Ala Gly Pro Ala Val His Leu Lys Ala Met Gln Leu Ser Trp Thr
1 5 10 15

Ser Leu Ala Leu Val Gly Ile Asp Ser Gln Gln Gly Lys Leu Ser Val
20 25 30

Leu Arg Leu Ser Pro Ser Met Gly His Pro Leu Glu Val Gly Leu Ala
35 40 45

Leu Arg His Leu

50

<210> 1908
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P99S"

<400> 1908
Glu Pro His Glu Ser Arg Thr Asn Ser Asp Ile Val Glu Ala Leu Asn
1 5 10 15

Lys Lys Glu His Arg Gly Cys Asp Ser Ser Ser Asp Pro Asp Thr Ser
20 25 30

Tyr Val Leu Thr Pro His Thr Glu Glu Lys Tyr Lys Lys Ile Asn Glu
35 40 45

Glu Phe Asp Asn
50

<210> 1909
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R127Q"

<400> 1909
Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu Glu Lys Tyr Lys Lys
1 5 10 15

Ile Asn Glu Glu Phe Asp Asn Met Met Gln Gln Asn His Lys Ile Ala
20 25 30

Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val Thr Val Pro Val
35 40 45

Thr Ser Pro Asn
50

<210> 1910
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R377H"

<400> 1910
Cys Pro Arg Cys Gln Asp Ser His Glu Arg Lys Ser Pro Gly Ser Leu
1 5 10 15

Ser Pro Gln Pro Leu Pro Gln Cys Lys His His His Leu Lys Gln Val
20 25 30

Gln Leu Leu Phe Cys Glu Asp His Asp Glu Pro Ile Cys Leu Ile Cys
35 40 45

Ser Leu Ser Gln
50

<210> 1911
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S1053L"

<400> 1911
Asn Pro Tyr Ala Thr Ile Lys Asp Pro Pro Val Leu Ile Pro Lys Ser
1 5 10 15

Ser Glu Cys Gly Tyr Val Glu Met Lys Leu Leu Pro Ala Arg Arg Asp
20 25 30

Ser Pro Tyr Ala Glu Ile Asn Asn Ser Thr Ser Ala Asn Arg Asn Val
35 40 45

Tyr Glu Val Glu
50

<210> 1912
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y393C"

<400> 1912
Arg Thr Cys Ile Asp Val Asp Asp Cys Ala Asp Ser Pro Cys Cys Gln
1 5 10 15

Gln Val Cys Thr Asn Asn Pro Gly Gly Cys Cys Glu Cys Gly Cys Tyr
20 25 30

Ala Gly Tyr Arg Leu Ser Ala Asp Gly Cys Gly Cys Glu Asp Val Asp
35 40 45

Glu Cys Ala Ser
50

<210> 1913
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A582fs"

<400> 1913
Asp Thr Phe Gly Lys Asn Cys Ser Phe Ser Cys Ser Cys Gln Asn Gly
1 5 10 15

Gly Thr Cys Asp Ser Val Thr Gly Ala Leu Pro Leu Pro Pro Gly Cys
20 25 30

Gln Trp Asn
35

<210> 1914
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H1094Y"

<400> 1914
Val Val Ile Gly Pro Ser Ser Leu Ile Val His Phe Asn Glu Val Ile
1 5 10 15

Gly Arg Gly His Phe Gly Cys Val Tyr Tyr Tyr Gly Thr Leu Leu Asp
20 25 30

Asn Asp Gly Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn Arg Ile
35 40 45

Thr Asp Ile Gly
50

<210> 1915
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M1250T"

<400> 1915
Leu Ala Arg Asp Met Tyr Asp Lys Glu Tyr Tyr Ser Val His Asn Lys
1 5 10 15

Thr Gly Ala Lys Leu Pro Val Lys Trp Thr Thr Ala Leu Glu Ser Leu

20 25 30

Gln Thr Gln Lys Phe Thr Thr Lys Ser Asp Val Trp Ser Phe Gly Val
35 40 45

Leu Leu Trp Glu
50

<210> 1916
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q53E"

<400> 1916
Val Trp Pro Asn Arg Ile His Thr Thr Ala Glu Lys Tyr Arg Glu Tyr
1 5 10 15

Glu Ala Arg Glu Gln Thr Asp Gln Thr Glu Glu Ala Gln Glu Leu His
20 25 30

Arg Ser Gln Asp Arg Asp Phe Glu Thr Met Ala Lys Leu His Ile Pro
35 40 45

Val Met Val Asp
50

<210> 1917
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R200Q"

<400> 1917
Glu Ile Ile Tyr Asp Phe Cys Met Cys Asn Pro Pro Phe Phe Ala Asn
1 5 10 15

Gln Leu Glu Ala Lys Gly Val Asn Ser Gln Gln Asn Pro Arg Arg Pro
20 25 30

Pro Pro Ser Ser Val Asn Thr Gly Gly Ile Thr Glu Ile Met Ala Glu
35 40 45

Gly Gly Glu Leu
50

<210> 1918
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R174Q"

<400> 1918
Glu Glu Thr Phe Thr Asp Leu Leu Gln Thr Leu Glu His Leu Cys Ser
1 5 10 15

Asn His Ser Val Ile Leu Leu Ala Cys Gln Gln Ile Arg Tyr Glu Arg
20 25 30

Asp Asn Asn Phe Leu Ala Met Leu Glu Arg Gln Phe Thr Val Arg Lys
35 40 45

Val His Tyr Asp
50

<210> 1919
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F56L"

<400> 1919
Asp Phe Lys Gln Gln Lys Leu Glu Gln Glu Ala Gln Lys Asn Trp Asp
1 5 10 15

Leu Phe Tyr Lys Arg Asn Ser Thr Asn Leu Leu Phe Lys Asp Arg His
20 25 30

Trp Thr Thr Arg Glu Phe Glu Glu Leu Arg Ser Cys Arg Glu Phe Glu
35 40 45

Asp Gln Lys Leu
50

<210> 1920
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y57F"

<400> 1920
Leu Tyr Val Asn Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Ala
1 5 10 15

Gly Gly Arg Lys Glu Asn His Gln Trp Phe Phe Val Cys Asn Arg Glu
20 25 30

Lys Leu Cys Glu Ser Leu Gln Ala Val Phe Val Gln Ser Tyr Leu Asp
35 40 45

Gln Gly Thr Gln
50

<210> 1921
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R534S"

<400> 1921
Ile Trp Thr Pro Phe Glu Pro Val Asn Pro Leu Ser Gly Phe Gly Ser
1   5   10   15

Asp Pro Ser Gly Asn Met Lys Thr Gln Ser Ser Arg Gly Ser Gln Pro
            20   25   30

Ser Thr Pro Arg Leu Ser Pro Thr Phe Pro Glu Ser Ile Glu His Pro
        35   40   45

Leu Ala Arg Arg
    50

<210> 1922
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.179_182AAAA>A"

<400> 1922
Ile Pro Gly Gly Ser Leu Gly Ser Val Leu Leu Pro Ala Ala Arg Phe
1   5   10   15

Asp Ala Arg Glu Ala Ala Ala Ala Ala Ala Gly Val Leu Tyr Gly Gly
            20   25   30

Asp Asp Ala Gln Gly Met Met Ala Ala Met Leu Ser His Ala Tyr Gly
        35   40   45

Pro Gly Gly Cys Gly Ala Ala Ala Ala Ala Leu Asn
    50   55   60

<210> 1923
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S7F"

<400> 1923
Met Ser Lys Gly Thr Ser Phe Phe Asp Thr Ser Leu Gly Arg Val Ser
1 5 10 15

Arg Ala Ala Phe Pro Ser Pro Thr Ala Ala Glu Met Ala Glu Ile Ser
20 25 30

Arg Ile

<210> 1924
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R162C"

<400> 1924
Thr Thr Pro Gln Asn Glu Glu Ile Arg Ala Val Gly Arg Leu Lys Arg
1 5 10 15

Glu Arg Ser Met Ser Glu Asn Ala Val Cys Cys Gln Asn Gly Gln Leu
20 25 30

Val Arg Asn Asp Ser Leu Trp His Arg Ser Asp Ser Ala Pro Arg Asn
35 40 45

Lys Ile Ser Arg
50

<210> 1925
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D170N"

<400> 1925
Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val
1 5 10 15

Ala Tyr Ser Leu Asn Gly His Glu Phe Asn Asn Phe Ile His Asp Val
20 25 30

Asn Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val
35 40 45

His Val Asn Leu
50

<210> 1926
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R280Q"

<400> 1926
Phe Glu Ala Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro
1 5 10 15

Ala Glu Trp Ile Pro Ala Thr Phe Ala Gln Gln Ala Ala Phe Trp Asn
20 25 30

His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser
35 40 45

Trp Ile Gly Leu
50

<210> 1927
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R2435Q"

<400> 1927
Trp Ser Asp Lys Leu Gln Lys Glu Ala Glu Ala Phe Ala Tyr Tyr Arg
1 5 10 15

Arg Thr His Thr Ala Asn Glu Arg Arg Gln Gln Arg Gly Glu Met Arg
20 25 30

Asp Leu Phe Glu Lys Leu Lys Ile Thr Leu Gly Leu Leu His Ser Ser
35 40 45

Lys Val Ser Lys
50

<210> 1928
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T444P"

<400> 1928
Ser Thr Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr
1 5 10 15

Leu Arg Glu Asp Phe Phe Trp Ala Phe Pro Pro Pro Ala Ala Gly Asp
20 25 30

Phe Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe
35 40 45

Phe Arg Ser Gly
50

<210> 1929
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T345M"

<400> 1929
Leu Ala Gln Lys Asn Val Ile Arg Phe Lys Pro Ser Leu Phe Gln His
1 5 10 15

Met Gly Tyr Tyr Ser Ser Tyr Lys Gly Met Met Glu Asn Lys Leu Lys
20 25 30

Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp Ile Pro Asp Asn Pro Pro
35 40 45

Ala Ser Leu Tyr
50

<210> 1930
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K102fs"

<400> 1930
Phe Ala Thr Cys Leu Gly Leu Val Tyr Ile Tyr Gly Arg His Leu Tyr
1 5 10 15

Phe Trp Gly Tyr Ser Glu Ala Ala Lys Asn Gly Ser Pro Val Ser Asp
20 25 30

<210> 1931
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G143fs"

<400> 1931
Ser Ile Ala Leu Leu Gly Leu Val Gly Thr Thr Val Cys Ser Ala Phe
1 5 10 15

Gln His Leu Gly Trp Val Lys Ser Gly Phe Gly Gln Trp Thr Gln Met
20 25 30

Leu Pro Leu Lys Asn Tyr Arg Gly Leu Lys Thr Leu Ile His Phe Lys
35 40 45

<210> 1932
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G318fs"

<400> 1932
His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln Ser His Trp Gln
1 5 10 15

Thr Phe His Val Ser Ala Val Ala Ala Leu Leu Phe Leu Leu Leu Leu
20 25 30

Phe Ser Met Ser Val Val Val Arg Arg Lys His Gln Leu Gln Arg Val
35 40 45

Gln Ser Ser
50

<210> 1933
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L131F"

<400> 1933
Glu Ser Glu Gly Gly Asp Val Ala Pro Asn Leu Pro Asp Met Thr Leu
1 5 10 15

Asp Lys Glu Gln Ile Ala Lys Asp Leu Phe Phe Ser Gly Glu Glu Glu
20 25 30

Glu Glu Thr Gln Ser Ser Ala Asp Asp Leu Thr Pro Ser Val Thr Ser
35 40 45

His Glu Ala Ser
50

<210> 1934
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1081S"

<400> 1934
Arg Glu Pro Ala Gly Asp Gly Lys Ser Ile Arg Thr Phe Lys Glu Ser
1 5 10 15

Pro Lys Gln Ile Leu Asp Pro Ala Ala Ser Ser Val Thr Gly Met Lys
20 25 30

Lys Trp Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser Leu Glu Asp Leu
35 40 45

Ala Gly Phe Lys
50

<210> 1935
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T1664fs"

<400> 1935
Val Gly Val Lys Glu Glu Leu Leu Ala Val Gly Lys Leu Thr Gln Thr
1 5 10 15

Ser Gly Glu Thr Thr His Thr His Thr Lys Ser Gln Gln Glu Met Val
20 25 30

Arg Ala

<210> 1936
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T1664fs"

<400> 1936
Val Gly Val Lys Glu Glu Leu Leu Ala Val Gly Lys Leu Thr Gln Thr
1 5 10 15

Ser Gly Glu Thr Thr His Thr His Thr Gln Ser Gln Gln Glu Met Val
20 25 30

Arg Ala

<210> 1937
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

<221> source
<223> /note="p.H2213D"

<400> 1937
Ala Gln Pro Leu Glu Asp Leu Ala Gly Leu Lys Glu Leu Phe Gln Thr
1 5 10 15

Pro Ile Cys Thr Asp Lys Pro Thr Thr Asp Asp Glu Lys Thr Thr Lys
20 25 30

Ile Ala Cys Arg Ser Pro Gln Pro Asp Pro Val Gly Thr Pro Thr Ile
35 40 45

Phe Lys Pro Gln
50

<210> 1938
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P307fs"

<400> 1938
His His Asn Tyr Gln Ala Ile Leu Pro Ala Pro Pro Lys Ser Ala Gly
1 5 10 15

Glu Ala Leu Gly Ser Ser Gly Thr Pro Gln Tyr Ala Ala Ser Pro Leu
20 25 30

Pro Ile Ala Ala Pro Ala Arg Ala Pro Leu Gly Pro Val Gly Trp His
35 40 45

Val Arg Thr Ala Pro His
50

<210> 1939
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F485L"

<400> 1939
Cys Met Leu Phe His Ser Lys Asn Arg Cys Leu Tyr Val Phe Gly Gly
1 5 10 15

Gln Arg Ser Lys Thr Tyr Leu Asn Asp Leu Leu Phe Ser Tyr Asp Val
20 25 30

Asp Ser Asp His Val Asp Ile Ile Ser Asp Gly Thr Lys Lys Asp Ser
35 40 45

Gly Met Val Pro
50

<210> 1940
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P448H"

<400> 1940
Pro Glu Gly Trp Gly Asp Glu Pro Pro Gly Pro Gly Gly Gly Ser Phe
1 5 10 15

Ser Ala Tyr Trp His Gln Leu Val Glu His His Val Arg Met Gly Glu
20 25 30

Gly Asn Met Leu Tyr Lys Ser Ile Lys Lys Glu Leu Val Val Leu Arg
35 40 45

Leu Ala Ser Leu
50

<210> 1941
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G270V"

<400> 1941
Tyr Tyr Ala Ser Arg Gly Val Cys Phe Arg Gly Glu Ser Cys Met Tyr
1 5 10 15

Leu His Gly Asp Ile Cys Asp Met Cys Val Val Leu Gln Thr Leu His
20 25 30

Pro Met Asp Ala Ala Gln Arg Glu Glu His Met Arg Ala Cys Ile Glu
35 40 45

Ala His Glu Lys
50

<210> 1942
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P647fs"

<400> 1942
Ala Ser Arg Leu Ser Pro Pro Pro Glu Asp Ser Pro Met Ser Pro Pro
1 5 10 15

Pro Glu Glu Ser Pro Met Ser Pro Pro Thr
20 25

<210> 1943
<211> 307
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P647fs"

<400> 1943
Glu Ala Ser Arg Leu Ser Pro Pro Pro Glu Asp Ser Pro Met Ser Pro
1 5 10 15

Pro Pro Glu Glu Ser Pro Met Ser Pro His Leu Arg Tyr Arg Ala Tyr
20 25 30

Pro Pro Cys Leu Trp Cys His Ala Cys Leu His Arg Leu Arg Asn Leu
35 40 45

Pro Cys Pro His Arg Leu Arg Ser Leu Pro Arg Pro Leu His Leu Arg
50 55 60

Leu His Ala Ser Pro His His Leu Arg Thr Pro Pro His Pro His His
65 70 75 80

Leu Arg Thr His Leu Leu Pro His His Arg Arg Thr Arg Ser Cys Pro
85 90 95

Cys Arg Trp Arg Ser His Pro Cys Cys His Tyr Leu Arg Ser Arg Asn
100 105 110

Ser Ala Pro Gly Pro Arg Gly Arg Thr Cys His Pro Gly Leu Arg Ser
115 120 125

Arg Thr Cys Pro Pro Gly Leu Arg Ser His Thr Tyr Leu Arg Arg Leu
130 135 140

Arg Ser His Thr Cys Pro Pro Ser Leu Arg Ser His Ala Tyr Ala Leu
145 150 155 160

Cys Leu Arg Ser His Thr Cys Pro Pro Arg Leu Arg Asp His Ile Cys
165 170 175

Pro Leu Ser Leu Arg Asn Cys Thr Cys Pro Pro Arg Leu Arg Ser Arg
180 185 190

Thr Cys Leu Leu Cys Leu Arg Ser His Ala Cys Pro Pro Asn Leu Arg
195 200 205

Asn His Thr Cys Pro Pro Ser Leu Arg Ser His Ala Cys Pro Pro Gly
210 215 220

Leu Arg Asn Arg Ile Cys Pro Leu Ser Leu Arg Ser His Pro Cys Pro
225 230 235 240

Leu Gly Leu Lys Ser Pro Leu Arg Ser Gln Ala Asn Ala Leu His Leu
245 250 255

Arg Ser Cys Pro Cys Ser Leu Pro Leu Gly Asn His Pro Tyr Leu Pro
260 265 270

Cys Leu Glu Ser Gln Pro Cys Leu Ser Leu Gly Asn His Leu Cys Pro
275 280 285

Leu Cys Pro Arg Ser Cys Arg Cys Pro His Leu Gly Ser His Pro Cys
290 295 300

Arg Leu Ser
305

<210> 1944
<211> 298
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L656fs"

<400> 1944
Glu Asp Ser Pro Met Ser Pro Pro Pro Glu Glu Ser Pro Met Ser Pro
1 5 10 15

Pro Pro Glu Val Ser Arg Leu Ser Pro Cys Leu Trp Cys His Ala Cys
20 25 30

Leu His Arg Leu Arg Asn Leu Pro Cys Pro His Arg Leu Arg Ser Leu
35 40 45

Pro Arg Pro Leu His Leu Arg Leu His Ala Ser Pro His His Leu Arg
50 55 60

Thr Pro Pro His Pro His His Leu Arg Thr His Leu Leu Pro His His
65 70 75 80

Arg Arg Thr Arg Ser Cys Pro Cys Arg Trp Arg Ser His Pro Cys Cys

85 90 95

His Tyr Leu Arg Ser Arg Asn Ser Ala Pro Gly Pro Arg Gly Arg Thr
100 105 110

Cys His Pro Gly Leu Arg Ser Arg Thr Cys Pro Pro Gly Leu Arg Ser
115 120 125

His Thr Tyr Leu Arg Arg Leu Arg Ser His Thr Cys Pro Pro Ser Leu
130 135 140

Arg Ser His Ala Tyr Ala Leu Cys Leu Arg Ser His Thr Cys Pro Pro
145 150 155 160

Arg Leu Arg Asp His Ile Cys Pro Leu Ser Leu Arg Asn Cys Thr Cys
165 170 175

Pro Pro Arg Leu Arg Ser Arg Thr Cys Leu Leu Cys Leu Arg Ser His
180 185 190

Ala Cys Pro Pro Asn Leu Arg Asn His Thr Cys Pro Pro Ser Leu Arg
195 200 205

Ser His Ala Cys Pro Pro Gly Leu Arg Asn Arg Ile Cys Pro Leu Ser
210 215 220

Leu Arg Ser His Pro Cys Pro Leu Gly Leu Lys Ser Pro Leu Arg Ser
225 230 235 240

Gln Ala Asn Ala Leu His Leu Arg Ser Cys Pro Cys Ser Leu Pro Leu
245 250 255

Gly Asn His Pro Tyr Leu Pro Cys Leu Glu Ser Gln Pro Cys Leu Ser
260 265 270

Leu Gly Asn His Leu Cys Pro Leu Cys Pro Arg Ser Cys Arg Cys Pro
275 280 285

His Leu Gly Ser His Pro Cys Arg Leu Ser
290 295

<210> 1945
<211> 54
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P2354fs"

<400> 1945
Ala Pro Leu Thr Pro Arg Ala Ser Gln Val Glu Pro Gln Ser Pro Gly
1 5 10 15

Leu Gly Leu Arg Pro Gln Glu Pro Pro Leu Pro Arg Leu Trp His Leu
20 25 30

Leu Leu Gln Val Thr Gln Thr Ser Phe Ala Leu Ala Pro Thr Leu Thr
35 40 45

His Met Leu Ser Pro His
50

<210> 1946
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q356K"

<400> 1946
Ile Asp Gln Ala Pro Glu Arg Ser Lys Glu Asp Ala Asn Cys Ala Val
1 5 10 15

Cys Asp Ser Pro Gly Asp Leu Leu Asp Lys Lys Phe Phe Cys Thr Thr
20 25 30

Cys Gly Gln His Tyr His Gly Met Cys Leu Asp Ile Ala Val Thr Pro
35 40 45

Leu Lys Arg Ala
50

<210> 1947
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N393K"

<400> 1947
Gly Met Cys Leu Asp Ile Ala Val Thr Pro Leu Lys Arg Ala Gly Trp
1 5 10 15

Gln Cys Pro Glu Cys Lys Val Cys Gln Lys Lys Cys Lys Gln Ser Gly
20 25 30

Glu Asp Ser Lys Met Leu Val Cys Asp Thr Cys Asp Lys Gly Tyr His
35 40 45

Thr Phe Cys Leu
50

<210> 1948
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F4496fs"

<400> 1948
Thr Ser Gly Cys His Arg Phe Arg Cys Thr Asn Ile Tyr His Phe Thr
1 5 10 15

Cys Ala Ile Lys Ala Gln Cys Met Phe Leu Arg Thr Lys Leu Cys Phe
20 25 30

Ala Pro Cys Thr Asn Gln Arg Glu Phe Met Ser Lys Asn
35 40 45

<210> 1949
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Y66C"

<400> 1949
Tyr Pro His Gln Leu Tyr Thr Ser Ser Ser His His Ser His Ser Tyr
1 5 10 15

Ile Gly Leu Pro Tyr Ala Asp His Asn Cys Cys Gly Ala Arg Pro Pro
20 25 30

Pro Thr Pro Pro Ala Ser Pro Pro Pro Ser Val Leu Ile Ser Lys Asn
35 40 45

Glu Val Gly Ile
50

<210> 1950
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S790R"

<400> 1950
Asn Trp Lys Phe Trp Val Phe Ser Ile Leu Ile Arg Pro Leu Phe Glu
1 5 10 15

Ser Phe Asn Gly Met Val Ser Thr Ala Arg Arg Val His Thr Leu Arg
20 25 30

Gln Thr Ser Leu Ala Trp Leu Asp Gln Tyr Cys Ser Leu Pro Ala Leu
35 40 45

Arg Pro Thr Val
50

<210> 1951

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R326C"

<400> 1951
Arg Ile Gln Ala Glu Tyr Val Ser Ala Leu Lys Leu Leu Arg Lys Arg
1 5 10 15

Ser Gln Val Trp Lys Pro Lys Val Ile Cys Cys Ile Ser Ala Arg Ser
20 25 30

Gly Glu Gly Ile Ser Glu Met Trp Asp Lys Met Lys Asp Phe Gln Asp
35 40 45

Leu Met Leu Ala
50

<210> 1952
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I64fs"

<400> 1952
Glu Asn Tyr Tyr Asp Leu Lys Lys Asp Val Lys Gln Phe Val Arg Arg
1 5 10 15

Lys Asp Ser Gly Pro Val Val Lys Lys Ser Glu Lys Cys Arg Ser Ser
20 25 30

Leu Asp Trp Arg
35

<210> 1953
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F917L"

<400> 1953
Gln Ala Leu Gln Leu Gln Val Leu Asn Ser Arg Phe Lys Ala Leu Glu
1 5 10 15

Ala Lys Ser Ile His Leu Ser Ile Asn Leu Leu Phe Ser Leu Asn Lys
20 25 30

Thr Leu His Glu Val Leu Thr Met Cys His Asn Ala Ser Thr Ser Val
35 40 45

Ser Glu Leu Asn
50

<210> 1954
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A1013S"

<400> 1954
Arg Ser Leu Pro Gly Ser Leu Ala Asn Val Val Lys Ser Gln Lys Gln
1 5 10 15

Val Lys Ser Leu Pro Lys Lys Ile Asn Ser Ser Leu Lys Lys Pro Thr
20 25 30

Val Asn Leu Thr Thr Val Leu Ile Gly Arg Thr Gln Arg Asn Thr Asp
35 40 45

Asn Ile Ile Tyr
50

<210> 1955
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D1005N"

<400> 1955
Ala Leu Thr Arg Leu Pro Thr Pro Val Leu Leu Pro Tyr Lys Pro Gln
1 5 10 15

Val Ile Arg Ala Leu Ala Lys Pro Leu Asn Asn Asp Lys Lys Arg Leu
20 25 30

Val Arg Lys Glu Ala Val Ser Ala Arg Gly Glu Trp Phe Leu Leu Gly
35 40 45

Ser Pro Gly Ser
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<210> 1956
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S472L"

<400> 1956
Ala Pro Pro Tyr Met Asn Val Ala Lys Arg Pro Arg Phe Asp Phe Pro
1 5 10 15

Gly Ser Ala Gly Val Asp Arg Cys Ala Leu Leu Trp Asn Gly Ser Met
20 25 30

His Asn Gly Ala Leu Asp Asn His Leu Ser Pro Ser Ala Tyr Pro Gly
35 40 45

Leu Pro Gly Glu
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<210> 1957
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S849P"

<400> 1957
Asn Gln His Val Phe Gln Lys Leu Ser Glu Ser Arg Glu Thr Lys Val
1 5 10 15

Asn Phe Gly Met Tyr Leu Met His Ala Pro Pro Leu Asp Leu Ser Ser
20 25 30

Pro Cys Phe Leu Ser Val Gly Ser Gln Val Leu Pro Val Leu Lys Glu
35 40 45

Asn Val Glu Gly
50

<210> 1958
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P22fs"

<400> 1958
Met Ser Ser Leu Glu Ile Ser Ser Ser Cys Phe Ser Leu Glu Thr Lys
1 5 10 15

Leu Pro Leu Ser Pro His
20

<210> 1959

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q66fs"

<400> 1959
Thr Arg Phe Trp Leu Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu
1 5 10 15

Asp Arg Asp Lys Pro Arg Gln Gly Gly Pro Ala His Pro Gly His Gln
20 25 30

Val Leu Asp Tyr Met Glu Val His Glu Gly Leu Phe Pro His Leu Ala
35 40 45

Gly Gln Asp Cys
50

<210> 1960
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D113Y"

<400> 1960
Lys Arg Leu Ser Thr Leu Lys Phe Ile Gly Gln Tyr Gly Asn Gly Leu
1 5 10 15

Lys Ser Gly Ser Met Arg Ile Gly Lys Tyr Tyr Phe Ile Leu Phe Thr
20 25 30

Lys Lys Glu Glu Thr Met Thr Cys Val Phe Phe Ser Gln Thr Phe Cys
35 40 45

Glu Glu Glu Ser
50

<210> 1961
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R740H"

<400> 1961
Ser Asp Ser Ala Gly Glu Glu Asp Ser Ala Asp Leu Lys Arg Ala Gln
1 5 10 15

Lys Asp Lys Gly Leu His Val Glu Val His His Val Asn Arg Glu Trp
20 25 30

Tyr Thr Gly Arg Val Thr Ala Val Glu Val Gly Lys His Val Val Arg
35 40 45

Trp Lys Val Lys
50

<210> 1962
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L804I"

<400> 1962
Val Arg Ile Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly
1 5 10 15

Tyr Val Ser Ala Lys Glu Asp Ser Phe Ile Ile Tyr Pro Pro His Ser
20 25 30

Cys Glu Glu Ala Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu
35 40 45

Ala Leu Val Gly
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<210> 1963
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.K1582fs"

<400> 1963
Lys Leu Thr Ile His Ala Glu Asn Pro Asp Ser Gln Ala Val Pro Ser
1   5   10   15

Ala Ala Gly Ala Ala Ser Gly Glu Lys Arg Thr Ala Pro Ser Leu
            20   25   30

<210> 1964
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A351fs"

<400> 1964
Ser Ser Asp Thr Arg Gln Gly Arg Ser Glu Lys Arg Ala Phe Pro Arg
1   5   10   15

Lys Arg Asp Phe Thr Asn Glu Ala Pro Gln Leu Leu Ser Gln Thr Pro
            20   25   30

Arg Leu Pro Pro Cys Leu His Thr Glu Glu Pro Ser His Trp Thr Gly
        35   40   45

Gly Pro Arg Ser Pro Pro
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<210> 1965
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S46L"

<400> 1965
Asp Ser Arg Thr His Ser Leu Arg Tyr Phe Arg Leu Gly Val Ser Asp
1 5 10 15

Pro Ile His Gly Val Pro Glu Phe Ile Leu Leu Val Gly Tyr Val Asp
20 25 30

Ser His Pro Ile Thr Thr Tyr Asp Ser Val Thr Arg Gln Lys Glu Pro
35 40 45

Arg Ala Pro Trp
50

<210> 1966
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L234I"

<400> 1966
Leu Arg Leu Glu Arg Glu Lys Arg Ala Arg Ile Lys Ala Arg Lys Glu
1 5 10 15

Asn Leu Glu Arg Lys Lys Ala Lys Ile Ile Ile Leu Lys Lys Phe Pro
20 25 30

His Leu Ala Glu Ala Gln Lys Ser Ser Leu Val
35 40

<210> 1967

<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E119del"

<400> 1967
Ser Asn Lys Glu Ile Met Glu His Ile Arg Lys Ile Leu Gly Lys Asn
1 5 10 15

Glu Glu Thr Leu Arg Glu Glu Glu Glu Lys Lys Gln Leu Ser His Pro
20 25 30

Ala Asn Phe Gly Pro Arg Lys Tyr Cys Leu Arg Glu Cys Ile Cys Glu
35 40 45

Val Glu Gly Gln Val
50

<210> 1968
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V99M"

<400> 1968
Ala Leu Met Ser Leu Ser Met Gly Ile Thr Met Met Cys Met Ala Ser
1 5 10 15

Asn Thr Tyr Gly Ser Asn Pro Ile Ser Met Met Tyr Ile Gly Tyr Thr
20 25 30

Ile Trp Gly Ser Val Met Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala
35 40 45

Ala Gly Ile Arg
50

<210> 1969
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S3L"

<400> 1969
Met Asn Leu Leu Met Thr Ser Ala Val Pro Val Ala Asn Ser Val Leu
1 5 10 15

Val Val Ala Pro His Asn Gly Tyr Pro Val Thr Pro Gly
20 25

<210> 1970
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K464N"

<400> 1970
Lys Asn Cys Asn Thr Pro Leu Leu Arg Ala Tyr Tyr Gly Ser Leu Glu
1 5 10 15

Asp Lys Arg Phe Gly Ile Ile Leu Glu Asn Asn Ile Lys Thr Val Ile
20 25 30

Asn Asp Asp Ala Arg Tyr Met Lys Gly Cys Leu Asn Met Arg Thr Gln
35 40 45

Lys Cys Tyr Ala
50

<210> 1971
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E730K"

<400> 1971
Tyr Val Pro Ala Glu Tyr Ser Ser Phe Arg Ile Ala Lys Gln Ile Phe
1 5 10 15

Thr Arg Ile Ser Thr Asp Asp Asp Ile Lys Lys Thr Asn Ser Ser Thr
20 25 30

Phe Met Lys Glu Met Lys Glu Ile Ala Tyr Ile Leu His Asn Ala Asn
35 40 45

Asp Lys Ser Leu
50

<210> 1972
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D576A"

<400> 1972
Gly His Thr Arg Ala Tyr Gly Val Cys Phe Val Asp Thr Ser Leu Gly
1 5 10 15

Lys Phe Phe Ile Gly Gln Phe Ser Asp Ala Ala Arg His Cys Ser Arg
20 25 30

Phe Arg Thr Leu Val Ala His Tyr Pro Pro Val Gln Val Leu Phe Glu
35 40 45

Lys Gly Asn Leu
50

<210> 1973
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.T1085fs"

<400> 1973
Leu Ala Asn Tyr Ser Arg Gly Gly Asp Gly Pro Met Cys Arg Pro Val
1 5 10 15

Ile Leu Leu Pro Glu Asp Thr Pro Pro Leu Leu Arg Ala
20 25

<210> 1974
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1095H"

<400> 1974
Gly Asp Gly Pro Met Cys Arg Pro Val Ile Leu Leu Pro Glu Asp Thr
1 5 10 15

Pro Pro Phe Leu Glu Leu Lys Gly Ser His His His Pro Cys Ile Thr
20 25 30

Lys Thr Phe Phe Gly Asp Asp Phe Ile Pro Asn Asp Ile Leu Ile Gly
35 40 45

Cys Glu Glu Glu
50

<210> 1975
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T68P"

<400> 1975
Met Thr Ser Ala Arg Arg Arg Thr Asp Val Gly Pro Arg Val Ala Phe
1 5 10 15

Thr Tyr Pro Cys Thr Gln Leu Ser Pro Pro Pro Arg Ala His Arg His
20 25 30

Leu Pro Val His Thr Val Thr Tyr Pro Cys Thr Gln Leu Ser Pro Thr
35 40 45

Arg Ala His Ser
50

<210> 1976
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N435fs"

<400> 1976
Ala Glu Thr Pro His Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His
1 5 10 15

Ala Gln Leu Glu Glu Asn Phe Cys Arg Thr Gln Met Gly Ile Ala Met
20 25 30

Gly Pro Gly Ala Thr Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val
35 40 45

Pro Cys Asp Ala Ala Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro
50 55 60

Gln Thr Arg Cys Ser Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp
65 70 75 80

Ile Ser Gly Val Pro Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr
85 90 95

His Pro Gly Gln Ser Ala Cys Gly Ile Gly Arg Ala Ser Ile Ser Ala
100 105 110

Gly Gly Leu
115

<210> 1977
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M464V"

<400> 1977
Phe Asn Gly Leu Leu Gly Pro Val Gln Val Thr Ala Leu Tyr Val Thr
1 5 10 15

Arg Leu Asp Asn Val Thr Val Ala His Val Val Gly Thr Met Asp Gly
20 25 30

Arg Ile Leu Gln Val Glu Leu Val Arg Ser Leu Asn Tyr Leu Leu Tyr
35 40 45

Val Ser Asn Phe
50

<210> 1978
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L105fs"

<400> 1978
Leu Asn Lys Met Asp Leu Ala Asp Leu Thr Glu Gln Gln Lys Ile Met
1 5 10 15

Gln His Leu Glu Gly Glu Gly Leu Lys Met Ser Phe Leu Pro Thr Val
20 25 30

<210> 1979
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H327fs"

<400> 1979
Asp Phe Leu Gln Thr Phe Arg Arg Gly Leu Leu Gly Ser Val Met Leu
1 5 10 15

Asp Leu Asp Val Leu Arg Gly His Pro Arg Leu Arg Leu Cys Pro Glu
20 25 30

Leu Val Arg Val Gly Arg Ala Gly Gly Met Trp Pro Pro Arg Pro Pro
35 40 45

Asp Leu Gly Gly
50

<210> 1980
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N109fs"

<400> 1980
Ser Thr Lys Ser Lys Lys Val Val Glu Val Trp Ile Gly Met Thr Ile
1 5 10 15

Glu Glu Leu Ala Arg Ala Met Glu Lys Thr Gln Ile Met Tyr Met Lys
20 25 30

Leu Tyr

<210> 1981
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.K193fs"

<400> 1981
Asp Glu Ala Leu Arg Lys Val Ala Thr Phe Arg His Gly Gly Arg Phe
1 5 10 15

Pro Val Leu Ser Tyr Tyr His Lys Lys Met Gly Trp
20 25

<210> 1982
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L1460P"

<400> 1982
Tyr Ala Met Lys His Phe Gly Glu Leu Glu Ile Gln Ala Thr Trp Tyr
1 5 10 15

Glu Lys Leu His Glu Trp Glu Asp Ala Pro Pro Val Ala Tyr Asp Lys
20 25 30

Lys Met Asp Thr Asn Lys Asp Asp Pro Glu Leu Met Leu Gly Arg Met
35 40 45

Arg Cys Leu Glu

50

<210> 1983
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.C1483F"

<400> 1983
Asp Ala Leu Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp Asp
1 5 10 15

Pro Glu Leu Met Leu Gly Arg Met Arg Phe Phe Leu Glu Ala Leu Gly
20 25 30

Glu Trp Gly Gln Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val
35 40 45

Asn Asp Glu Thr
50

<210> 1984
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S2215Y"

<400> 1984
Glu Asp Leu Arg Gln Asp Glu Arg Val Met Gln Leu Phe Gly Leu Val
1 5 10 15

Asn Thr Leu Leu Ala Asn Asp Pro Thr Tyr Tyr Leu Arg Lys Asn Leu
20 25 30

Ser Ile Gln Arg Tyr Ala Val Ile Pro Leu Ser Thr Asn Ser Gly Leu
35 40 45

Ile Gly Trp Val
50

<210> 1985
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1005W"

<400> 1985
Tyr Pro Lys Gln Arg Thr Ala Ala Ala Arg Asn Gly Phe Pro Pro Lys
1 5 10 15

Pro Asp Pro Gln Ala Arg Glu Ala Glu Trp Trp Gln Leu Val Leu Arg
20 25 30

Leu Lys Glu Arg Cys Glu Gln Gln Thr Arg Gln Leu Gly Val Ala Gln
35 40 45

Gly Glu Leu Lys
50

<210> 1986
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P5119S"

<400> 1986
Leu Pro Asn Phe Ser Ser Thr Ser Asp Lys Ile Leu Ala Thr Ser Lys
1 5 10 15

Asp Ser Lys Asp Thr Lys Glu Ile Phe Ser Ser Ser Ile Asn Thr Glu
20 25 30

Glu Thr Asn Val Lys Ala Asn Asn Ser Gly His Glu Ser His Ser Pro
35 40 45

Ala Leu Ala Asp
50

<210> 1987
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A6156T"

<400> 1987
Pro Asp Ile Ser Pro Glu Ala Ser Ser Ser His Ser Asn Ser Pro Pro
1 5 10 15

Leu Thr Ile Ser Thr His Lys Thr Ile Thr Thr Thr Gln Thr Gly Pro
20 25 30

Ser Gly Val Thr Ser Leu Gly Gln Leu Thr Leu Asp Thr Ser Thr Ile
35 40 45

Ala Thr Ser Ala
50

<210> 1988
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R8606H"

<400> 1988
Glu Ser Ile Ser Ser Ser Pro His Pro Val Thr Ala Leu Leu Thr Leu
1 5 10 15

Gly Pro Val Lys Thr Thr Asp Met Leu His His Thr Ser Ser Glu Pro
20 25 30

Glu Thr Ser Ser Pro Pro Asn Leu Ser Ser Thr Ser Ala Glu Ile Leu
35 40 45

Ala Thr Ser Glu
50

<210> 1989
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P10452fs"

<400> 1989
Gly Ile Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala Ala His Arg
1 5 10 15

Gly Thr Ile Arg Pro Val Lys Gly Pro Ser Asp Ile His Phe Ala Cys
20 25 30

Gln Ser

<210> 1990
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T11005I"

<400> 1990
Val Leu Pro Glu Val Pro Gly Met Val Thr Ser Leu Val Ala Ser Ser
1 5 10 15

Arg Ala Val Thr Ser Thr Thr Leu Pro Ile Ile Leu Thr Leu Ser Pro

20 25 30

Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu
35 40 45

Ala Ser Ser Thr
50

<210> 1991
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P11260A"

<400> 1991
Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu Ala Ser Ser Val Val
1 5 10 15

Pro Thr Leu Thr Val Ser Thr Gly Glu Ala Ala Phe Thr Asn Ile Ser
20 25 30

Leu Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu Pro Arg Thr Thr
35 40 45

Ser Arg Phe Ser
50

<210> 1992
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N11594K"

<400> 1992
Tyr Glu Pro Glu Thr Thr Ala Thr Trp Leu Thr His Pro Ala Glu Thr
1 5 10 15

Ser Thr Thr Val Ser Gly Thr Ile Pro Lys Lys Phe Ser His Arg Gly
20 25 30

Ser Asp Thr Ala Pro Ser Met Val Thr Ser Pro Gly Val Asp Thr Arg
35 40 45

Ser Gly Val Pro
50

<210> 1993
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R12774H"

<400> 1993
Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala
1 5 10 15

Thr Gly Val Asp Ala Ile Cys Thr His His His Leu Asp Pro Lys Ser
20 25 30

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
35 40 45

Asn Gly Ile Lys
50

<210> 1994
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R4415H"

<400> 1994
Leu Val Tyr Gly Leu Val Gly Ala Gly Val Val Leu Met Leu Ile Ile
1 5 10 15

Leu Val Ala Leu Leu Met Leu Val Phe His His Ser Lys Arg Glu Val
20 25 30

Lys Arg Gln Lys Tyr Arg Leu Ser Gln Leu Tyr Lys Trp Gln Glu Glu
35 40 45

Asp Ser Gly Pro
50

<210> 1995
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V77M"

<400> 1995
Cys Gln Gln Leu Ser Gln His Val Arg Thr Gly Ser Ala Ala Asn Thr
1 5 10 15

Ala Thr Gly Thr Thr Ser Thr Asn Val Met Met Glu Pro Arg Met Tyr
20 25 30

Leu Ser Cys Ser Thr Asn Pro Glu Met Thr Ser Ile Glu Ser Ser Val
35 40 45

Thr Ser Asp Thr
50

<210> 1996
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R1227fs"

<400> 1996
Pro Thr Ala Glu Val Thr Ser Met Pro Thr Ser Thr Pro Gly Glu Arg
1 5 10 15

Ser Thr Pro Leu Thr Ser Met Pro Val Ser Thr His Ala Ser Gly Gln
20 25 30

Phe

<210> 1997
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H1228fs"

<400> 1997
Thr Ala Glu Val Thr Ser Met Pro Thr Ser Thr Pro Gly Glu Arg Ser
1 5 10 15

Thr Pro Leu Thr Ser Met Pro Val Arg Pro Arg Gln Trp Pro Val Leu
20 25 30

Arg Leu Ala Pro Phe Gln His Leu Pro Leu Thr Pro Ala His Leu
35 40 45

<210> 1998
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T2279N"

<400> 1998
Ser Thr Glu Ala Thr Ser Ser Pro Thr Thr Ala Glu Gly Thr Ser Ile

1020

1 5 10 15

Pro Thr Ser Thr Leu Ser Glu Gly Thr Asn Asn Pro Leu Thr Ser Ile
20 25 30

Pro Val Ser His Thr Leu Val Ala Asn Ser Glu Val Ser Thr Leu Ser
35 40 45

Thr Thr Pro Val
50

<210> 1999
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T1568M"

<400> 1999
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
1 5 10 15

Thr Thr Thr Pro Ile Thr Thr Thr Thr Met Met Val Thr Pro Thr Pro
20 25 30

Thr Pro Thr Gly Thr Gln Thr Pro Thr Ser Thr Pro Ile Thr Thr Thr
35 40 45

Thr Thr Val Thr
50

<210> 2000
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T1580N"

<400> 2000
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Val Thr
1 5 10 15

Pro Thr Pro Thr Pro Thr Gly Thr Gln Asn Asn Pro Thr Ser Thr Pro
20 25 30

Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
35 40 45

Gln Thr Pro Thr
50

<210> 2001
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T1582R"

<400> 2001
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
1 5 10 15

Pro Thr Pro Thr Gly Thr Gln Thr Pro Arg Arg Ser Thr Pro Ile Thr
20 25 30

Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
35 40 45

Pro Thr Thr Thr
50

<210> 2002
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<400> 2002
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Ser Thr Pro Ile Thr
1 5 10 15

Thr Thr Thr Thr Val Thr Pro Thr Pro Ile Ile Pro Thr Gly Thr Gln
20 25 30

Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Val Thr Pro Thr
35 40 45

Pro Thr Pro Thr
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<210> 2003
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polypeptide"

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<400> 2003
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
1 5 10 15

Thr Pro Thr Ser Thr Pro Ile Thr Thr Ile Ile Thr Thr Val Thr Pro
20 25 30

Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Pro Thr Pro Ile Ser
35 40 45

Thr Thr Thr Thr
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<210> 2004
<211> 52
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polypeptide"

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<400> 2004
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
1 5 10 15

Thr Ser Thr Pro Ile Thr Thr Thr Thr Met Met Val Thr Pro Thr Pro
20 25 30

Thr Pro Thr Gly Thr Gln Thr Pro Thr Pro Thr Pro Ile Ser Thr Thr
35 40 45

Thr Thr Val Thr
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<210> 2005
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.G1715S"

<400> 2005
Pro Thr Gly Thr Gln Thr Pro Thr Ser Thr Pro Ile Thr Thr Thr Thr
1 5 10 15

Thr Val Thr Pro Thr Pro Thr Pro Thr Ser Ser Thr Gln Thr Pro Thr
20 25 30

Pro Thr Pro Ile Ser Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
35 40 45

Thr Gly Thr Gln
50

<210> 2006
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

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<223> /note="p.T1722I"

<400> 2006
Thr Ser Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
1 5 10 15

Pro Thr Gly Thr Gln Thr Pro Thr Pro Ile Ile Pro Ile Ser Thr Thr
20 25 30

Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
35 40 45

Thr Thr Pro Ile
50

<210> 2007
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

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<223> /note="p.S681G"

<400> 2007
Tyr Met Gly Ile Phe Leu Val Ile Glu Thr His Gly Met Ala Val Ser
1 5 10 15

Trp Asp Arg Lys Thr Ser Val Phe Ile Gly Gly Leu His Gln Asp Tyr
20 25 30

Lys Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp Asp Asn Ala Ile
35 40 45

Asn Asp Phe Ala
50

<210> 2008
<211> 52

<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.D682G"

<400> 2008
Met Gly Ile Phe Leu Val Ile Glu Thr His Gly Met Ala Val Ser Trp
1 5 10 15

Asp Arg Lys Thr Ser Val Phe Ile Arg Gly Arg His Gln Asp Tyr Lys
20 25 30

Gly Arg Val Cys Gly Leu Cys Gly Asn Phe Asp Asp Asn Ala Ile Asn
35 40 45

Asp Phe Ala Thr
50

<210> 2009
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.P1569fs"

<400> 2009
Ile Thr Pro Asn Pro Thr Ser Thr Arg Thr Arg Thr Pro Val Ala His
1 5 10 15

Thr Asn Ser Ala Thr Ser Ser Arg Pro Thr Thr Thr Leu His His Thr
20 25 30

Leu Pro Thr Tyr Arg Glu Gln Ser Leu Leu Phe His Arg Ser His Asp
35 40 45

Gly Asn Ile Leu Gln Asp His His Tyr Leu Ser Asn Pro Ile Thr Pro
50 55 60

Ser Asp His Thr Ser His Ser Arg Ser Thr Phe Leu His Leu Phe Gly
65 70 75 80

Asp Ser Lys Tyr Ser His Ser His His Pro Tyr Pro Cys Thr Asp Gly
85 90 95

His Phe Cys Leu His Pro Leu Asn Ala Asn Arg His Asp Ser Ser Thr
100 105 110

Asp Asn Ala Gln Gly His Arg Val His Pro His Ser Ala Asn Asn Asp
115 120 125

Ala Asp His Gln Arg Asp Gln Pro Ser Pro Glu Leu Ile Lys His Ser
130 135 140

Gln Asn Leu Tyr Ile Pro Thr Phe Thr His Phe Leu His Thr Pro Cys
145 150 155 160

<210> 2010
<211> 52
<212> PRT
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<220>
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polypeptide"

<220>
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<223> /note="p.P1977H"

<400> 2010
Ala His Thr Thr Ser Ala Ser Ser Ser Arg Leu Pro Thr Pro Phe Thr
1 5 10 15

Thr His Ser Pro Pro Thr Gly Ser Ser His His Phe Ser Ser Thr Gly
20 25 30

Pro Met Thr Ala Thr Ser Phe Gln Thr Thr Thr Thr Tyr Pro Thr Pro
35 40 45

Ser His Pro Gln
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<210> 2011
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

<220>
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<223> /note="p.H2000Q"

<400> 2011
Ser Ser Pro Phe Ser Ser Thr Gly Pro Met Thr Ala Thr Ser Phe Gln
1 5 10 15

Thr Thr Thr Thr Tyr Pro Thr Pro Ser Gln Gln Pro Gln Thr Thr Leu
20 25 30

Pro Thr His Val Pro Pro Phe Ser Thr Ser Leu Val Thr Pro Ser Thr
35 40 45

His Thr Val Ile
50

<210> 2012
<211> 54
<212> PRT
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polypeptide"

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<223> /note="p.2129_2130SS>S"

<400> 2012
Ser Pro Ile Thr Thr Gln Leu Pro His Leu Ser Ser Ala Thr Thr Pro
1 5 10 15

Val Ser Thr Thr Asn Gln Leu Ser Ser Ser Phe Ser Pro Ser Pro Ser
20 25 30

Ala Pro Ser Thr Val Ser Ser Tyr Val Pro Ser Ser His Ser Ser Pro
35 40 45

Gln Thr Ser Ser Pro Ser
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<210> 2013

<211> 52
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<220>
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<220>
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<223> /note="p.S336L"

<400> 2013
Pro Asn Ser Ser Pro Thr Thr Leu Ala Pro Asp Thr Ser Glu Thr Ser
1 5 10 15

Ala Ala Pro Thr His Gln Thr Thr Thr Leu Leu Val Thr Thr Gln Thr
20 25 30

Thr Thr Thr Lys Gln Pro Thr Ser Ala Pro Gly Gln Asn Lys Ile Ser
35 40 45

Arg Phe Leu Leu
50

<210> 2014
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P138fs"

<400> 2014
Tyr Leu Ser Ile Cys Arg Lys Gln Arg Ala Leu Pro Ser Leu Asp Ile
1 5 10 15

Val Val Trp Ser Glu Leu Pro Pro Gly Arg Ala Trp Ala Pro Ala Pro
20 25 30

Pro Thr Arg Cys Val Trp Gln Gln Pro Ser
35 40

<210> 2015
<211> 52

<212> PRT
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<220>
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<223> /note="p.D324Y"

<400> 2015
Glu Glu Asp Gly Gly Ser Gln Leu Ile Leu Glu Lys Phe Gln Leu Pro
1 5 10 15

Gln Trp Ser Ile Ser Leu Asn Met Thr Tyr Tyr Glu His Gly Asn Met
20 25 30

Val Asn Leu Val Cys Asp Ile Lys Lys Pro Met Asp Val Tyr Lys Ile
35 40 45

His Leu Asn Gln
50

<210> 2016
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R481fs"

<400> 2016
Glu Ser Ser Leu Asp Pro Pro Lys Val Leu Pro Pro Ala Arg His Ser
1 5 10 15

Thr Ile Pro Leu Val Ile Leu Arg Lys Asn Gly Ala Arg Pro Ala Pro
20 25 30

<210> 2017
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R646H"

<400> 2017
Thr Asn Pro Val Gly Glu Asp Val Ala Ser Ile Phe Leu Gln Val Val
1 5 10 15

Asp Val Pro Asp Pro Pro Glu Ala Val His His Ile Thr Ser Val Gly
20 25 30

Glu Asp Trp Ala Ile Leu Val Trp Glu Pro Pro Met Tyr Asp Gly Gly
35 40 45

Lys Pro Val Thr
50

<210> 2018
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M240T"

<400> 2018
Thr Cys Val Trp Ser Ile Ala Ser Glu Leu Ile Glu Lys Arg Leu Ala
1 5 10 15

Arg Arg Pro Arg Gly Gly Cys Arg Arg Thr Thr Val Val Val Val Ser
20 25 30

Asp Asp Tyr Leu Gln Ser Lys Glu Cys Asp Phe Gln Thr Lys Phe Ala
35 40 45

Leu Ser Leu Ser
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<210> 2019
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S251N"

<400> 2019
Glu Lys Arg Leu Ala Arg Arg Pro Arg Gly Gly Cys Arg Arg Met Val
1 5 10 15

Val Val Val Ser Asp Asp Tyr Leu Gln Asn Asn Lys Glu Cys Asp Phe
20 25 30

Gln Thr Lys Phe Ala Leu Ser Leu Ser Pro Gly Ala His Gln Lys Arg
35 40 45

Leu Ile Pro Ile
50

<210> 2020
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.L273P"

<400> 2020
Tyr Leu Gln Ser Lys Glu Cys Asp Phe Gln Thr Lys Phe Ala Leu Ser
1 5 10 15

Leu Ser Pro Gly Ala His Gln Lys Arg Pro Pro Ile Pro Ile Lys Tyr
20 25 30

Lys Ala Met Lys Lys Glu Phe Pro Ser Ile Leu Arg Phe Ile Thr Val
35 40 45

Cys Asp Tyr Thr
50

<210> 2021

<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K323E"

<400> 2021
Leu Phe Asp Arg Pro Met His Val Lys Met Asp Asp Lys Ser Val Pro
1 5 10 15

His Glu Glu Tyr Arg Ser His Asp Gly Glu Glu Thr Pro Gln Leu Pro
20 25 30

Arg Gly Leu Gly Gly Ile Gly Met Gly Leu Gly Pro Gly Gly Gln Pro
35 40 45

Ile Ser Ala Ser
50

<210> 2022
<211> 90
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L269fs"

<400> 2022
Cys Ser Thr Trp Gly Leu Pro Leu Arg Val Ala Gly Ser Trp Leu Thr
1 5 10 15

Val Val Thr Val Glu Ala Leu Gly Gly Gly Ala Trp Glu Leu Gly Gly
20 25 30

Leu Ala Arg Trp Gly Pro Leu Cys Thr His Pro Gln Cys Gln Val Leu
35 40 45

Leu Leu Ser Ser Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser
50 55 60

Ser Leu Val Glu Asp Val Leu Cys Ala Lys Trp Phe Ile Cys Pro Ala
65 70 75 80

Ser Phe Asn Pro Gln Asn Asp Ser Met Arg
85 90

<210> 2023
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L302H"

<400> 2023
Arg Arg Thr Gly Gln Val Gly Pro Thr Met His Pro Pro Pro Val Ser
1 5 10 15

Gly Ala Ser Pro Leu Leu Leu His His His His Leu Leu Leu Leu Leu
20 25 30

Ile Ile Ile Leu Thr Cys
35

<210> 2024
<211> 44
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.L1091fs"

<400> 2024
Met Ile Ser Asp Leu Glu Glu Arg Leu Lys Lys Glu Glu Lys Thr Arg
1 5 10 15

Gln Glu Leu Glu Lys Ala Lys Arg Lys Pro Arg Arg Gly Asp Asp Arg
20 25 30

Pro Ala Gly Pro Asp Arg Arg Ala Ala Gly Ala Asp
35 40

<210> 2025
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E993K"

<400> 2025
Glu Glu Glu Ala Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala
1 5 10 15

Glu Ala Lys Ile Lys Lys Leu Glu Asp Lys Lys Ile Leu Val Met Asp
20 25 30

Asp Gln Asn Asn Lys Leu Ser Lys Glu Arg Lys Leu Leu Glu Glu Arg
35 40 45

Ile Ser Asp Leu
50

<210> 2026
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K1263del"

<400> 2026
Lys Glu Asn Ala Asp Leu Ala Gly Glu Leu Arg Val Leu Gly Gln Ala
1 5 10 15

Lys Gln Glu Val Glu His Lys Lys Lys Leu Glu Ala Gln Val Gln Glu
20 25 30

Leu Gln Ser Lys Cys Ser Asp Gly Glu Arg Ala Arg Ala Glu Leu Asn
35 40 45

Asp Lys Val His Lys
50

<210> 2027
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D311N"

<400> 2027
His Ile Phe Tyr Gln Ile Met Ser Asn Lys Lys Pro Glu Leu Ile Asp
1 5 10 15

Leu Leu Leu Ile Ser Thr Asn Pro Phe Asn Asn Phe Pro Phe Val Ser
20 25 30

Gln Gly Glu Val Thr Val Ala Ser Ile Asp Asp Ser Glu Glu Leu Leu
35 40 45

Ala Thr Asp Asn
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<210> 2028
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T790M"

<400> 2028
Thr Lys Val Phe Phe Lys Ala Gly Leu Leu Gly Thr Leu Glu Glu Met
1 5 10 15

Arg Asp Glu Lys Leu Ala Gln Leu Ile Met Met Arg Thr Gln Ala Ile

20 25 30

Cys Arg Gly Phe Leu Met Arg Val Glu Phe Arg Lys Met Met Glu Arg
35 40 45

Arg Glu Ser Ile
50

<210> 2029
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T847M"

<400> 2029
Ala Phe Met Gly Val Lys Asn Trp Pro Trp Met Lys Leu Tyr Phe Lys
1 5 10 15

Ile Lys Pro Leu Leu Lys Ser Ala Glu Met Met Glu Lys Glu Met Ala
20 25 30

Thr Met Lys Glu Glu Phe Gly Arg Ile Lys Glu Thr Leu Glu Lys Ser
35 40 45

Glu Ala Arg Arg
50

<210> 2030
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A1487T"

<400> 2030
Glu Ser Gln Ser Glu Leu Glu Ser Ser Gln Lys Glu Ala Arg Ser Leu
1 5 10 15

Ser Thr Glu Leu Phe Lys Leu Lys Asn Thr Thr Tyr Glu Glu Ser Leu
20 25 30

Glu His Leu Glu Thr Phe Lys Arg Glu Asn Lys Asn Leu Gln Glu Glu
35 40 45

Ile Ser Asp Leu
50

<210> 2031
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1689C"

<400> 2031
Asn Asp Asp Leu Lys Glu Asn Ile Ala Ile Val Glu Arg Arg Asn Asn
1 5 10 15

Leu Leu Gln Ala Glu Leu Glu Glu Leu Cys Cys Ala Val Val Glu Gln
20 25 30

Thr Glu Arg Ser Arg Lys Leu Ala Glu Gln Glu Leu Ile Glu Thr Ser
35 40 45

Glu Arg Val Gln
50

<210> 2032
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A785V"

<400> 2032
Lys Phe Gly His Thr Lys Val Phe Phe Lys Ala Gly Leu Leu Gly Leu
1 5 10 15

Leu Glu Glu Met Arg Asp Glu Lys Leu Val Val Gln Ile Ile Thr Arg
20 25 30

Thr Gln Ala Val Cys Arg Gly Phe Leu Met Arg Val Glu Tyr Gln Lys
35 40 45

Met Leu Gln Arg
50

<210> 2033
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H1006N"

<400> 2033
Leu Thr Glu Glu Met Ala Gly Leu Asp Glu Thr Ile Ala Lys Leu Ser
1 5 10 15

Lys Glu Lys Lys Ala Leu Gln Glu Thr Asn Asn Gln Gln Thr Leu Asp
20 25 30

Asp Leu Gln Ala Glu Glu Asp Lys Val Asn Ile Leu Thr Lys Ala Lys
35 40 45

Thr Lys Leu Glu
50

<210> 2034
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R1048Q"

<400> 2034
Leu Thr Lys Ala Lys Thr Lys Leu Glu Gln Gln Val Asp Asp Leu Glu
1 5 10 15

Gly Ser Leu Glu Gln Glu Lys Lys Leu Gln Gln Met Asp Leu Glu Arg
20 25 30

Ala Lys Arg Lys Leu Glu Gly Asp Leu Lys Leu Ala Gln Glu Ser Thr
35 40 45

Met Asp Met Glu
50

<210> 2035
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1117C"

<400> 2035
Asn Leu Ile Ser Lys Ile Glu Asp Glu Gln Ala Val Glu Ile Gln Leu
1 5 10 15

Gln Lys Lys Ile Lys Glu Leu Gln Ala Cys Cys Ile Glu Glu Leu Gly
20 25 30

Glu Glu Ile Glu Ala Glu Arg Ala Ser Arg Ala Lys Ala Glu Lys Gln
35 40 45

Arg Ser Asp Leu
50

<210> 2036
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P209fs"

<400> 2036
Pro Arg Pro Gly His Arg Ser Arg Ala Pro Glu Leu Val Thr Lys Lys
1 5 10 15

Phe Pro Val Asp Leu Arg Leu Pro Pro Trp Cys Pro Cys Pro His Leu
20 25 30

Pro Ser Gly Ser Trp Ser Cys Asn Asp Gly Pro Leu Glu Thr Leu Ala
35 40 45

Ser Pro Cys Gly Ala Gln Pro Cys Trp Ile Gly Ala Pro Arg Ala Arg
50 55 60

Pro Val Gly Val Trp Ser Thr Leu Leu Ser Leu Val Gln Ala Pro Arg
65 70 75 80

Thr Trp Pro Trp Gly Trp Cys Gln Glu Ile Asp Trp Trp Arg Leu Met
85 90 95

Gly Thr Met Trp Arg Ala Ser Pro Gly Met Arg Leu Trp Arg
100 105 110

<210> 2037
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T109M"

<400> 2037
Ala Ala Tyr Lys Ala Met Lys Arg Arg Ser Lys Asp Thr Cys Ile Val
1 5 10 15

Ile Ser Gly Glu Ser Gly Ala Gly Lys Met Met Glu Ala Ser Lys Tyr
20 25 30

Ile Met Gln Tyr Ile Ala Ala Ile Thr Asn Pro Ser Gln Arg Ala Glu
35 40 45

Val Glu Arg Val
50

<210> 2038
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E246K"

<400> 2038
Leu Gln Lys Ser Leu Ser Ser Tyr Asn Tyr Ile His Val Gly Ala Gln
1 5 10 15

Leu Lys Ser Ser Ile Asn Asp Ala Ala Lys Lys Phe Arg Val Val Ala
20 25 30

Asp Ala Met Lys Val Ile Gly Phe Lys Pro Glu Glu Ile Gln Thr Val
35 40 45

Tyr Lys Ile Leu
50

<210> 2039
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N525H"

<400> 2039
Ala Val Val Gly Ala Gln Ile Ser Glu Tyr Leu Leu Glu Lys Ser Arg
1 5 10 15

Val Ile His Gln Ala Ile Gly Glu Lys His His Phe His Ile Phe Tyr
20 25 30

Tyr Ile Tyr Ala Gly Leu Ala Glu Lys Lys Lys Leu Ala His Tyr Lys
35 40 45

Leu Pro Glu Asn
50

<210> 2040
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N525S"

<400> 2040
Ala Val Val Gly Ala Gln Ile Ser Glu Tyr Leu Leu Glu Lys Ser Arg
1 5 10 15

Val Ile His Gln Ala Ile Gly Glu Lys Ser Ser Phe His Ile Phe Tyr
20 25 30

Tyr Ile Tyr Ala Gly Leu Ala Glu Lys Lys Lys Leu Ala His Tyr Lys
35 40 45

Leu Pro Glu Asn
50

<210> 2041
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A405V"

<400> 2041
Lys Leu Val Thr Thr Ser Glu Thr Tyr Val Lys Thr Met Ser Leu Gln
1 5 10 15

Gln Val Ile Asn Ala Arg Asn Ala Leu Val Val Lys His Ile Tyr Ala
20 25 30

Gln Leu Phe Gly Trp Ile Val Glu His Ile Asn Lys Ala Leu His Thr
35 40 45

Ser Leu Lys Gln
50

<210> 2042
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R708L"

<400> 2042
Val Leu Glu Thr Ile Arg Ile Ser Ala Ala Gly Tyr Pro Ser Arg Trp
1 5 10 15

Ala Tyr His Asp Phe Phe Asn Arg Tyr Leu Leu Val Leu Val Lys Lys
20 25 30

Arg Glu Leu Ala Asn Thr Asp Lys Lys Ala Ile Cys Arg Ser Val Leu
35 40 45

Glu Asn Leu Ile
50

<210> 2043
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q914fs"

<400> 2043
Glu Gln Ile Gln Lys Glu Tyr Asp Ala Leu Val Lys Ser Ser Glu Glu

1 5 10 15

Leu Leu Ser Ala Leu Gln Lys Lys Lys Thr Ala Gly Arg Gly Ser Arg
20 25 30

Lys Ala Glu Ala Tyr Ser Arg Arg Asn Gly Lys Gly Lys Lys Lys Thr
35 40 45

<210> 2044
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1180N"

<400> 2044
Ile Pro Ala Arg Gln Arg Glu Ile Glu Met Asn Arg Gln Gln Arg Phe
1 5 10 15

Phe Arg Ile Pro Phe Ile Arg Pro Ala Asn Asn Gln Tyr Lys Asp Pro
20 25 30

Gln Ser Lys Lys Lys Gly Trp Trp Tyr Ala His Phe Asp Gly Pro Trp
35 40 45

Ile Ala Arg Gln
50

<210> 2045
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P2040H"

<400> 2045
Lys Gln Thr Ser Glu Pro Ser Tyr Pro Asp Val Ile Leu Ile Ala Ile
1 5 10 15

Asn Arg His Gly Val Leu Leu Ile His His His Lys Thr Lys Asp Leu
20 25 30

Leu Thr Thr Tyr Pro Phe Thr Lys Ile Ser Ser Trp Ser Ser Gly Ser
35 40 45

Thr Tyr Phe His
50

<210> 2046
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R167Q"

<400> 2046
Gln Pro Gln Gln Lys Asp Phe Asp Asp Leu Cys Ser Leu Pro Asp Leu
1 5 10 15

Asn Glu Lys Thr Leu Leu Glu Asn Leu Gln Gln Asn Arg Phe Lys His
20 25 30

Glu Lys Ile Tyr Thr Tyr Val Gly Ser Ile Leu Ile Val Ile Asn Pro
35 40 45

Phe Lys Phe Leu
50

<210> 2047
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R2179Q"

<400> 2047
Phe Leu Arg Ala Met Gly Leu Gln Glu Arg Lys Glu Thr Ile Arg Gly
1 5 10 15

Val Tyr Ser Val Ile Asp Gln Leu Ser Gln Gln Thr His Leu Asn Thr
20 25 30

Leu Glu Arg Leu Ile Phe His Leu Val Arg Ile Ala Leu Gln Glu Asp
35 40 45

Thr Asn Arg Met
50

<210> 2048
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R94L"

<400> 2048
Lys Glu Ser Gly Gly Glu Glu Trp Val Leu Asp Ala Asn Asp Ser Pro
1 5 10 15

Val His Arg Val Leu Leu Trp Pro Arg Leu Leu Ala Gln Asp Glu His
20 25 30

Pro Gln Glu Asp Gly Tyr Tyr Phe Leu Leu Gln Glu Arg Asn Ala Asp
35 40 45

Gly Thr Ile Lys
50

<210> 2049
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.T493M"

<400> 2049
Ala Gly Ser Leu Pro Asp Thr Phe Asn Asp Ala Ser Pro Ser Phe Gly
1 5 10 15

Leu His Pro Ser Pro Val His Val Cys Met Met Glu Glu Ser Leu Met
20 25 30

Ser Ser Leu Asn Gly Gly Ser Val Pro Ser Glu Leu Asp Gly Leu Asp
35 40 45

Ser Glu Lys Asp
50

<210> 2050
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G226fs"

<400> 2050
Glu Asn Asp Arg Asn Asp Ser Ala Ser Gln Pro Ser His Gln Ser Asp
1 5 10 15

Ala Gly Lys Gln Gly Leu Gly Pro Pro Ala Pro Pro
20 25

<210> 2051
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q310del"

<400> 2051
Ala Tyr Ala Arg Leu Leu Gln Gln Gln Gln Leu Phe Leu Gln Leu Gln

1 5 10 15

Ile Leu Ser Gln Gln Gln Gln Gln His Arg Phe Ser Tyr Leu Gly
20 25 30

Met His Gln Ala Gln Leu Lys Glu Pro Asn Glu Gln Met Val Arg Asn
35 40 45

Pro Asn Ser Ser Ser
50

<210> 2052
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G165fs"

<400> 2052
Pro Gly Met Gly Gly Asp Gly Glu Glu Asp Glu Gly Asp Glu Asp Arg
1 5 10 15

Leu Asp Asn Ala Val Arg Gly Pro Gly Ala Gln Gly Ala Ser Trp Asp
20 25 30

Gly Val Gly Ser Ser Ala Cys Ser Glu Ala His Gln Ser Lys Glu Gln
35 40 45

Pro Ala Asp Ala Val Lys
50

<210> 2053
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R63Q"

<400> 2053
Val Tyr Thr Gln Gly Ser Thr Ala Tyr Ser Ser Arg Ser Ser Ala Ala
1 5 10 15

His Arg Arg Glu Ser Glu Ala Phe Arg Gln Gln Ala Ser Ala Ser Ser
20 25 30

Ser Gln Gln Gln Ala Ser Gln His Ala Leu Ser Ser Glu Val Ser Arg
35 40 45

Lys Ala Ala Ser
50

<210> 2054
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D988N"

<400> 2054
Asp His Ser Lys Leu Tyr Leu Lys Asn Pro Asp Lys Glu Asp Leu Gly
1 5 10 15

Thr Tyr Ser Val Ser Val Ser Asp Thr Asn Asn Gly Val Ser Ser Ser
20 25 30

Phe Val Leu Asp Pro Glu Glu Leu Glu Arg Leu Met Ala Leu Ser Asn
35 40 45

Glu Ile Lys Asn
50

<210> 2055
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E251K"

<400> 2055
Leu Ser Gly Arg Arg Ser Phe Asn Arg Thr Pro Lys Gly Trp Ile Ser
1 5 10 15

Glu Asn Ile Pro Ile Val Ile Thr Thr Lys Lys Pro Thr Asp Asp Thr
20 25 30

Thr Val Pro Glu Ser Glu Asp Leu
35 40

<210> 2056
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E226K"

<400> 2056
Ala Ala Glu Gly Ala Ala Ser Glu Glu Gly Glu Lys Gly Leu Phe Ile
1 5 10 15

Gln Pro Glu Asp Ala Glu Glu Val Val Lys Lys Val Thr Thr Glu Arg
20 25 30

Ser Gln Asp Leu Cys Pro Gln Ser Leu Glu Asp Ala Ala Ser Glu Glu
35 40 45

Ser Ser Lys Gln
50

<210> 2057
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P351Q"

<400> 2057
Ser Leu Glu Cys Leu Arg Asn Gln Cys Phe Asp Leu Ala Arg Lys Leu
1 5 10 15

Ser Glu Thr Asn Pro Gln Glu Arg Asn Gln Gln Gln Gln Asn Met Asn
20 25 30

Ile Arg Gln His Val Arg Pro Glu Glu Asp Phe Pro Gly Arg Thr Pro
35 40 45

Asp Arg Asn Tyr
50

<210> 2058
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R506C"

<400> 2058
Ser Thr Lys Asn Lys Lys Arg Arg Lys Lys Arg Ile Phe Asn Leu Val
1 5 10 15

Pro Asn Phe Asp Leu Leu Gly Gln Ser Cys Cys Ile Gly Val Lys Glu
20 25 30

Arg Glu Lys Cys Asp Leu Leu Thr Lys Asn His Gly Leu Lys Ile Thr
35 40 45

Leu Gly Glu Glu
50

<210> 2059
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T184K"

<400> 2059
Arg Arg Gln Met Asp Leu Lys Lys Gly Gly Tyr Val Val Leu Gly Ser
1 5 10 15

Arg Glu Asn Gln Glu Thr Gln Gly Ser Lys Lys Leu Ser Asp Ser Glu
20 25 30

Glu Ala Cys Gln Gln Lys Asn Pro Ala Thr Glu Glu Ser Gly Ser Asp
35 40 45

Ser Lys Glu Pro
50

<210> 2060
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.H514fs"

<400> 2060
Cys Ile Ser Ala Tyr Gln Arg Leu Gly Arg Tyr Gly Asp Ala Leu Lys
1 5 10 15

Lys Cys His Glu Val Glu Arg His Phe Leu Arg
20 25

<210> 2061
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S807Y"

<400> 2061
Asp Ile Tyr Glu Leu Asp Thr Ser Gly Leu Glu Asp Thr Met Glu Ile
1 5 10 15

Gln Glu Arg Ile Glu Asn Ser Phe Lys Tyr Tyr Leu Leu Asp Gln Leu
20 25 30

Lys Asp Val Phe Ser Lys Cys Lys Gly Asp Leu Leu Glu Val Lys Asp
35 40 45

Gly Asn Leu Lys
50

<210> 2062
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L72F"

<400> 2062
Glu Glu Phe Leu Glu Ile Met Ala Leu Val Gly Met Ala Ser Lys Pro
1 5 10 15

Leu His Val Arg Arg Leu Gln Lys Ala Phe Phe Arg Asp Trp Val Thr
20 25 30

Asn Pro Gly Leu Phe Asn Gln Pro Leu Thr Ser Leu Pro Val Ser Ser
35 40 45

Ile Pro Ile Tyr
50

<210> 2063
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S183L"

<400> 2063
Lys Thr Gln Asp Thr Gly His Arg Arg Gly Gly Gly Gly Gly Ala Gly
1 5 10 15

Phe Arg Gly Ala Gly Lys Ser Glu Pro Leu Leu Pro Ser Cys Ser Pro
20 25 30

Ser Met Ser Thr
35

<210> 2064
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P353R"

<400> 2064
Met Ile Gln Lys Tyr Asp Glu Pro Ile Leu Lys Phe Leu Ser Asp Val
1 5 10 15

Ser Leu Lys Phe Ser Lys Pro Gly Gln Arg Arg Val Ser Tyr Thr Phe
20 25 30

Glu Phe His Phe Leu Pro Asn Pro Tyr Phe Arg Asn Glu Val Leu Val
35 40 45

Lys Thr Tyr Ile
50

<210> 2065
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P285Q"

<400> 2065
Val Thr Val Lys Thr Ile Lys Lys Lys Gln Lys His Lys Gly Arg Gly
1 5 10 15

Thr Val Arg Thr Ile Thr Lys Gln Val Gln Gln Asn Glu Ser Phe Phe
20 25 30

Asn Phe Phe Asn Pro Leu Lys Ala Ser Gly Asp Gly Glu Ser Leu Asp
35 40 45

Glu Asp Ser Glu Phe
50

<210> 2066
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R121Q"

<400> 2066
Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Arg Arg Cys His Phe
1 5 10 15

Phe Ser Val Pro Cys Trp Leu His His Gln Gln Phe Asp Pro Lys Ala
20 25 30

Ser Ser Ser Phe Gln Ala Asn Gly Thr Lys Phe Ala Ile Gln Tyr Gly
35 40 45

Thr Gly Arg Val
50

<210> 2067
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P240R"

<400> 2067
Ala Phe Leu Thr Val Ser Gly Gln Leu His Leu Glu Val Met Ser Gly
1   5   10   15

Ala Phe Thr Gln Val Phe Thr Phe Gly Arg Arg Thr Phe Arg Ala Glu
            20   25   30

Asn Ser Gln Ser Arg Arg His Leu Ala Glu Phe Tyr Met Ile Glu Ala
        35   40   45

Glu Ile Ser Phe
    50

<210> 2068
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.I393T"

<400> 2068
Ile Gln Tyr Ile His Pro Ala Asp Ala Val Lys Leu Gly Gln Ala Glu
1   5   10   15

Leu Val Val Ile Asp Glu Ala Ala Ala Thr Thr Pro Leu Pro Leu Val
            20   25   30

Lys Ser Leu Leu Gly Pro Tyr Leu Val Phe Met Ala Ser Thr Ile Asn
        35   40   45

Gly Tyr Glu Gly
    50

<210> 2069
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E810K"

<400> 2069
Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu
1 5 10 15

Asn Glu Ser Asp Asp Glu Glu Glu Glu Lys Lys Lys Gly Pro Val Ser
20 25 30

Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser
35 40 45

Trp Asp Glu Gly
50

<210> 2070
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R25C"

<400> 2070
Met Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn
1 5 10 15

Ile Leu Glu Ile Asn Glu Lys Leu Cys Cys Pro Gln Leu Ala Glu Asn
20 25 30

Lys Gln Gln Phe Gly Asn Leu Lys Glu Arg Cys Phe Val Thr Gln Leu
35 40 45

Ala Gly Phe
50

<210> 2071
<211> 31
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D449fs"

<400> 2071
Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu
1 5 10 15

Asp Arg Cys Tyr Ser Thr Pro Ser Asp Ile Leu Asn Cys Leu Thr
20 25 30

<210> 2072
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D491V"

<400> 2072
Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg
1 5 10 15

Glu Leu Pro Glu Val Val Glu Pro Glu Val Val Leu Gln Asp Ser Leu
20 25 30

Asp Arg Trp Tyr Ser Thr Pro Phe Ser Tyr Pro Glu Leu Pro Asp Ser
35 40 45

Cys Gln Pro Tyr
50

<210> 2073
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.G698C"

<400> 2073
Gly Tyr Ser Glu Pro Thr Val Tyr Glu Phe Ser Met Pro Pro Lys Pro
1 5 10 15

Asn Ile Ile Lys Asp Thr Leu Phe Asn Cys Cys Leu Gly Leu Gly Ala
20 25 30

Val Ile Gly Leu Gly Val Ala Ala Leu Leu Leu Ile Leu Val Val Thr
35 40 45

Asp Val Ser Cys
50

<210> 2074
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R220L"

<400> 2074
Val Ser Leu Val Thr Gly Cys Cys Tyr Arg Leu Leu Glu Asn Pro Thr
1 5 10 15

Ile Asn His Gln Lys Asn Arg Pro Thr Leu Leu Glu Ala Ile Thr His
20 25 30

Leu Leu Gly Val Ala Leu Thr Arg Tyr Asn His Met Leu Ser Ala Thr
35 40 45

Val Lys Ile Ile
50

<210> 2075
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q909fs"

<400> 2075
Ala Ser Ser Ala Asp Ala Asp His Ser Pro Ser Ser Gln Gly Ser Ser
1 5 10 15

Glu Ala Pro Ala Ser Gln Pro Pro Pro Arg Ser Glu Val Leu Ser Cys
20 25 30

Pro Leu

<210> 2076
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T466fs"

<400> 2076
His Trp Arg Phe Arg Pro Arg Arg Lys Gln Asp Ala Pro Ser Gln Ser
1 5 10 15

Glu Asn Lys Lys Lys Ser Thr Lys Lys Ile Leu Lys Leu Thr Leu Lys
20 25 30

Met Ile Leu Thr Leu Met Tyr Ile Leu Glu Lys Gln Arg Leu Leu Leu
35 40 45

Phe

<210> 2077
<211> 55
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q1253fs"

<400> 2077
Arg Ser Arg Glu Leu Leu Ser His His Phe Arg Gln Gln Arg Val Ala
1 5 10 15

Met Met Met Gln Gln Gln Gln Gln Gln Thr Ala Ala Ala Ala Ala Ala
20 25 30

Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Ala Ala Thr Ala Ala Asn
35 40 45

Pro Gly Leu Gln Pro Thr Ser
50 55

<210> 2078
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R562Q"

<400> 2078
Ala Asp Trp Val Leu Pro Gly Lys Lys Met Gly Asn Leu Ser Gln Leu
1 5 10 15

Ser Ser Gly Glu Asp Lys Trp Leu Leu Gln Gln Lys Lys Ala Gln Glu
20 25 30

Val Leu Leu Asn Ser Pro Leu Gln Glu Glu His Asn Phe Pro Pro Asp
35 40 45

His Tyr Gly Leu
50

<210> 2079
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E369D"

<400> 2079
Asp Ser Arg Pro Ile Val Pro Leu Glu Lys Ser Thr Gly His Thr Pro
1 5 10 15

Thr Lys Pro Ser Gly Ser Ser Val Ser Asp Asp Lys Leu Lys Lys Leu
20 25 30

Asp Ser Ser Arg Glu Thr Ser His Gly Ser Pro Thr Val Thr Lys Leu
35 40 45

Ser Lys Glu Pro
50

<210> 2080
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1561Q"

<400> 2080
Pro Gly Val Asp Pro Val Val Ser His Ser Pro Phe Asp Pro His His
1 5 10 15

Arg Gly Ser Thr Ala Gly Glu Val Tyr Gln Gln Ser His Leu Pro Thr
20 25 30

His Leu Asp Pro Ala Met Pro Phe His Arg Ala Leu Asp Pro Ala Ala
35 40 45

Ala Ala Tyr Leu
50

<210> 2081
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R258W"

<400> 2081
Thr Tyr Leu Leu Thr Thr Glu Thr Gly Leu Gln Lys Asp His Ala Leu
1 5 10 15

Trp Asp His Thr Ala Gln Asn Leu Leu Trp Trp Met Gly Leu Ala Phe
20 25 30

Leu Val Leu Val Ala Leu Val Trp Phe Leu Val Glu Asp Trp Leu Ser
35 40 45

Arg Lys Arg Thr
50

<210> 2082
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V427I"

<400> 2082
Leu Asn Lys Lys Phe Ala Leu Glu His Gly Ile Pro Thr Asp Met Gly
1 5 10 15

Tyr Ala Val Ala Pro His His Ser Gly Ile Ile Tyr Pro Val His Val
20 25 30

Gln Leu Tyr Glu Ala Trp Lys Lys Val Trp Asn Ile Lys Ile Thr Ser
35 40 45

Thr Glu Glu Tyr

50

<210> 2083
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P194del"

<400> 2083
Asp Met Glu His Gly Trp Glu Val Val Asp Ser Asn Asp Ser Ala Ser
1 5 10 15

Gln His Gln Glu Glu Leu Pro Pro Pro Leu Pro Pro Gly Trp Glu Glu
20 25 30

Lys Val Asp Asn Leu Gly Arg Thr Tyr Tyr Val Asn His Asn Asn Arg
35 40 45

Thr Thr Gln Trp His
50

<210> 2084
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A798T"

<400> 2084
Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys Glu Gln Leu Lys
1 5 10 15

Thr Ile Val Met Ala Thr Lys Met Ala Thr Thr Leu His Tyr Pro Ser
20 25 30

Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp Leu Ser Arg
35 40 45

Asn Ala Gln Leu
50

<210> 2085
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A316T"

<400> 2085
Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro Gln Leu
1 5 10 15

Gly Gln Ser Val Gly Ser Gln Asn Asp Thr Thr Tyr Asp Val Pro Arg
20 25 30

Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala Asn
35 40 45

Pro Gln Glu Arg
50

<210> 2086
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E645K"

<400> 2086
Ser Pro Val Lys Glu Glu Ala Lys Ser Pro Ala Glu Val Lys Ser Pro
1 5 10 15

Glu Lys Ala Lys Ser Pro Thr Lys Glu Lys Lys Ala Lys Ser Pro Glu
20 25 30

Lys Ala Lys Ser Pro Glu Lys Glu Glu Ala Lys Ser Pro Glu Lys Ala
35 40 45

Lys Ser Pro Val
50

<210> 2087
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.665_666insEE"

<400> 2087
Pro Thr Lys Glu Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Glu
1 5 10 15

Lys Glu Glu Ala Lys Ser Pro Glu Lys Glu Glu Glu Glu Ala Lys Ser
20 25 30

Pro Val Lys Ala Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val
35 40 45

Lys Ala Glu Ala Lys Ser Pro Glu Lys Ala
50 55

<210> 2088
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V670E"

<400> 2088
Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Glu Lys Glu Glu Ala
1 5 10 15

Lys Ser Pro Glu Lys Ala Lys Ser Pro Glu Glu Lys Ala Glu Ala Lys
20 25 30

Ser Pro Glu Lys Ala Lys Ser Pro Val Lys Ala Glu Ala Lys Ser Pro
35 40 45

Glu Lys Ala Lys
50

<210> 2089
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A213V"

<400> 2089
Arg Phe Glu Glu Glu Ala Arg Leu Arg Asp Asp Thr Glu Ala Ala Ile
1 5 10 15

Arg Ala Leu Arg Lys Asp Ile Glu Glu Val Val Ser Leu Val Lys Val
20 25 30

Glu Leu Asp Lys Lys Val Gln Ser Leu Gln Asp Glu Val Ala Phe Leu
35 40 45

Arg Ser Asn His
50

<210> 2090
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R608C"

<400> 2090
Glu Val Tyr Leu Ala Arg Leu Arg Gln Ile Arg Leu Gln Asn Phe Asn

1 5 10 15

Glu Arg Gln Gln Ile Lys Ala Lys Leu Cys Cys Gly Glu Lys Lys Glu
20 25 30

Ala Asn His Ser Glu Gly Gln Glu Gly Ser Glu Glu Ala Asp Met Arg
35 40 45

Arg Lys Lys Ile
50

<210> 2091
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R374Q"

<400> 2091
Lys Leu Gln Ala Ala Asp Glu Lys Ala Arg Lys Leu Lys Lys Ile Val
1 5 10 15

Glu Glu Lys Tyr Glu Glu Asn Ser Lys Gln Gln Met Gln Glu Leu Arg
20 25 30

Ser Arg Asn Phe Gln Gln Leu Ser Val Asp Val Leu His Glu Lys Thr
35 40 45

His Leu Lys Gly
50

<210> 2092
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R239S"

<400> 2092
Pro Pro Phe Thr Ala Phe Ser Gln Lys Glu Leu Ala Gly Lys Ile Arg
1 5 10 15

Glu Gly Lys Phe Arg Arg Ile Pro Tyr Ser Ser Tyr Ser Asp Glu Leu
20 25 30

Asn Glu Ile Ile Thr Arg Met Leu Asn Leu Lys Asp Tyr His Arg Pro
35 40 45

Ser Val Glu Glu
50

<210> 2093
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V690fs"

<400> 2093
Val Thr Ser Val Ser Cys Cys His Gly Asn Thr Leu Leu Ala Val Arg
1 5 10 15

Ser Val Thr Asp Glu Pro Val Pro Pro Glu Ala Pro Gly Phe Thr Ser
20 25 30

Gly Pro Pro
35

<210> 2094
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G170D"

<400> 2094
Gln Thr His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp
1 5 10 15

His Arg Tyr Leu Glu Leu Glu Ser Ser Asp Asp His Arg Asn Glu Val
20 25 30

Arg Leu His Tyr Arg Ser Gly Ser His Arg Pro His Thr Glu Val Phe
35 40 45

Pro Tyr Ile Leu
50

<210> 2095
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V611L"

<400> 2095
Leu Lys Ser Leu Glu Lys Glu Asn Lys Glu Leu Leu Lys Asp Val Glu
1 5 10 15

Val Val Arg Pro Leu Glu Lys Glu Ala Leu Leu Gly Gln Leu Lys Pro
20 25 30

Thr Gly Lys Glu Asp Thr Gln Thr Leu Gln Ser Leu Gln Lys Glu Asn
35 40 45

Gln Glu Leu Met
50

<210> 2096
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.T676fs"

<400> 2096
Pro Gly Ala Ser Leu Arg Lys Gly Lys Gly Asn Ser Ser Met Asp Ser
1 5 10 15

Ala Ala Gly Cys Ser Gly Thr Pro Pro Asp Leu Pro Thr Ser Pro Asp
20 25 30

Gln Thr Arg Ser Gly Pro Val His Val Ser Val Glu Pro
35 40 45

<210> 2097
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F1658fs"

<400> 2097
Ala Lys Pro Tyr Glu Ile Val Val Asp Leu Thr His Thr Gly Pro Ser
1 5 10 15

Asn Arg Phe Lys Thr Asp Phe Leu Ser Gly Leu Leu Phe Phe Leu Ala
20 25 30

Leu Leu Thr Thr Thr Ser Pro Gln Ser Ile Ser Ile Thr Val Thr Pro
35 40 45

Gly Ser Gly Ser Thr Pro Ser Ile Met Ser Gly Cys
50 55 60

<210> 2098
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V256I"

<400> 2098
Gln Phe Glu Glu Asp Gln Phe Gln Pro Gly Val Trp His Asp His Ser
1 5 10 15

Lys Tyr Pro Gly Ser Val Asn Ser Ala Ile Ile Leu Arg Leu Ser Pro
20 25 30

Tyr Val Asn Tyr Gln Phe Arg Val Ile Ala Ile Asn Glu Val Gly Ser
35 40 45

Ser His Pro Ser
50

<210> 2099
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q906E"

<400> 2099
Gln Gln Gln Gln Gln Gln Gln Gln Val Met Glu Ser Ser Ala Ala Met
1 5 10 15

Val Met Glu Met Gln Gln Ser Ile Cys Glu Glu Ala Ala Ala Gln Ile
20 25 30

Gln Ser Glu Leu Phe Pro Ser Thr Ala Ser Ala Asn Gly Asn Leu Gln
35 40 45

Gln Ser Pro Val
50

<210> 2100
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R34G"

<400> 2100
Pro Gly Leu Pro Ser Gln Gln Asp Met Asp Leu Ile Asp Ile Leu Trp
1 5 10 15

Arg Gln Asp Ile Asp Leu Gly Val Ser Gly Gly Glu Val Phe Asp Phe
20 25 30

Ser Gln Arg Arg Lys Glu Tyr Glu Leu Glu Lys Gln Lys Lys Leu Glu
35 40 45

Lys Glu Arg Gln
50

<210> 2101
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R34Q"

<400> 2101
Pro Gly Leu Pro Ser Gln Gln Asp Met Asp Leu Ile Asp Ile Leu Trp
1 5 10 15

Arg Gln Asp Ile Asp Leu Gly Val Ser Gln Gln Glu Val Phe Asp Phe
20 25 30

Ser Gln Arg Arg Lys Glu Tyr Glu Leu Glu Lys Gln Lys Lys Leu Glu
35 40 45

Lys Glu Arg Gln
50

<210> 2102
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E79K"

<400> 2102
Leu Glu Lys Glu Arg Gln Glu Gln Leu Gln Lys Glu Gln Glu Lys Ala
1 5 10 15

Phe Phe Ala Gln Leu Gln Leu Asp Glu Lys Lys Thr Gly Glu Phe Leu
20 25 30

Pro Ile Gln Pro Ala Gln His Ile Gln Ser Glu Thr Ser Gly Ser Ala
35 40 45

Asn Tyr Ser Gln
50

<210> 2103
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E79Q"

<400> 2103
Leu Glu Lys Glu Arg Gln Glu Gln Leu Gln Lys Glu Gln Glu Lys Ala
1 5 10 15

Phe Phe Ala Gln Leu Gln Leu Asp Glu Gln Gln Thr Gly Glu Phe Leu
20 25 30

Pro Ile Gln Pro Ala Gln His Ile Gln Ser Glu Thr Ser Gly Ser Ala
35 40 45

Asn Tyr Ser Gln
50

<210> 2104
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G81S"

<400> 2104
Lys Glu Arg Gln Glu Gln Leu Gln Lys Glu Gln Glu Lys Ala Phe Phe
1 5 10 15

Ala Gln Leu Gln Leu Asp Glu Glu Thr Ser Ser Glu Phe Leu Pro Ile
20 25 30

Gln Pro Ala Gln His Ile Gln Ser Glu Thr Ser Gly Ser Ala Asn Tyr
35 40 45

Ser Gln Val Ala
50

<210> 2105
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D29H"

<400> 2105
Leu Glu Leu Pro Pro Pro Gly Leu Pro Ser Gln Gln Asp Met Asp Leu
1 5 10 15

Ile Asp Ile Leu Trp Arg Gln Asp Ile His His Leu Gly Val Ser Arg
20 25 30

Glu Val Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu Glu Lys
35 40 45

Gln Lys Lys Leu
50

<210> 2106

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L30F"

<400> 2106
Glu Leu Pro Pro Pro Gly Leu Pro Ser Gln Gln Asp Met Asp Leu Ile
1 5 10 15

Asp Ile Leu Trp Arg Gln Asp Ile Asp Phe Phe Gly Val Ser Arg Glu
20 25 30

Val Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu Glu Lys Gln
35 40 45

Lys Lys Leu Glu
50

<210> 2107
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G31A"

<400> 2107
Leu Pro Pro Pro Gly Leu Pro Ser Gln Gln Asp Met Asp Leu Ile Asp
1 5 10 15

Ile Leu Trp Arg Gln Asp Ile Asp Leu Ala Ala Val Ser Arg Glu Val
20 25 30

Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu Glu Lys Gln Lys
35 40 45

Lys Leu Glu Lys
50

<210> 2108
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L294F"

<400> 2108
Ser Val Thr Glu Leu Val Arg Val Ser Gln Thr Pro Ile Ala Ala Gly
1 5 10 15

Thr Gly Pro Asn Phe Ser Leu Ser Asp Phe Phe Glu Ser Ser Ser Tyr
20 25 30

Tyr Ser Met Ser Pro Gly Ala Met Arg Arg Ser Leu Pro Ser Thr Ser
35 40 45

Ser Thr Ser Ser
50

<210> 2109
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R109Q"

<400> 2109
Leu Lys Asp Ala Ala His Pro Ser Glu Ala Thr Phe Ser Cys Asp Cys
1 5 10 15

Val Ala Asp Ala Leu Ile Leu Arg Val Gln Gln Ser Glu Leu Ser Gly
20 25 30

Leu Pro Phe Tyr Trp Asn Phe His Cys Met Leu Ala Ser Pro Ser Leu
35 40 45

Val Ser Gln His
    50

<210> 2110
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.F204fs"

<400> 2110
Asp Val Thr Ile Thr Asn Asp Cys His Val Val Val Thr Asp Ala Gly
1   5   10   15

Asp Arg Ser Ile Lys Val Phe Asp Phe Leu Ala Arg Ser Ser Leu Ser
            20   25   30

Leu Glu Ala Asn Ser Pro Tyr Leu Gly Val Trp Arg Pro Pro Leu Arg
        35   40   45

Met Gly Leu Trp
    50

<210> 2111
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R84C"

<400> 2111
Asp Ala Glu Pro Leu Glu Ile Ile Leu His Leu Pro Leu Leu Cys Glu
1   5   10   15

Asp Lys Asn Val Pro Tyr Val Phe Val Cys Cys Ser Lys Gln Ala Leu
            20   25   30

Gly Arg Ala Cys Gly Val Ser Arg Pro Val Ile Ala Cys Ser Val Thr
35 40 45

Ile Lys Glu Gly
50

<210> 2112
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1561N"

<400> 2112
Ala Thr Glu Ile Leu Lys Ser Pro Ile Leu Pro Lys Pro Pro Gly Glu
1 5 10 15

Leu Thr Ala Glu Ser Pro Gln Ser Thr Asn Asn Asp Ala His Gln Gly
20 25 30

Ser Gln Gly Ala Glu Ala Leu Ser Pro Leu Ser Pro Cys Ser Pro Arg
35 40 45

Val Asn Ala Glu
50

<210> 2113
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1035fs"

<400> 2113
Glu Pro Thr Gln Arg Pro Pro Thr Ile Cys Glu Arg Trp Arg Glu Asn
1 5 10 15

Leu Leu Glu His Tyr Gly Gly Thr Pro Gly Met Thr Ser Thr Cys Pro

20 25 30

Ser Ala Met Thr Trp Ala Thr Ser Ser Pro Cys Ser Ala Thr Glu Arg
35 40 45

Ala Thr Ser Ala Gly Val Trp Thr Lys Met Ala Glu Arg Cys Arg Ala
50 55 60

Pro Ala Pro Ser Gln Ala Pro Pro Leu Arg Val Tyr Pro Pro Ser Leu
65 70 75 80

His Pro Trp Ser Gly Pro Arg Pro Gly Gln Met
85 90

<210> 2114
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1366C"

<400> 2114
Val Arg Ala Leu Gln Ala Thr Glu Glu Lys Gln Arg Gly Ala Glu Lys
1 5 10 15

Gln Ser Arg Leu Leu Glu Glu Lys Val Cys Cys Ala Leu Asn Lys Leu
20 25 30

Val Ser Arg Ile Ala Pro Ala Ala Leu Ser Val
35 40

<210> 2115
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P286fs"

<400> 2115
Ala Gly Ile Glu Asn Tyr Thr Ser Gln Phe Gly Pro Gly Ser Pro Ser
1 5 10 15

Val Ala Gln Lys Ser Glu Leu Pro Pro Pro His Leu Gln Ser His Ser
20 25 30

Ile Ser Leu Pro
35

<210> 2116
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.H447del"

<400> 2116
Gly Tyr Ala Val Pro Val Ile Gln Arg His Glu His His His His His
1 5 10 15

Glu His His His His His His His His Phe His Pro Ser
20 25

<210> 2117
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C190fs"

<400> 2117
Lys Lys Met Pro Asn Val Phe Gln Asn Leu Val Ser Cys Lys Arg Val
1 5 10 15

Phe Arg Glu Leu Lys Met Leu Cys Phe Leu Ser Met Ile Met Tyr Ser
20 25 30

Leu Pro Leu Thr Tyr Ser Asn Leu His Thr Leu Thr Ile Leu Lys Lys
35 40 45

Tyr Met Leu Ser Gln Asn
50

<210> 2118
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E409K"

<400> 2118
Ser Asp Phe Ile Arg Ser Leu Asp His Cys Gly Asp Leu Ala Leu Glu
1 5 10 15

Gly Val Phe Ser His Lys Phe Asp Phe Lys Lys Leu Gln Asp Val Ser
20 25 30

Ser Val Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr
35 40 45

Thr Ala Gln Arg
50

<210> 2119
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D593N"

<400> 2119
Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys Ser
1 5 10 15

Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asn Asn Tyr Leu Phe Asp Phe
20 25 30

Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu
35 40 45

Asp Phe Tyr Gly
50

<210> 2120
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R288W"

<400> 2120
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr
1 5 10 15

Thr Thr Thr Glu Cys Leu Arg His Ile Trp Trp Gln Phe Gly Ala Leu
20 25 30

Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile
35 40 45

Arg Glu Val Leu
50

<210> 2121
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R157C"

<400> 2121
Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg Lys Tyr Val Arg Ser Arg

1 5 10 15

Phe Gln Cys Ile Glu Asp Arg Asn Ala Cys Cys Leu Gly Glu Ser Val
20 25 30

Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu Ile Lys Glu His Arg
35 40 45

Ser Gln Gln Glu
50

<210> 2122
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V229I"

<400> 2122
Leu Ile Ser Arg Glu Trp Pro Asp Pro Ala Ala Pro Ile Thr Glu Ile
1 5 10 15

Val Ser Gln Pro Glu Arg Leu Leu Phe Ile Ile Ile Asp Ser Phe Glu
20 25 30

Glu Leu Gln Gly Gly Leu Asn Glu Pro Asp Ser Asp Leu Cys Gly Asp
35 40 45

Leu Met Glu Lys
50

<210> 2123
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R392H"

<400> 2123
Leu Gly Ser Val Leu Asn Asn Asp Thr Lys Leu Cys Lys Asp Trp Ala
1 5 10 15

Glu Lys Gln Pro Pro Phe Thr Leu Ile His His Ser Leu Leu Arg Lys
20 25 30

Val Leu Leu Pro Glu Ser Phe Leu Ile Val Thr Val Arg Asp Val Gly
35 40 45

Thr Glu Lys Leu
50

<210> 2124
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R737W"

<400> 2124
Leu Pro Ile Asn Gln Asn Leu Asp Leu Ile Ala Ser Ser Phe Cys Leu
1 5 10 15

Gln His Cys Pro Tyr Leu Arg Lys Ile Trp Trp Val Asp Val Lys Gly
20 25 30

Ile Phe Pro Arg Asp Glu Ser Ala Glu Ala Cys Pro Val Val Pro Leu
35 40 45

Trp Met Arg Asp
50

<210> 2125
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E611G"

<400> 2125
Cys Pro Gly Val Ala Pro Glu Val Thr Glu Gly Ala Lys Gly Leu Glu
1 5 10 15

Asp Thr Glu Glu Pro Glu Glu Glu Glu Gly Gly Gly Glu Glu Pro Asn
20 25 30

Tyr Pro Leu Glu Leu Leu Tyr Cys Leu Tyr Glu Thr Gln Glu Asp Ala
35 40 45

Phe Val Arg Gln
50

<210> 2126
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E75K"

<400> 2126
Gln Lys Met Arg Ile Glu Val Gly Leu Asp Leu Leu His Phe Ala Leu
1 5 10 15

Ala Glu Ala Asp Arg Leu Asp Val Leu Lys Lys Lys Tyr Arg Gly Lys
20 25 30

Cys Glu Pro Thr Phe Leu Phe Tyr Ala Gly Gly Glu Leu Val Ala Val
35 40 45

Val Arg Gly Ala
50

<210> 2127
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.A18E"

<400> 2127
Met Leu Arg Thr Glu Ser Cys Arg Pro Arg Ser Pro Ala Gly Gln Val
1 5 10 15

Ala Glu Glu Ala Ser Pro Leu Leu Leu Leu Leu Leu Leu Leu Ala Trp
20 25 30

Cys Ala Gly Ala Cys Arg Gly Ala Pro Ile Leu Pro
35 40

<210> 2128
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A19E"

<400> 2128
Met Leu Arg Thr Glu Ser Cys Arg Pro Arg Ser Pro Ala Gly Gln Val
1 5 10 15

Ala Ala Glu Glu Ser Pro Leu Leu Leu Leu Leu Leu Leu Leu Ala Trp
20 25 30

Cys Ala Gly Ala Cys Arg Gly Ala Pro Ile Leu Pro Gln
35 40 45

<210> 2129
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="p.E233K"

<400> 2129
Glu Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala
1 5 10 15

Ala Val Lys Glu Ala Gly Tyr Thr Ile Lys Lys Trp Phe Glu Val Ile
20 25 30

Ser Gln Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser
35 40 45

Leu Val Ala Arg
50

<210> 2130
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S58A"

<400> 2130
Pro Arg Arg Arg Leu Gly Ser Leu Arg Trp Cys Gly Arg Arg Arg Leu
1 5 10 15

Arg Trp Arg Leu Leu Gln Ala Gln Ala Ala Ala Gly Val Asp Trp Arg
20 25 30

Glu Gly Ala Arg Gln Val Ser Arg Ala Ala Ala Ala Arg Arg Pro Asn
35 40 45

Thr Ala Thr Pro
50

<210> 2131
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T428M"

<400> 2131
Val Thr Thr Lys Ser Pro Ala Val Lys Pro Ala Ala Ala Pro Lys Gln
1 5 10 15

Pro Val Gly Gly Gly Gln Lys Leu Leu Met Met Arg Lys Ala Asp Ser
20 25 30

Ser Ser Ser Glu Glu Glu Ser Ser Ser Ser Glu Glu Glu Lys Thr Lys
35 40 45

Lys Met Val Ala
50

<210> 2132
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R24G"

<400> 2132
Met Ala Ala Ser Arg Ser Ala Gly Glu Ala Gly Pro Gly Gly Ser Gln
1 5 10 15

Gly Arg Val Val Arg Met Lys Gly Gly Arg Gly Gly Arg Gly Pro Arg
20 25 30

Arg Gly Pro Ala Gly Gly Gly Glu Lys Ala Leu Lys Arg Leu Lys Leu
35 40 45

Ala Val
50

<210> 2133
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q306del"

<400> 2133
Leu Gly Thr Glu Thr Pro Leu Ser Thr His His Gln Met Gln Leu Leu
1 5 10 15

Gln Gln Leu Leu Gln Gln Gln Gln Gln Thr Gln Val Ala Val Ala Gln
20 25 30

Val His Leu Leu Lys Asp Gln Leu Ala Ala Glu Ala Ala Ala Arg Leu
35 40 45

Glu Ala Gln Ala Arg
50

<210> 2134
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P2514fs"

<400> 2134
Ser Tyr Ser Ser Pro Val Asp Asn Thr Pro Ser His Gln Leu Gln Val
1 5 10 15

Pro Glu His Pro Phe Leu Thr Pro Ser Arg Val Pro
20 25

<210> 2135
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P6fs"

<400> 2135
Met Pro Ala Leu Arg Arg Ser Ala Val Gly Ala Ala Gly Ala Leu Ala
1 5 10 15

Val Leu Arg Gly Pro Arg Ala Cys Ile Ala Val Ser Arg Trp Leu
20 25 30

<210> 2136
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.C19W"

<400> 2136
Met Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala Leu Trp
1 5 10 15

Leu Cys Trp Trp Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp Gly
20 25 30

Tyr Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr
35 40 45

<210> 2137
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R2105L"

<400> 2137
Leu Ser Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys
1 5 10 15

His Thr Pro Met Gly Lys Lys Ser Arg Leu Leu Pro Ser Ala Lys Ser

20 25 30

Thr Met Pro Thr Ser Leu Pro Asn Leu Ala Lys Glu Ala Lys Asp Ala
35 40 45

Lys Gly Ser Arg
50

<210> 2138
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R2298W"

<400> 2138
Ala Pro Ala Glu Gly Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro
1 5 10 15

Pro Glu Gly Lys His Ile Thr Thr Pro Trp Trp Glu Pro Leu Pro Pro
20 25 30

Ile Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala
35 40 45

Gly Ala Pro Gln
50

<210> 2139
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.C404fs"

<400> 2139
Ser Leu Pro Arg Leu Ala Val Asp Gly Pro Phe Gly Thr Ala Leu Thr
1 5 10 15

Asp Val Phe His Tyr Pro Val Cys Val Arg Cys Arg Gly Asp Arg Ser
20 25 30

His Ser Leu Arg Cys Ser Ser Glu Ile Tyr Met Val Gln Met Gln
35 40 45

<210> 2140
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P467fs"

<400> 2140
Ala Val Cys Ile Met Glu Val Asn Leu Leu Pro Ser Lys Val Thr His
1 5 10 15

Leu Leu Ile Lys Arg Pro Pro Phe Phe Thr Ile Asp Leu Val Thr Thr
20 25 30

Cys Ile

<210> 2141
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D6E"

<400> 2141
Met Ala Ser Leu Gly Glu Glu Leu Val Arg Ala Trp His Leu Gly Ala
1 5 10 15

Gln Ala Val Asp Arg Gly Asp Trp Ala Arg Ala Leu His Leu Phe Ser
20 25 30

<210> 2142
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G3fs"

<400> 2142
Met Ala Gly Pro Pro Ile Pro Ser Phe Ser Ala Arg Gly Ser Pro Gly
1 5 10 15

Ala Asp Gln Glu Ala Pro Asn Val Cys Leu Leu Cys Ala Leu Val Arg
20 25 30

Arg Gln Arg His Leu Arg Ala Gln Glu Leu Gly Arg Ile Gln Ala Ala
35 40 45

Gln Glu Asp Pro Gln Gly Asp Leu Pro Gly Gly Gly Gly Pro Ala Ala
50 55 60

Glu Ile
65

<210> 2143
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q201R"

<400> 2143
Asp Ser Ile Thr Pro Leu Leu Gly His Leu Pro Ser Asp Val Met Asp
1 5 10 15

Gln Asn Leu Leu Asn Phe Leu Pro Glu Arg Arg Glu His Ser Glu Val
20 25 30

Tyr Lys Ile Leu Ser Ser His Met Leu Val Thr Asp Ser Pro Ser Pro
35 40 45

Glu Tyr Leu Lys
50

<210> 2144
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E451K"

<400> 2144
Gly Ala Asp Val Pro Phe Gly Pro Pro Leu Asp Ile Gln Ile Leu His
1 5 10 15

Gln Val Leu Asp Leu Gln Ile Ala Ile Lys Lys Asn Ile Thr Ala Ser
20 25 30

Tyr Asp Asn Glu Thr Val Thr Leu Gln Asp Ile Cys Leu Ala Pro Leu
35 40 45

Ser Pro Tyr Asn
50

<210> 2145
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A271V"

<400> 2145
Gln Pro Pro Pro Pro Thr Gln Gln His Ser Ile Ile Asp Asn Ser Leu
1 5 10 15

Ser Leu Lys Thr Pro Ser Glu Leu Ser Val Val His Ser Pro Ser Thr

20 25 30

Leu Ser Ser Thr Leu Ser Gly
35

<210> 2146
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L287fs"

<400> 2146
Lys Val Glu Ala Lys Phe Ile Asn Tyr Val Lys Asn Cys Phe Arg Met
1 5 10 15

Thr Asp Gln Glu Ala Ile Gln Asp Leu Cys Leu Ala Val Glu Glu Val
20 25 30

Ser Leu Arg Lys
35

<210> 2147
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L287fs"

<400> 2147
Lys Val Glu Ala Lys Phe Ile Asn Tyr Val Lys Asn Cys Phe Arg Met
1 5 10 15

Thr Asp Gln Glu Ala Ile Gln Asp Leu Leu Leu Ala Val Glu Glu Val
20 25 30

Ser Leu Arg Lys
35

<210> 2148
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W288fs"

<400> 2148
Lys Val Glu Ala Lys Phe Ile Asn Tyr Val Lys Asn Cys Phe Arg Met
1 5 10 15

Thr Asp Gln Glu Ala Ile Gln Asp Leu Cys Leu Ala Val Glu Glu Val
20 25 30

Ser Leu Arg Lys
35

<210> 2149
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y138H"

<400> 2149
Leu Phe Ser Leu Val Asp Arg Val Ala Ala Ala Arg Gly Ala Lys Pro
1 5 10 15

Asp Leu Ile Leu Gly Pro Val Cys Glu His His Ala Ala Ala Pro Val
20 25 30

Ala Arg Leu Ala Ser His Trp Asp Leu Pro Met Leu Ser Ala Gly Ala
35 40 45

Leu Ala Ala Gly
50

<210> 2150
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R235Q"

<400> 2150
Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu Thr Ile
1 5 10 15

Ile Ser Ile Met Tyr Gly Ile Val Ile Gln Gln Thr Ile Trp Ile Lys
20 25 30

Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly Lys Leu
35 40 45

Cys Ser Ser Tyr
50

<210> 2151
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A263T"

<400> 2151
Tyr Met Tyr Ala Lys Val Lys Lys Ser Leu Pro Glu Met Tyr Ala Phe
1 5 10 15

Thr Val Cys Met Trp Leu Lys Ser Ser Thr Thr Thr Pro Gly Val Gly
20 25 30

Thr Pro Phe Ser Tyr Ala Val Pro Gly Gln Ala Asn Glu Leu Val Leu
35 40 45

Ile Glu Trp Gly
50

<210> 2152
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A371T"

<400> 2152
Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys
1 5 10 15

Thr Ser Leu Lys Gln Ala Ser Pro Val Thr Thr Phe Lys Lys Ile Asn
20 25 30

Asn Asn Asp Asp Asn Glu Lys Ile
35 40

<210> 2153
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S270I"

<400> 2153
His Pro Ser Gly Val Lys Thr Glu Ser Ala Val Leu Met Thr Ser Asp
1 5 10 15

Lys Ala Glu Ser Cys Gln Gly Asp Leu Ile Ile Thr Leu Ala Asn Val
20 25 30

Val Thr Ser Leu Ala Asn Leu Gly Lys Thr Lys Asp Leu Ser Gln Asn
35 40 45

Ser Asn Glu Met

50

<210> 2154
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R314L"

<400> 2154
Arg Thr Val Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn
1 5 10 15

Cys Pro Val Asp Lys Arg Arg Arg Asn Leu Leu Cys Gln Tyr Cys Arg
20 25 30

Phe Gln Lys Cys Leu Ala Val Gly Met Val Lys Glu Val Val Arg Thr
35 40 45

Asp Ser Leu Lys
50

<210> 2155
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E80K"

<400> 2155
Ser His Gly Glu Gln Gly Gln Met Pro Glu Asn Met Gln Val Ser Gln
1 5 10 15

Phe Lys Met Val Asn Tyr Ser Tyr Asp Lys Lys Asp Leu Glu Glu Leu
20 25 30

Cys Pro Val Cys Gly Asp Lys Val Ser Gly Tyr His Tyr Gly Leu Leu
35 40 45

Thr Cys Glu Ser
50

<210> 2156
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E327K"

<400> 2156
Tyr Glu Glu His Arg Gly Lys Gly Ser Phe Pro Ala Met Ile Thr Pro
1 5 10 15

Ala Tyr Gln Asn Ala Lys Lys Ala His Lys Lys Leu Ala Ser Asp Ile
20 25 30

Lys Tyr Arg Gln Asp Phe Asn Lys Met Lys Gly Ala Ala His Tyr His
35 40 45

Ser Leu Pro Ala
50

<210> 2157
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61K"

<400> 2157
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Lys Lys Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 2158
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q61R"

<400> 2158
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Arg Arg Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 2159
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61L"

<400> 2159
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly Leu Leu Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 2160
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61H"

<400> 2160
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys
1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly His His Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 2161
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q61H"

<400> 2161
Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly Glu Thr Cys

1 5 10 15

Leu Leu Asp Ile Leu Asp Thr Ala Gly His His Glu Glu Tyr Ser Ala
20 25 30

Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys Val Phe
35 40 45

Ala Ile Asn Asn
50

<210> 2162
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12C"

<400> 2162
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Cys Cys Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 2163
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G12D"

<400> 2163
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Asp Asp Gly Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu
35

<210> 2164
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G13R"

<400> 2164
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Arg Arg Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu Asp
35

<210> 2165
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G13D"

<400> 2165
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Asp Asp Val Gly
1 5 10 15

Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu
20 25 30

Tyr Asp Pro Thr Ile Glu Asp
35

<210> 2166
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V481L"

<400> 2166
Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala Val Ser Pro Phe
1 5 10 15

Met Glu Glu Glu Arg Pro Leu Leu Leu Leu Leu Thr Pro Pro Arg Leu
20 25 30

Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe His
35 40 45

His Asn Pro Ala
50

<210> 2167
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T246M"

<400> 2167
Leu Lys Lys Glu Val Gly Lys Ile Leu Cys Thr Asp Cys Ala Thr Arg
1 5 10 15

Pro Lys Leu Lys Lys Met Lys Ser Gln Met Met Gly Gln Val Gly Glu
20 25 30

Lys Gln Ser Leu Lys Cys Glu Ala Ala Ala Gly Asn Pro Gln Pro Ser
35 40 45

Tyr Arg Trp Phe
50

<210> 2168
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G21fs"

<400> 2168
Ala Asn Arg Ser Arg Arg Ala Leu Trp Ser Gln Ser Gln Val Val Leu
1 5 10 15

Pro Glu Trp Gly Ala Val Val Met
20

<210> 2169
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R103C"

<400> 2169
Phe Glu Thr Pro Glu Ala Tyr Ile Ser Leu Pro Lys Trp Asn Thr Lys
1 5 10 15

Arg Met Gly Ser Ile Ser Phe Asp Phe Cys Cys Thr Thr Glu Pro Asn
20 25 30

Gly Leu Ile Leu Phe Thr His Gly Lys Pro Gln Glu Arg Lys Asp Ala
35 40 45

Arg Ser Gln Lys

50

<210> 2170
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P23H"

<400> 2170
Met Leu Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro Ser Thr
1 5 10 15

Ala Asp Leu Pro Gly Ser His His Val Ser Asn Asn Phe Met Gly Cys
20 25 30

Leu Lys Glu Val Val Tyr Lys Asn Asn Asp Ile Arg Leu Glu Leu Ser
35 40 45

Arg

<210> 2171
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D244N"

<400> 2171
Tyr Phe Gln Ser Asn Ala Glu Pro Arg Cys Pro His Cys Asn Asp Tyr
1 5 10 15

Trp Pro His Glu Ile Pro Lys Val Phe Asn Asn Pro Glu Lys Glu Arg
20 25 30

Glu Ser Gly Val Leu Lys Ser Asn Lys Lys Ser Leu Arg Ser Arg Gln
35 40 45

His

<210> 2172
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q31fs"

<400> 2172
Ser Asn Ser Gly Ser Thr Gly Phe Ile Ser Phe Ser Gly Val Glu Ser
1 5 10 15

Ala Leu Ser Ser Leu Lys Asn Phe Gln Ser Leu Tyr Gln Leu Trp Tyr
20 25 30

Gly His Ser Phe
35

<210> 2173
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.A3P"

<400> 2173
Met Arg Pro Pro Pro Ser Met Asp Arg Ala Ala Val Ala Arg Val Gly
1 5 10 15

Ala Val Ala Ser Ala Ser Val Cys Ala Leu Val Ala Gly
20 25

<210> 2174
<211> 58
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P206fs"

<400> 2174
Ala Glu Pro Thr Pro Ser Trp Glu His Val Leu Phe Thr Ala Cys His
1 5 10 15

Asn Gln His Leu Gln Leu Gln Pro Pro Ala Ala Gly Cys Thr Arg Gly
20 25 30

Arg Thr Thr Gly Arg Pro Phe Trp Thr Ala Ser Gly Pro Ala Glu Leu
35 40 45

Asp Cys Ala Ser Gly Ser Ser Val Gly Leu
50 55

<210> 2175
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G333C"

<400> 2175
Ile Met Leu Phe Glu Val Lys Thr Thr Ala Leu Thr Pro Trp Lys Gly
1 5 10 15

Pro Gly Ala Val Ser Glu Val Ser Asn Cys Cys Thr Ser Arg Arg Ala
20 25 30

Gly Cys Val Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys
35 40 45

Phe

<210> 2176
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E59K"

<400> 2176
Cys Asn Pro Arg Met Gly Asn Leu Ala Leu Gly Arg Lys Leu Trp Ala
1 5 10 15

Asp Thr Thr Cys Gly Gln Asn Ala Thr Lys Lys Leu Tyr Cys Phe Tyr
20 25 30

Ser Glu Asn Thr Asp Leu Thr Cys Arg Gln Pro Lys Cys Asp Lys Cys
35 40 45

Asn Ala Ala Tyr
50

<210> 2177
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G173C"

<400> 2177
Arg Arg Leu Ser Glu Arg Glu Thr Arg His Phe Phe Arg Gln Ile Val
1 5 10 15

Ser Ala Val His Tyr Cys His Lys Asn Cys Cys Val Val His Arg Asp
20 25 30

Leu Lys Leu Glu Asn Ile Leu Leu Asp Asp Asn Cys Asn Ile Lys Ile
35 40 45

Ala Asp Phe Gly

50

<210> 2178
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R373Q"

<400> 2178
Arg Leu Val His Ile Lys Gly Asn Cys Gly Lys Glu Lys Val Leu Phe
1 5 10 15

Leu Arg Leu Tyr Leu Leu Gln Gly Ile Gln Gln Asn Tyr His Ser Gly
20 25 30

Asn Asp Val Glu Ala Tyr Glu Tyr Leu Asn Lys Ala Arg Gln Leu Phe
35 40 45

Lys Glu Leu Tyr
50

<210> 2179
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S83Y"

<400> 2179
Glu Cys Ala Gln Arg Glu Thr Trp Glu Glu Ala Ala Leu His Leu Lys
1 5 10 15

Asn Val His Phe Ala Ser Val Val Asn Tyr Tyr Phe Ile Glu Lys Glu
20 25 30

Asn Tyr His Tyr Val Thr Ile Leu Met Lys Gly Glu Val Asp Val Thr
35 40 45

His Asp Ser Glu
    50

<210> 2180
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.W13fs"

<400> 2180
Met Ser Val Val Pro Pro Asn Arg Ser Gln Thr Gly Trp Ala Pro Gly
1   5   10   15

Gly His Ser Val Arg Gln Gln Val His Pro Ala Asp Glu Ala Pro His
            20   25   30

Pro Gly Ala His His Gln Pro Val Pro Ser Tyr Gln Leu Tyr Phe Trp
        35   40   45

Tyr Lys Arg Ala Pro Leu Arg Glu Gly Gln Leu Cys Cys Ser Gln Ile
    50   55   60

Ser Ala His Glu Gly Arg Ile
65   70

<210> 2181
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S340L"

<400> 2181
Lys Glu Ser Leu Asn Leu Glu Asp Gln Ile Glu Ser Asp Glu Ser Glu
1   5   10   15

Leu Lys Lys Leu Lys Thr Glu Glu Asn Leu Leu Phe Lys Arg Leu Met
20 25 30

Ile Val Lys Lys Glu Lys Leu Ala Thr Ala Gln Phe Lys Ile Asn Lys
35 40 45

Lys His Glu Asp
50

<210> 2182
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R224fs"

<400> 2182
Thr Asn Gly Tyr Met Gly Lys Gly Ala Asp Asn Asp Gly Ser Gly Ser
1 5 10 15

Glu Ser Gly Tyr Thr Thr Pro Lys Lys Gly Lys Leu Gly Ala Ile Val
20 25 30

Pro Arg Val Val Lys Thr Leu Ile
35 40

<210> 2183
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q29del"

<400> 2183
Lys Pro Gly Gln Pro Gln Pro Gln His His His Ser His His His Pro
1 5 10 15

His His His Pro Gln Gln Gln Gln Gln Pro His His His His His Tyr
20 25 30

Tyr Phe Tyr Asn His Ser His Asn His His His His His His His Gln
35 40 45

Gln Pro His Gln Tyr
50

<210> 2184
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.L135fs"

<400> 2184
Asp Ala Ile Val Asp Leu Ile His Asp Ile Gln Ile Val Ser Thr Thr
1 5 10 15

Arg Glu Leu Tyr Leu Glu Asp Ser Pro Trp Ser
20 25

<210> 2185
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A302V"

<400> 2185
Phe Leu Thr Tyr Ile Ser Leu Leu His Ser Pro Gly Asn Ile Gly Lys
1 5 10 15

Leu Leu Gly Pro Leu Pro Met His Pro Val Val Ala Glu Asp Asn Tyr
20 25 30

Gly Tyr Asp Ala Cys Ala Val Leu Cys Leu Pro Cys Val Pro Asn Ile

35 40 45

Leu Val Ile Ala
50

<210> 2186
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E14K"

<400> 2186
Met Asp Thr Glu Gly Phe Gly Glu Leu Leu Gln Gln Ala Lys Lys Gln
1 5 10 15

Leu Ala Ala Glu Thr Glu Gly Ile Ser Glu Leu Pro His Val Glu Arg
20 25 30

Asn Leu Gln Glu Ile Gln Gln Ala
35 40

<210> 2187
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P480S"

<400> 2187
Asp Lys Ala Val Ser Tyr Thr Met Val Tyr Ser Ala Val Lys Val Thr
1 5 10 15

Thr His Ser Val Leu Pro Ala Gly Pro Ser Ser Leu Gly Ala Gly Glu
20 25 30

Pro Lys Thr Glu Lys Glu Ile Ser Val Leu His Gly Met Leu Cys Thr
35 40 45

Ser Ser Arg Pro
    50

<210> 2188
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P437L"

<400> 2188
Ser Ser Pro Pro Pro Pro Ser Thr Leu Tyr Arg Thr Gln Ser Pro His
1   5   10   15

Gly Tyr Pro Lys Ser His Ser Thr Ser Leu Leu Ser Pro Val Ser Met
            20   25   30

Gly Arg Ser Leu Thr Pro Leu Ser Leu Lys Arg Pro Pro Pro Tyr Asp
        35   40   45

Ala Val His Ser
    50

<210> 2189
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R197Q"

<400> 2189
Arg Thr Glu Ala Ser Ala Lys Pro Arg Pro His Ser Asp Glu Tyr Ser
1   5   10   15

Lys Lys Ile Pro Pro Pro Lys Pro Lys Gln Gln Asn Pro Asn Thr Gln
            20   25   30

Leu Ser Thr Ser Phe Asp Glu Thr Tyr Ile Lys Lys His Gly Pro Arg
35 40 45

Arg Thr Ser Leu
50

<210> 2190
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G113fs"

<400> 2190
Ala Phe Leu Gly Ala Gln Gly Leu Phe Leu Asp Cys Leu Cys Trp Ser
1 5 10 15

Thr Leu Ala Tyr Leu Val Pro Gly Pro Leu Ala Pro
20 25

<210> 2191
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R4516W"

<400> 2191
Leu Leu Leu Arg Ser Ala Gln Pro His His Ala Gly Glu Val Thr Phe
1 5 10 15

Ala Cys Arg Asp Ala Val Ala Ser Ala Trp Trp Leu Thr Val Leu Gly
20 25 30

Leu Pro Asp Pro Pro Glu Asp Ala Glu Val Val Ala Arg Ser Ser His
35 40 45

Thr Val Thr Leu
    50

<210> 2192
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A908T"

<400> 2192
Val Ser Glu Pro Lys Val Val Phe Ala Lys Glu Gln Leu Ala Arg Arg
1   5   10   15

Lys Leu Gln Ala Glu Ala Gly Ala Ser Thr Thr Thr Leu Ser Cys Glu
            20   25   30

Val Ala Gln Ala Gln Thr Glu Val Thr Trp Tyr Lys Asp Gly Lys Lys
        35   40   45

Leu Ser Ser Ser Ser
    50

<210> 2193
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G997fs"

<400> 2193
Leu Asp Val Lys Glu Pro Lys Val Val Phe Ala Lys Asp Gln Val Ala
1   5   10   15

His Ser Glu Val Gln Ala Glu Ala Gly Gly Gln Cys His Ala Glu Leu
            20   25   30

Arg Gly Gly Pro Gly Pro Asp Gly Gly Asp Val Val Gln Arg Trp Glu

35 40 45

Glu Ala Glu Leu Gln Leu Glu Ser Ala Cys Arg Gly Gln Gly Leu Gln
50 55 60

Thr Glu Ala Gly Gly Ala Ala Gly Arg Gln Asp Arg Cys Arg Gly Leu
65 70 75 80

Gln Leu Arg Gly Gln Gly Pro Glu Gly Leu Leu Pro Pro Ala His His
85 90 95

Arg Ala Gln Asp Asp Val Cys Lys Gly Ala Val Ser Ala
100 105

<210> 2194
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1642K"

<400> 2194
Arg Cys Ala Ala Arg Leu Ile Val Arg Glu Val Pro Val Thr Ile Val
1 5 10 15

Arg Gly Pro His Asp Leu Glu Val Thr Lys Lys Gly Asp Thr Ala Thr
20 25 30

Phe Glu Cys Glu Leu Ser Gln Ala Leu Ala Asp Val Thr Trp Glu Lys
35 40 45

Asp Gly Asn Ala
50

<210> 2195
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K407fs"

<400> 2195
Thr Thr Leu Ala Ala Leu Lys Asp Glu Val Val Ser Val Glu Asn Glu
1 5 10 15

Leu Ser Glu Leu Gln Glu Val Glu Lys Asn Arg Lys Pro Leu Leu Lys
20 25 30

Cys Ile Lys Leu Arg Tyr Lys Ser Cys Lys Lys Gln Leu Lys
35 40 45

<210> 2196
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E294K"

<400> 2196
Asp Gln Glu Ala Lys Leu Ser Glu Thr Ile Ser Ala Ser Asn Ala Trp
1 5 10 15

Lys Ser His Tyr Glu Lys Ile Val Ile Lys Lys Lys Thr Glu Leu Glu
20 25 30

Val Gln Ile Glu Thr Met Lys Lys Gln Ile Ile Asn Leu Leu Glu Asp
35 40 45

Leu Lys Lys Met
50

<210> 2197
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R61C"

<400> 2197
Thr Gly Glu Leu Gly Gln Asp Gly Arg Leu Leu Ser Ser Thr Leu Ser
1 5 10 15

Leu Ser Ser Asn Arg Ser Leu Gly Gln Cys Cys Gln Asn Ser Pro Leu
20 25 30

Pro Phe Gln Trp Arg Ile Thr His Ser Phe Arg Trp Met Ala Gln Val
35 40 45

Leu Ala Ser Glu
50

<210> 2198
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R366M"

<400> 2198
His Leu Phe Gly Leu Thr Trp Gln Leu Gln Pro Val Glu Gly Glu Leu
1 5 10 15

Tyr Ala Asn Gly Val Ser Lys Gly Asn Met Met Gly Thr Glu Ser Met
20 25 30

Asp Thr Thr Tyr Ser Pro Ile Gly Gly Lys Val Ser Asp Lys Ser Glu
35 40 45

Lys Lys Val Phe
50

<210> 2199
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R2556W"

<400> 2199
Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala Asp Ile
1 5 10 15

Ile Gly Val Ala Asn Glu Asp Ser Arg Trp Trp Leu Ala Ala Ile Leu
20 25 30

Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Arg
35 40 45

Asp Thr His Tyr
50

<210> 2200
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.W628fs"

<400> 2200
Lys Ala Ala Cys Pro Val Leu Cys Ser Gly Asn Gly Gln Tyr Ser Lys
1 5 10 15

Gly Thr Cys Gln Cys Tyr Ser Gly Trp Glu Arg Cys Arg Val Arg Arg
20 25 30

Ala His Glu Ser Val His Arg Ser Phe Leu Arg Gly Pro Arg Leu Leu
35 40 45

His

<210> 2201
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P218Q"

<400> 2201
Ser Ala Gln His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu
1 5 10 15

Thr Asn Arg Arg Asn Gln Ser Pro Ala Gln Gln Pro Ala Ala Leu Pro
20 25 30

Ala Glu Leu Gln Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp
35 40 45

Val Leu Gly Ser
50

<210> 2202
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I78fs"

<400> 2202
Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp Leu Glu Asn Pro Lys Ser
1 5 10 15

Val His Lys Ser Trp Asp Ile Phe Phe Ala Thr Arg Met Pro Glu Pro
20 25 30

His Arg Ala Leu Pro Thr Arg Val Pro Phe Pro
35 40

<210> 2203
<211> 27
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.Y948fs"

<400> 2203
Val Ala Ile Thr Arg Ile Glu Gln Leu Ser Pro Phe Pro Phe Asp Leu
1 5 10 15

Leu Leu Lys Glu Val Gln Lys Tyr Pro Gln Cys
20 25

<210> 2204
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A427T"

<400> 2204
Thr Lys Ala Glu Gln Phe Tyr Arg Gly Asp Ala Gln Gly Lys Lys Val
1 5 10 15

Met Ser Ile Leu Val His Gly Asp Ala Thr Thr Phe Ala Gly Gln Gly
20 25 30

Val Val Tyr Glu Thr Phe His Leu Ser Asp Leu Pro Ser Tyr Thr Thr
35 40 45

Asn Gly Thr Val
50

<210> 2205
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R57C"

<400> 2205
Arg Leu Leu Pro Ser Arg Leu Gly Val Gln Ala Ala Arg Leu Leu Ala
1 5 10 15

Ala His Asp Val Pro Val Phe Gly Trp Cys Cys Ser Arg Ser Ser Gly
20 25 30

Pro Pro Ala Thr Phe Pro Ser Ser Lys Gly Gly Gly Gly Ser Ser Tyr
35 40 45

Met Glu Glu Met
50

<210> 2206
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G477fs"

<400> 2206
Ser Lys Ala Glu Phe Ala Leu Asp Leu Ile Leu Tyr Cys Gly Cys Glu
1 5 10 15

Gly Trp Glu Pro Glu Tyr Gly Gly Phe Phe Phe Leu Leu Leu Thr Leu
20 25 30

Pro Lys Val Lys Met Lys Ser Cys
35 40

<210> 2207
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.S557T"

<400> 2207
Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala
1 5 10 15

Gly Pro Ala Gly Asp Glu Pro Ala Glu Thr Thr Pro Ser Glu Thr Pro
20 25 30

Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro
35 40 45

Ser Glu Thr Pro
50

<210> 2208
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R508S"

<400> 2208
Phe Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys Arg Val Leu
1 5 10 15

Val Cys Gly Val Leu Asp Glu Arg Ser Ser Ser Cys Ala Gln Gly Cys
20 25 30

His Arg Arg Met Arg Arg Gly Ala Gly Gly Glu Asp Ser Ala Gly Leu
35 40 45

Gln Gly Gln Thr
50

<210> 2209
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K132N"

<400> 2209
His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val Arg Glu
1 5 10 15

Tyr Val Gln Leu Ile Ser Val Tyr Glu Asn Asn Lys Leu Leu Asn Leu
            20 25 30

Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser Tyr Thr Glu
        35 40 45

Leu Asp Phe Glu
    50

<210> 2210
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R445Q"

<400> 2210
Met Glu Phe Val Asp Ser Leu His Gly Gln Pro Lys Met Pro Glu Trp
1 5 10 15

Leu Ser Thr His Pro Ser His Gly Asn Gln Gln Val Glu Tyr Leu Asp
            20 25 30

Arg Leu Ile Pro Gln Ala Leu Lys Ile Arg Glu Met Cys Asn Cys Pro
        35 40 45

Pro Leu Ser Asn
    50

<210> 2211
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L424M"

<400> 2211
Thr Leu His Ala Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Leu
1 5 10 15

Gln Ile Thr Ile Ser Gln Gln Leu Gly Met Met Glu Leu Ser Thr Val
20 25 30

Ser Asn Phe Phe Met Asn Ala Arg Arg Arg Ser Leu Asp Lys Trp Gln
35 40 45

Asp Glu Gly Ser
50

<210> 2212
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R101C"

<400> 2212
Thr Ser Gln Ala Leu Leu Thr Val Asp Ile Val Asp Ser Gly Asn Leu
1 5 10 15

Val Glu Ile Thr Val Phe Gly Arg Pro Cys Cys Val Gln Asn Arg Val
20 25 30

Lys Ser Met Leu Leu Cys Leu Ala Trp Phe His Arg Glu His Arg Ala
35 40 45

Arg Ala Glu Lys
50

<210> 2213
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A900D"

<400> 2213
Gln Gln Glu Gly Ala Val Phe Leu Ser Phe Lys Leu Val Gln Gly Gly
1 5 10 15

Val Phe Gln Glu Glu Ala Val Thr Glu Asp Asp Leu Arg Ala Pro Gly
20 25 30

Lys Val Pro Asn Cys Ser Gly Thr Arg Asn Leu His Asp Asn Leu Ser
35 40 45

Asp Leu Arg Ala
50

<210> 2214
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P283H"

<400> 2214
Ser Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Val Val Met
1 5 10 15

Ile Phe Ala Tyr Cys Val Cys Trp Gly His His Tyr Thr Phe Phe Ala
20 25 30

Cys Phe Ala Ala Ala Asn Pro Gly Tyr Ala Phe His Pro Leu Met Ala
35 40 45

Ala Leu Pro Ala
50

<210> 2215
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A285T"

<400> 2215
Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Val Val Met Val Leu
1 5 10 15

Ala Phe Cys Phe Cys Trp Gly Pro Tyr Thr Thr Phe Phe Ala Cys Phe
20 25 30

Ala Ala Ala Asn Pro Gly Tyr Pro Phe His Pro Leu Met Ala Ala Leu
35 40 45

Pro Ala Phe Phe
50

<210> 2216
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C27F"

<400> 2216
Glu Pro Ala Pro Ser Ala Gly Ala Glu Leu Gln Pro Pro Leu Phe Ala
1 5 10 15

Asn Ala Ser Asp Ala Tyr Pro Ser Ala Phe Phe Pro Ser Ala Gly Ala
20 25 30

Asn Ala Ser Gly Pro Pro Gly Ala Arg Ser Ala Ser Ser Leu Ala Leu
35 40 45

Ala Ile Ala Ile

50

<210> 2217
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R353H"

<400> 2217
Lys Ile Cys Val Phe Ile Phe Ala Phe Ile Met Pro Val Leu Ile Ile
1 5 10 15

Thr Val Cys Tyr Gly Leu Met Ile Leu His His Leu Lys Ser Val Arg
20 25 30

Met Leu Ser Gly Ser Lys Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr
35 40 45

Arg Met Val Leu
50

<210> 2218
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R462C"

<400> 2218
Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn
1 5 10 15

Ile Glu Gln Gln Asn Ser Thr Arg Ile Cys Cys Gln Asn Thr Arg Asp
20 25 30

His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu
35 40 45

Asn Leu Glu Ala
50

<210> 2219
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P24fs"

<400> 2219
Met Ser His Gln Pro Leu Ser Cys Leu Thr Glu Lys Glu Asp Ser Pro
1 5 10 15

Ser Glu Ser Thr Gly Asn Gly Pro Pro Thr Trp Pro Thr Gln Thr Trp
20 25 30

Thr Arg Leu Pro Arg Arg Ser Cys Cys Ser Arg
35 40

<210> 2220
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F73V"

<400> 2220
Ile Ile Ser Leu Asn Gln Ser Leu His Val Pro Met Tyr Leu Phe Leu
1 5 10 15

Leu Asn Leu Ser Val Val Glu Val Ser Val Val Ser Ala Val Ile Thr
20 25 30

Pro Glu Met Leu Val Val Leu Ser Thr Glu Lys Thr Met Ile Ser Phe
35 40 45

Val Gly Cys Phe
    50

<210> 2221
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S93Y"

<400> 2221
Val Val Glu Val Ser Phe Ser Ala Val Ile Thr Pro Glu Met Leu Val
1   5   10   15

Val Leu Ser Thr Glu Lys Thr Met Ile Tyr Tyr Phe Val Gly Cys Phe
            20   25   30

Ala Gln Met Tyr Phe Ile Leu Leu Phe Gly Gly Thr Glu Cys Phe Leu
        35   40   45

Leu Gly Ala Met
    50

<210> 2222
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.M199I"

<400> 2222
Val Ile His His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala
1   5   10   15

Cys Glu Asn Lys Thr Ser Ser Val Ile Ile Ile Gly Val Met Leu Val
            20   25   30

Cys Val Thr Ala Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr
35 40 45

Val Phe Ile Val
50

<210> 2223
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L157Q"

<400> 2223
Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Met Val Ile Met
1 5 10 15

Asn Lys Arg Leu Arg Ile Gln Leu Val Gln Gln Gly Ala Cys Ser Ile
20 25 30

Gly Leu Ile Val Ala Ile Thr Gln Val Thr Ser Val Phe Arg Leu Pro
35 40 45

Phe Cys Ala Arg
50

<210> 2224
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R244Q"

<400> 2224
Val Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr
1 5 10 15

Ile Leu Lys Ile Ala Ser Val Glu Gly Gln Gln Lys Lys Ala Phe Ala

20 25 30

Thr Cys Ala Ser His Leu Thr Val Val Ile Val His Tyr Ser Cys Ala
35 40 45

Ser Ile Ala Tyr
50

<210> 2225
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L298I"

<400> 2225
Ile Val Tyr Leu Lys Pro Glu Ala Ser Gly Asp Asp Thr Leu Ile Ala
1 5 10 15

Val Pro Tyr Thr Val Ile Thr Pro Phe Ile Ile Ser Pro Ile Ile Phe
20 25 30

Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly
35 40 45

Asn Thr Val Ala
50

<210> 2226
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L205F"

<400> 2226
Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr Gly Pro Ser
1 5 10 15

Glu Leu Arg Ile Phe Ile Leu Ser Leu Phe Phe Val Leu Leu Val Ser
            20   25   30

Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala Ile Leu
        35   40   45

Arg Ile Pro Ser
    50

<210> 2227
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.H154P"

<400> 2227
Leu Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Ala Ile Cys Arg Pro
1   5   10   15

Leu Leu Tyr Pro Asn Ile Met Thr Gly Pro Pro Leu Cys Ala Lys Leu
            20   25   30

Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Ile
        35   40   45

Val Leu Ile Ser
    50

<210> 2228
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.L9V"

<400> 2228
Met Glu Trp Glu Asn His Thr Ile Val Val Val Glu Phe Phe Leu Lys
1 5 10 15

Gly Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile
20 25 30

Phe Ile Met
35

<210> 2229
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R258H"

<400> 2229
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Thr Leu Tyr
1 5 10 15

Tyr Ser Pro Val Ile Tyr Thr Tyr Ile His His Pro Ala Ser Ser Tyr
20 25 30

Thr Phe Glu Arg Asp Lys Val Val Ala Ala Leu Tyr Thr Leu Val Thr
35 40 45

Pro Thr Leu Asn
50

<210> 2230
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="p.G160C"

<400> 2230

Asp Arg Ser Thr Cys Val Gln Arg Ala Thr Val Ser Trp Leu Tyr Gly
1 5 10 15

Gly Leu Ile Ala Val Met His Thr Ala Cys Cys Thr Phe Ser Leu Ser
20 25 30

Tyr Cys Gly Ser Asn Met Val His Gln Phe Phe Cys Asp Ile Pro Gln
35 40 45

Leu Leu Ala Ile
50

<210> 2231
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V69I"

<400> 2231
Leu Ile Ile Leu Ala Ile Ser Ile Asp Ser His Leu His Thr Pro Met
1 5 10 15

Tyr Phe Phe Leu Ala Asn Leu Ser Leu Ile Ile Asp Phe Cys Leu Ala
20 25 30

Thr Asn Thr Ile Pro Lys Met Leu Val Ser Leu Gln Thr Gly Ser Lys
35 40 45

Ala Ile Ser Tyr
50

<210> 2232
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M80I"

<400> 2232
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asp Ile
1 5 10 15

Ala Cys Ala Cys Ser Thr Val Pro Gln Ile Ile Leu Val Asn Leu Leu
20 25 30

His Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met Thr Gln Met Phe
35 40 45

Leu Phe Leu Ser
50

<210> 2233
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S105C"

<400> 2233
Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly
1 5 10 15

Cys Met Thr Gln Met Phe Leu Phe Leu Cys Cys Phe Ala His Thr Glu
20 25 30

Cys Leu Leu Leu Val Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys
35 40 45

His Pro Leu Arg
50

<210> 2234
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S71L"

<400> 2234
Gly Leu Ile Trp Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe
1 5 10 15

Leu Ser His Leu Ala Ile Ile Asp Ile Leu Leu Tyr Ala Ser Asn Asn
20 25 30

Val Pro Lys Met Leu Thr Asn Leu Gly Leu Asn Lys Arg Lys Thr Ile
35 40 45

Ser Phe Val Pro
50

<210> 2235
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G249W"

<400> 2235
Thr Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val
1 5 10 15

Thr Cys Ser Ser His Leu Ile Val Val Trp Trp Met Phe Tyr Gly Ala
20 25 30

Ala Thr Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln
35 40 45

Asp Asn Ile Ile
50

<210> 2236
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.W37C"

<400> 2236
Leu Val Ser Ala Met Lys Thr Gly Asn Gln Ser Phe Gly Thr Asp Phe
1 5 10 15

Leu Leu Val Gly Leu Phe Gln Tyr Gly Cys Cys Ile Asn Ser Leu Leu
20 25 30

Phe Val Val Ile Ala Thr Leu Phe Thr Val Ala Leu Thr Gly Asn Ile
35 40 45

Met Leu Ile His
50

<210> 2237
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> source
<223> /note="p.V45I"

<400> 2237
Asn Gln Ser Phe Gly Thr Asp Phe Leu Leu Val Gly Leu Phe Gln Tyr
1 5 10 15

Gly Trp Ile Asn Ser Leu Leu Phe Val Ile Ile Ile Ala Thr Leu Phe
20 25 30

Thr Val Ala Leu Thr Gly Asn Ile Met Leu Ile His Leu Ile Arg Leu
35 40 45

Asn Thr Arg Leu
50

<210> 2238
<211> 36
<212> PRT
<213> Artificial Sequence

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polypeptide"

<220>
<221> source
<223> /note="p.G10V"

<400> 2238
Met Lys Ser Asp Asn His Ser Phe Leu Val Val Asp Ser Pro Lys Ala
1 5 10 15

Phe Ile Leu Leu Gly Val Ser Asp Arg Pro Trp Leu Glu Leu Pro Leu
20 25 30

Phe Val Val Leu
35

<210> 2239
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.V287I"

<400> 2239
Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe Gly Leu Phe Tyr Ala
1 5 10 15

Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Ile Tyr Thr Leu Arg Asn
20 25 30

Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly Lys Glu Arg Asp
35 40 45

Ser Arg Glu Ser
50

<210> 2240
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L205F"

<400> 2240
Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu Ile
1 5 10 15

Gln Val Ala Val Ala Ser Val Phe Ile Phe Phe Val Val Pro Leu Ser
20 25 30

Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu Arg Ile
35 40 45

Asn Ser Ala Lys
50

<210> 2241
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G234W"

<400> 2241
Leu Ile Pro Leu Ile Leu Ile Leu Thr Thr Tyr Gly Ala Ile Ala Arg
1 5 10 15

Ala Val Leu Ser Met Gln Ser Thr Thr Trp Trp Leu Gln Lys Val Phe
20 25 30

Arg Thr Cys Gly Ala His Leu Met Val Val Ser Leu Phe Phe Ile Pro
35 40 45

Val Met Cys Met
50

<210> 2242
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M106I"

<400> 2242
Ala Tyr Asn Phe Leu Ser Gly Gln Lys Gly Ile Ser Phe Leu Gly Cys
1 5 10 15

Gly Val Gln Ser Phe Phe Phe Leu Thr Ile Ile Ala Cys Ser Glu Gly
20 25 30

Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys His
35 40 45

Ser Leu Tyr Tyr
50

<210> 2243
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T242A"

<400> 2243
Cys Gly Arg Val Leu Phe Ala Val Tyr His Met His Ser Lys Glu Gly
1 5 10 15

Arg Lys Lys Ala Phe Thr Thr Ile Ser Ala Ala His Leu Thr Val Val
20 25 30

Ile Phe Tyr Tyr Ala Pro Phe Val Tyr Thr Tyr Leu Arg Pro Arg Asn
35 40 45

Leu Arg Ser Pro
50

<210> 2244
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L67I"

<400> 2244
Leu Ser Met Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro
1 5 10 15

Met Tyr Phe Leu Leu Ser Gln Leu Ser Ile Ile Ile Asp Leu Asn Tyr
20 25 30

Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp Phe Leu Ser Gly Asn
35 40 45

Lys Ser Ile Ser
50

<210> 2245
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.M1I"

<400> 2245
Ile Ile Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly
1 5 10 15

Phe Phe Pro Pro Ser Arg Ile Gly Leu Phe Leu
20 25

<210> 2246
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K294R"

<400> 2246
Glu Asp Lys Val Leu Ala Val Phe Tyr Thr Thr Leu Thr Pro Met Leu
1 5 10 15

Asn Pro Ile Ile Tyr Ser Leu Arg Asn Arg Arg Glu Val Met Gly Ala
20 25 30

Leu Thr Arg Val Ser Gln Arg Ile Cys Ser Gly Lys Met
35 40 45

<210> 2247
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R121C"

<400> 2247
Cys Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala
1 5 10 15

Leu Leu Leu Ala Ser Met Ala Tyr Asp Cys Cys Tyr Ile Ala Ile Cys
20 25 30

Phe Pro Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu
35 40 45

Met Ile Thr Gly
50

<210> 2248
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R171S"

<400> 2248
Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr
1 5 10 15

Val Leu His Ile Pro Tyr Cys Arg Ser Ser Ser Ala Ile Asn His Phe
20 25 30

Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
35 40 45

Val Tyr Glu Gly
50

<210> 2249
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S201fs"

<400> 2249
Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
1 5 10 15

Val Tyr Glu Gly Thr Val Phe Leu Ser His His Leu Ser Arg Val Ser
20 25 30

Leu His Trp Tyr Phe Met Phe Leu Trp Pro Gly Ser Leu Cys Cys Leu
35 40 45

Pro His Glu Ile Cys Arg Arg Glu Glu Glu Ser Leu Phe Asp Leu Gln
50 55 60

His Pro Pro His Cys Ser Asn Phe Leu Leu Cys Thr Phe Cys Leu His
65 70 75 80

Leu Ser Thr Ser Lys Ile Pro Ala Ile Ser Asn Arg Gly Gln Gly Ser
85 90 95

Gly Cys Leu Leu His His Pro His Pro Asn Ala Gln Pro His His Leu
100 105 110

<210> 2250
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A95fs"

<400> 2250
Asp Leu Met Leu Ile Cys Thr Thr Val Pro Lys Met Ala Phe Asn Tyr
1 5 10 15

Leu Ser Gly Ser Lys Ser Ile Ser Met Val Val Val Ser His Lys Phe
20 25 30

Ser Ser Ile Tyr His Cys Leu Ala Leu Asn Val Phe Phe Trp Leu Leu
35 40 45

Trp Leu Met Thr Ala Ile Leu Leu Phe Ala Thr Leu
50 55 60

<210> 2251
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F177L"

<400> 2251
Gly Ser Thr Asp Gly Ile Ile Asp Ala Val Ala Thr Phe Ser Phe Ser
1 5 10 15

Phe Cys Gly Ser Arg Glu Ile Ala His Leu Leu Phe Cys Glu Phe Pro
20 25 30

Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe Glu Glu Val
35 40 45

Ile Phe Ile Cys
50

<210> 2252
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F323L"

<400> 2252
Thr Arg Ala Phe Met Lys Ile Leu Gly Lys Gly Lys Ser Glu Ser Glu
1 5 10 15

Leu Pro His Lys Leu Tyr Val Leu Leu Leu Leu Ala Lys Phe Phe Phe
20 25 30

Leu Ile Ser Ile Phe Phe Tyr Asp Val Lys Ile Leu Ala Leu Ile Met
35 40 45

Tyr Ile Ala
50

<210> 2253
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R235H"

<400> 2253

Pro Val Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val
1 5 10 15

Ile His Met Gly Ser Gly Glu Gly Arg His His Lys Ala Phe Thr Thr
20 25 30

Cys Ser Ser His Leu Leu Val Val Gly Met Tyr Tyr Gly Ala Ala Leu
35 40 45

Phe Met Tyr Ile
50

<210> 2254
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M273I"

<400> 2254
Val Gly Met Tyr Tyr Gly Ala Ala Leu Phe Met Tyr Ile Arg Pro Thr
1 5 10 15

Ser Asp Arg Ser Pro Thr Gln Asp Lys Ile Ile Val Ser Val Phe Tyr
20 25 30

Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn
35 40 45

Lys Glu Val Thr
50

<210> 2255
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.V205L"

<400> 2255
Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
1 5 10 15

Glu Lys Val Leu Phe Ile Cys Cys Ile Leu Leu Met Ile Val Phe Pro
20 25 30

Val Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile
35 40 45

His Met Gly Ser
50

<210> 2256
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R184H"

<400> 2256
Val Ala Thr Leu Ser Phe Pro Tyr Cys Gly Ala His Glu Ile Asp His
1 5 10 15

Phe Phe Cys Glu Ala Pro Val Leu Val His His Leu Ala Cys Ala Asp
20 25 30

Thr Ser Val Phe Glu Asn Ala Met Tyr Ile Cys Cys Val Leu Met Leu
35 40 45

Leu Val Pro Phe
50

<210> 2257
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M258L"

<400> 2257
Lys Lys Ala Phe Ala Thr Cys Ser Ser His Val Ala Val Val Gly Leu
1 5 10 15

Phe Tyr Gly Ala Gly Ile Phe Thr Tyr Leu Leu Arg Pro Lys Ser His
20 25 30

Arg Ser Thr Asn His Asp Lys Val Val Ser Ala Phe Tyr Thr Met Phe
35 40 45

Thr Pro Leu Leu
50

<210> 2258
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F13V"

<400> 2258
Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Val Val Val Leu
1 5 10 15

Thr Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile
20 25 30

Val Phe Ser Ile Phe Val Val
35

<210> 2259
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D11Y"

<400> 2259
Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Tyr Tyr Phe Ile Leu Leu
1 5 10 15

Gly Leu Phe Ser Asn Ala Arg Phe Pro Trp Leu Leu Phe Ala Leu Ile
20 25 30

Leu Leu Val Phe Leu
35

<210> 2260
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R120S"

<400> 2260
Cys Gly Val Gln Ile Phe Phe Leu Pro Thr Leu Gly Gly Gly Glu Cys
1 5 10 15

Phe Leu Leu Ala Ala Met Ala Tyr Asp Ser Ser Tyr Ala Ala Val Cys
20 25 30

His Pro Leu Arg Tyr Pro Thr Leu Met Ser Trp Gln Leu Cys Leu Arg
35 40 45

Met Thr Met Ser
50

<210> 2261
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P165Q"

<400> 2261
Leu Arg Met Thr Met Ser Cys Trp Leu Leu Gly Ala Ala Asp Gly Leu
1 5 10 15

Leu Gln Ala Val Val Thr Leu Ser Phe Gln Gln Tyr Cys Gly Ala His
20 25 30

Glu Ile Asp His Phe Phe Cys Glu Thr Pro Val Leu Val Arg Leu Ala
35 40 45

Cys Ala Asp Thr
50

<210> 2262
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C246F"

<400> 2262
Ser Ser Tyr Thr Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala
1 5 10 15

Ala Gly Arg Arg Lys Ala Leu Ala Thr Phe Phe Ser Ser His Met Ile
20 25 30

Ile Val Leu Leu Leu Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Arg
35 40 45

Ser Ser Tyr His
50

<210> 2263
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V137L"

<400> 2263
Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Ile Ser Ala Pro
1 5 10 15

Glu Cys Gly Met Gln Met Phe Phe Tyr Leu Leu Thr Leu Ala Gly Ser
            20 25 30

Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile
        35 40 45

Cys His Pro Leu Arg
    50

<210> 2264
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V213L"

<400> 2264
Ala Cys Gly Asp Lys Thr Thr Tyr Glu Thr Val Met Tyr Val Cys Cys
1 5 10 15

Val Ala Met Leu Leu Ile Pro Phe Ser Leu Leu Val Thr Ala Ser Tyr
            20 25 30

Thr Arg Ile Leu Ile Thr Val His Gln Met Thr Ser Ala Glu Gly Arg
        35 40 45

Lys Lys Ala Phe
    50

<210> 2265
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F248L"

<400> 2265
Leu Lys Asn Asn Ser Leu Glu Gly Arg Cys Lys Ala Leu Ser Thr Cys
1 5 10 15

Ile Ser His Ile Ile Val Val Val Leu Leu Leu Phe Val Pro Cys Ile
20 25 30

Phe Val Tyr Leu Arg Ser Val Thr Thr Leu Pro Ile Asp Lys Ala Val
35 40 45

Ala Val Phe Tyr
50

<210> 2266
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M279I"

<400> 2266
Phe Val Tyr Leu Arg Ser Val Thr Thr Leu Pro Ile Asp Lys Ala Val
1 5 10 15

Ala Val Phe Tyr Thr Met Val Val Pro Ile Ile Leu Asn Pro Val Val
20 25 30

Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp
35 40 45

Arg Lys Lys Val
50

<210> 2267
<211> 27
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.D309Y"

<400> 2267
Val Tyr Thr Leu Arg Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu
1 5 10 15

Trp Arg Lys Lys Val Thr Ser Asp Asn Tyr Tyr
20 25

<210> 2268
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y63F"

<400> 2268
Leu Gly Asn Leu Leu Ile Ile Ile Ser Val Lys Thr Ser Gln Ala Leu
1 5 10 15

Lys Asn Pro Met Phe Phe Phe Leu Phe Phe Phe Leu Ser Leu Ser Asp
20 25 30

Thr Cys Leu Ser Thr Ser Ile Thr Pro Arg Met Ile Val Asp Ala Leu
35 40 45

Leu Lys Lys Thr
50

<210> 2269
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.S135R"

<400> 2269
Ile Phe Ile Leu Ile Leu Thr Ala Val Asp Arg Tyr Val Asp Ile Cys
1 5 10 15

Lys Pro Leu His Tyr Met Thr Ile Ile Arg Arg Gln Trp Val Cys Gly
20 25 30

Val Leu Met Ala Val Ala Trp Val Gly Ser Cys Val His Ser Leu Val
35 40 45

Gln Ile Phe Leu
50

<210> 2270
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L162M"

<400> 2270
Trp Val Cys Gly Val Leu Met Ala Val Ala Trp Val Gly Ser Cys Val
1 5 10 15

His Ser Leu Val Gln Ile Phe Leu Ala Met Met Ser Leu Pro Phe Cys
20 25 30

Gly Pro Asn Val Ile Asn His Cys Phe Cys Asp Leu Gln Pro Leu Leu
35 40 45

Lys Gln Ala Cys
50

<210> 2271
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.H130fs"

<400> 2271
Ile Ala Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys
1 5 10 15

Met Ala Gln Leu Phe Gly Ala His Phe Phe Gly Arg Cys
20 25

<210> 2272
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R226Q"

<400> 2272
Thr Asn Ser Gly Thr Ile Ser Leu Ser Cys Phe Leu Ala Val Val Thr
1 5 10 15

Ser Tyr Met Val Ile Leu Val Ser Leu Gln Gln Lys His Ser Ala Glu
20 25 30

Gly Arg Gln Lys Ala Leu Ser Thr Cys Ser Ala His Phe Met Val Val
35 40 45

Ala Leu Phe Phe
50

<210> 2273
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.C254F"

<400> 2273
Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr Ala His Phe
1 5 10 15

Ile Val Val Phe Leu Phe Phe Gly Pro Phe Phe Ile Phe Ile Tyr Met
20 25 30

Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser Val Phe Tyr
35 40 45

Thr Ile Phe Thr
50

<210> 2274
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F177fs"

<400> 2274
Val His Thr Leu Ser Gln Leu Ser Phe Thr Val Asn Leu Pro Phe Cys
1 5 10 15

Gly Pro Asn Val Val Asp Ser Phe Phe Val Ile Phe Leu Glu Ser Pro
20 25 30

Asn Leu Pro Ala Trp Thr Leu Thr Ser Leu Lys Tyr
35 40

<210> 2275
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G41E"

<400> 2275
Gly Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe
1 5 10 15

Leu Ser Phe Tyr Leu Phe Ile Leu Pro Glu Glu Asn Ile Leu Ile Ile
20 25 30

Cys Thr Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu
35 40 45

Leu Ala Asn Leu
50

<210> 2276
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A119S"

<400> 2276
Phe Asp Gly Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala
1 5 10 15

Ser Glu Met Phe Leu Leu Thr Val Met Ser Ser Phe Asp Leu Tyr Thr
20 25 30

Ala Ile Cys Arg Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu
35 40 45

Cys Cys Ile Leu
50

<210> 2277
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.A161S"

<400> 2277
Met Asn Gln Arg Leu Cys Cys Ile Leu Val Ala Leu Ser Trp Arg Gly
1 5 10 15

Gly Phe Ile His Ser Ile Ile Gln Val Ser Ser Leu Ile Val Arg Leu
20 25 30

Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser Tyr Phe Cys Asp Ile Thr
35 40 45

Gln Val Val Arg
50

<210> 2278
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S268F"

<400> 2278
Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser Ile Tyr
1 5 10 15

Ile Tyr Ala Arg Pro Phe Asp Ser Phe Phe Phe Leu Asp Lys Val Val
20 25 30

Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile Tyr
35 40 45

Thr Leu Arg Asn
50

<210> 2279
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.G41E"

<400> 2279
Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Val
1 5 10 15

Leu Ile Phe Tyr Phe Ile Ile Leu Pro Glu Glu Asn Phe Leu Ile Ile
20 25 30

Phe Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe
35 40 45

Leu Gly Asn Leu
50

<210> 2280
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L150fs"

<400> 2280
Ile Cys Arg Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys
1 5 10 15

Tyr Ala Met Met Leu Ala Leu Trp Leu Trp Gly Phe Cys Pro Leu His
20 25 30

Tyr Pro Gly Gly Pro His Pro Pro Leu Ala Phe Leu Trp Pro Lys Pro
35 40 45

Ala Gly Gln Leu Leu Leu
50

<210> 2281
<211> 54

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L150fs"

<400> 2281
Ile Cys Arg Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys
1 5 10 15

Tyr Ala Met Met Leu Ala Leu Trp Leu Trp Gly Phe Cys Pro Leu His
20 25 30

Tyr Pro Gly Gly Pro His Pro Pro Leu Ala Phe Leu Trp Pro Lys Pro
35 40 45

Ala Gly Gln Leu Leu Leu
50

<210> 2282
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L124R"

<400> 2282
Ala Gln Glu Phe Phe Ile His Gly Phe Thr Val Met Glu Ser Ser Val
1 5 10 15

Leu Leu Ile Met Ser Leu Asp Arg Phe Arg Arg Ala Ile His Asn Pro
20 25 30

Leu Arg Tyr Ser Ser Ile Leu Thr Ser Asn Arg Val Ala Lys Met Gly
35 40 45

Leu Ile Leu Ala
50

<210> 2283
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S163L"

<400> 2283
Arg Val Ile Ala Leu Gly Val Gly Val Phe Leu Arg Gly Phe Val Ser
1 5 10 15

Ile Leu Pro Val Ile Leu Arg Leu Phe Leu Leu Phe Ser Tyr Cys Lys
20 25 30

Ser His Val Ile Thr Arg Ala Phe Cys Leu His Gln Glu Ile Met Arg
35 40 45

Leu Ala Cys Ala
50

<210> 2284
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A66fs"

<400> 2284
Gly Thr Leu Leu Leu Leu Ile Lys Glu Asp His Asn Leu His Glu Pro
1 5 10 15

Met Tyr Phe Phe Leu Ala Met Leu Ala Gly Pro Asp His Asn Ala His
20 25 30

Gly Ala Gly Ser Pro Leu Ala Gly Ser Gln Gly Asp Trp Lys Cys Gly
35 40 45

Leu Leu Phe Pro Gly Leu Leu Tyr Thr Leu Thr Phe Leu Ser Arg Val
50 55 60

Trp His Ser Ala Cys His Gly Leu
65 70

<210> 2285
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R67P"

<400> 2285
Ser Ile Pro Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser
1 5 10 15

Met Ile Leu Phe Val Val Leu Cys Glu Pro Pro Ser Leu His Lys Pro
20 25 30

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser
35 40 45

Leu Cys Thr Leu
50

<210> 2286
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R159Q"

<400> 2286
Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu Thr Asn Gly Val Ile
1 5 10 15

Ser Lys Ile Ser Leu Ala Ile Ser Phe Gln Gln Cys Leu Gly Leu His

20 25 30

Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr Cys Leu Pro Gln
35 40 45

Val Leu Thr His
50

<210> 2287
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P298T"

<400> 2287
Phe Gly Lys His Leu Ser Pro Val Ala His Val Leu Ile Gly Asn Ile
1 5 10 15

Tyr Ile Leu Phe Pro Pro Leu Met Asn Thr Thr Ile Ile Tyr Ser Val
20 25 30

Lys Thr Gln Gln Ile His Thr Arg Met Leu Arg Leu Phe Ser Leu Lys
35 40 45

Arg Tyr
50

<210> 2288
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R133C"

<400> 2288
Phe Val His Ala Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met
1 5 10 15

Ala Cys Asp Arg Ala Ala Ala Ile Gly Cys Cys Pro Leu His Tyr Pro
20 25 30

Val Leu Val Thr Lys Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Ala
35 40 45

Leu Lys Ala Val
50

<210> 2289
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K89N"

<400> 2289
Gln His Leu Ala Phe Val Asp Ile Cys Tyr Thr Ser Ala Ile Thr Pro
1 5 10 15

Lys Met Leu Gln Ser Phe Thr Glu Glu Asn Asn Asn Leu Met Leu Phe
20 25 30

Gln Gly Cys Val Ile Gln Phe Leu Val Tyr Ala Thr Phe Ala Thr Ser
35 40 45

Asp Cys Tyr Leu
50

<210> 2290
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M39I"

<400> 2290
Phe Val Gly Phe Thr Asp Tyr Leu Pro Leu Arg Val Thr Leu Phe Leu
1 5 10 15

Val Phe Leu Leu Val Tyr Thr Leu Thr Ile Ile Val Gly Asn Ile Leu
20 25 30

Leu Ile Ile Leu Val Asn Ile Asn Ser Ser Leu Gln Ile Pro Met Tyr
35 40 45

Tyr Phe Leu Ser
50

<210> 2291
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R312H"

<400> 2291
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Cys Leu Phe
1 5 10 15

Phe Gly Thr Thr Leu Phe Met Tyr Leu His His Pro Arg Ser Ser Tyr
20 25 30

Ser Leu Thr Gln Asp Arg Thr Val Ala Val Ile Tyr Thr Val Val Ile
35 40 45

Pro Val Leu Asn
50

<210> 2292
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.S289C"

<400> 2292
His Phe Met Gly Thr Asp Lys Met Ala Ser Val Phe Tyr Ala Ile Val
1 5 10 15

Ile Pro Met Leu Asn Pro Leu Val Tyr Cys Cys Leu Arg Asn Lys Glu
20 25 30

Val Lys Ser Ala Phe Lys Lys Thr Val Gly Lys Ala Lys Ala Ser Ile
35 40 45

Gly Phe Ile Phe
50

<210> 2293
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R163H"

<400> 2293
Val Cys Ala Cys Leu Ala Ile Gly Cys Tyr Val Ile Gly Phe Leu Asn
1 5 10 15

Ala Ser Ile Gln Ile Gly Asp Thr Phe His His Leu Ser Phe Cys Met
20 25 30

Ser Asn Val Ile His His Phe Phe Cys Asp Lys Pro Ala Val Ile Thr
35 40 45

Leu Thr Cys Ser
50

<210> 2294
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M266I"

<400> 2294
Ser His Leu Ile Ala Ile Phe Leu Phe Tyr Ile Thr Val Ile Ile Met
1   5   10   15

Tyr Ile Arg Pro Ser Ser Ser His Ser Ile Ile Asp Thr Asp Lys Ile
            20   25   30

Ala Ser Val Phe Tyr Thr Met Ile Ile Pro Met Leu Ser Pro Ile Val
        35   40   45

Tyr Thr Leu Arg
    50

<210> 2295
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R236C"

<400> 2295
Ser Ser Leu Ile Ile Ile Leu Thr Ser Tyr Met Leu Ile Phe Thr Thr
1   5   10   15

Ile Met Lys Met Arg Ser Ala Ser Gly Cys Cys Gln Lys Thr Phe Ser
            20   25   30

Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile
        35   40   45

Leu Phe Leu Tyr
    50

<210> 2296
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.H246N"

<400> 2296
Val Phe Ile Phe Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg
1 5 10 15

His Lys Ala Phe Ser Thr Trp Ala Ser Asn Asn Leu Thr Ser Ile Thr
20 25 30

Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys
35 40 45

Asn Ser Arg Gln
50

<210> 2297
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P264T"

<400> 2297
Val Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His
1 5 10 15

Gly Thr Ile Leu Phe Leu Tyr Cys Val Thr Thr Asn Ser Lys Asn Ser
20 25 30

Arg His Thr Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
35 40 45

Leu Leu Asn Pro
50

<210> 2298
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T271K"

<400> 2298
Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys
1 5 10 15

Val Pro Asn Ser Lys Asn Ser Arg His Lys Lys Val Lys Val Ala Ser
20 25 30

Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser
35 40 45

Leu Arg Asn Lys
50

<210> 2299
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G44V"

<400> 2299
Asp Thr Leu Glu Leu Gln Ile Ile Leu Phe Leu Phe Phe Leu Val Ile
1 5 10 15

Tyr Thr Leu Thr Val Leu Gly Asn Leu Val Val Met Ile Leu Leu Ile
20 25 30

Arg Ile Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn
35 40 45

Leu Ser Phe Val
50

<210> 2300
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A36S"

<400> 2300
Glu Phe Ile Leu Leu Gly Leu Thr Asp His Ala Glu Leu Lys Ala Val
1 5 10 15

Leu Phe Val Val Phe Leu Val Ile Tyr Ser Ser Ile Thr Leu Leu Arg
20 25 30

Asn Leu Gly Met Ile Leu Leu Ile Gln Ile Thr Ser Lys Leu His Thr
35 40 45

Pro Met Tyr Phe
50

<210> 2301
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T275N"

<400> 2301
Val Phe His Gly Thr Val Leu Ser Ile Tyr Cys Arg Pro Ser Ser Gly
1 5 10 15

Asn Ser Gly Asp Ala Asp Lys Val Ala Asn Asn Val Phe Tyr Thr Val
20 25 30

Val Ile Pro Met Leu Asn Ser Val Ile Tyr Ser Leu Arg Asn Lys Asp
35 40 45

Val Lys Glu Ala

50

<210> 2302
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T89fs"

<400> 2302
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
1 5 10 15

Leu Glu Asn Leu Leu Ser Asp Lys Lys Gln Leu Leu Met Leu Val Val
20 25 30

<210> 2303
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A100V"

<400> 2303
Pro Asn Met Leu Val Asn Phe Leu Val Glu Arg Asn Thr Val Ser Tyr
1 5 10 15

Leu Gly Cys Ala Ile Gln Leu Gly Ser Val Val Ala Phe Phe Ala Thr
20 25 30

Val Glu Cys Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Phe Val Ala
35 40 45

Ile Cys Ser Pro
50

<210> 2304
<211> 37

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I154fs"

<400> 2304
Thr Thr Ile Met Ser Asn Lys Val Cys Asn Trp Leu Val Ile Ser Ser
1 5 10 15

Trp Leu Ala Gly Phe Leu Ile Ile Phe Ser Pro Arg Asp Tyr Gly Pro
20 25 30

Pro Thr Gly Phe Leu
35

<210> 2305
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G94W"

<400> 2305
Ile Ser Phe Thr Ser Val Cys Ile Pro Arg Phe Leu Val Thr Val Val
1 5 10 15

Thr Gly Asn Arg Thr Ile Ser Tyr Asn Trp Trp Cys Val Ala Gln Leu
20 25 30

Phe Phe Phe Ile Phe Leu Gly Val Thr Glu Phe Tyr Leu Leu Ala Ala
35 40 45

Met Ser Tyr Asp
50

<210> 2306
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P79Q"

<400> 2306
His Leu His Thr Pro Met Tyr Thr Phe Ile Ser Ala Leu Ser Phe Leu
1 5 10 15

Glu Ile Trp Tyr Thr Thr Ala Thr Ile Gln Gln Lys Met Leu Ser Ser
20 25 30

Leu Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys Leu Leu Gln Met
35 40 45

Tyr Phe Phe His
50

<210> 2307
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F311L"

<400> 2307
Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe Trp Asp Thr Ala Ile
1 5 10 15

Ala Val Thr Phe Val Ile Leu Ala Pro Leu Leu Phe Asn Pro Ile Ile
20 25 30

Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile Gly Arg Leu Phe
35 40 45

His Tyr Gln Lys
50

<210> 2308
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R293C"

<400> 2308
Leu Thr Leu Asp Arg Thr Leu Ala Ile Val Tyr Ser Val Leu Thr Pro
1 5 10 15

Met Val Asn Pro Ile Ile Tyr Ser Leu Cys Cys Asn Lys Glu Ile Ile
20 25 30

Lys Ala Ile Lys Arg Thr Ile Phe Gln Lys Gly Asp Lys Ala Ser Leu
35 40 45

Ala His Leu
50

<210> 2309
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I248fs"

<400> 2309
Val Leu Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr
1 5 10 15

Cys Gly Ser His Leu Thr Leu Val Phe Met Ala Thr Val Val Pro Ser
20 25 30

Phe Cys Met Ser Gly Leu Ala Lys Leu Thr Leu Cys Lys Ser Gly Arg
35 40 45

Ser Trp Pro Trp

50

<210> 2310
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F104fs"

<400> 2310
Pro Lys Met Leu Leu Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr
1 5 10 15

Ala Gly Cys Leu Ser Gln Ile Phe Phe Ser Leu His Leu Asp Ala Trp
20 25 30

Thr Ile Tyr Ser
35

<210> 2311
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C179fs"

<400> 2311
Met Gly Ser Leu Leu Glu Thr Leu Thr Val Leu Arg Leu Ser Phe Cys
1 5 10 15

Thr Glu Met Glu Ile Pro His Phe Phe Val Ile Tyr Leu Lys Ser
20 25 30

<210> 2312
<211> 69
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L7fs"

<400> 2312
Met Ser Tyr Phe Pro Ile Leu Phe Phe Phe Phe Pro Gln Lys Val Ser
1 5 10 15

Glu Leu His Arg Ala Thr Glu Ser His Arg Cys Leu Arg Ile Pro Pro
20 25 30

Pro Gly Thr Leu Arg Gly Ser Arg Thr Ala Ala Gly Pro Arg Trp Ala
35 40 45

Val Pro Val His Val Pro Gly His Gly Ala Gly Glu Pro Ala His His
50 55 60

Pro Gly Cys Gln Leu
65

<210> 2313
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R306M"

<400> 2313
Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp
1 5 10 15

Val Lys Asn Ala Leu Lys Lys Met Thr Met Met Gly Arg Gln Ser Ser
20 25 30

<210> 2314
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L166F"

<400> 2314
Cys Leu Ala Leu Ile Thr Gly Pro Tyr Val Ile Gly Phe Ile Asp Ser
1 5 10 15

Phe Val Asn Val Val Ser Met Ser Arg Phe Phe His Phe Tyr Asp Ser
20 25 30

Asn Val Ile His His Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu
35 40 45

Ser Cys Thr Asp
50

<210> 2315
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<400> 2315
Val Val Ser Arg Arg Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu
1 5 10 15

Tyr Gly Phe Ser Thr Ala Ile Val Val Leu Leu Pro Cys Ile Phe Ser
20 25 30

Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Ile
35 40 45

Ala Pro Leu Leu
50

<210> 2316
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

<220>
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<223> /note="p.K235N"

<400> 2316
Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala Ile
1 5 10 15

Leu Arg Met Asn Ser Ala Gly Arg Gln Asn Asn Ala Phe Ser Thr Cys
20 25 30

Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe
35 40 45

Met Tyr Val Gln
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<210> 2317
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.A99V"

<400> 2317
Ser Ser Val Ile Val Pro Lys Met Leu Glu Asn Leu Leu Ser Gln Arg
1 5 10 15

Lys Thr Ile Ser Val Glu Gly Cys Leu Val Val Gln Val Phe Phe Val
20 25 30

Phe Val Thr Ala Gly Thr Glu Ala Cys Leu Leu Ser Gly Met Ala Tyr
35 40 45

Asp Arg His Ala
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<210> 2318

<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R289W"

<400> 2318
Val Glu Tyr Asn Lys Ile Val Ser Leu Leu Val Ser Val Leu Thr Pro
1 5 10 15

Phe Leu Asn Pro Phe Ile Phe Thr Leu Trp Trp Asn Asp Lys Val Lys
20 25 30

Glu Ala Leu Arg Asp Gly Met Lys Arg Cys Cys Gln Leu Leu Lys Asp
35 40 45

<210> 2319
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R169L"

<400> 2319
Val Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr
1 5 10 15

Lys Lys Thr Phe Ser Phe Asn Phe Cys Leu Leu Glu Asn Ile Ile Asp
20 25 30

Asp Phe Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu
35 40 45

Lys Gly Gly Tyr
50

<210> 2320
<211> 52

<212> PRT
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<220>
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<400> 2320
Phe Ser Glu Leu Ala Leu Thr Leu Asn Ala Trp Glu Ser Gly Thr Ala
1 5 10 15

Pro Thr Asp Ser Arg Leu Arg Pro Asp His His Arg Leu Met Glu Asn
20 25 30

Gly Arg Trp Asp Glu Ala Asn Ala Glu Lys Gln Arg Leu Glu Glu Lys
35 40 45

Gln Arg Leu Ser
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<210> 2321
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H627fs"

<400> 2321
Glu Thr Phe Glu Leu Asp Arg Leu Asp Asp Met Gly Leu Arg Ser Leu
1 5 10 15

Cys Glu Gln Val Ser His His Pro Pro Leu Ser Cys Ala Leu Arg Val
20 25 30

Leu Gln Ala Trp Leu Glu Pro Leu Ala Gly Asp His His Leu Gln Gln
35 40 45

Val Pro Gly Lys Ile His Leu His His Ala Ala Arg Cys His Pro Leu
50 55 60

Arg Ile Pro Gly Gln Trp Glu Ser Leu Arg Val Glu Glu Glu His Leu
65 70 75 80

Asn Cys Ser Gln His His Arg Gly Gln Ala Leu Asp Arg Pro Val Arg
85 90 95

Gly His Arg Asp Cys Glu Pro
100

<210> 2322
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2322
Ser Glu Asp Asn Thr Ser Val Ala Asp Asn Ile Ser Arg Gln Ile Leu
1 5 10 15

Asn Gly Glu Leu Thr Gly Gly Ala Phe Gln Gln Asn Gly Arg Arg Ala
20 25 30

Cys Leu Pro Ala Pro Cys Pro Asp Thr Ser Asn Ile Asn Leu Trp Asn
35 40 45

Ile Leu Arg Asn
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<210> 2323
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R115Q"

<400> 2323

Pro Leu Asp Arg Leu Ser Ala Gly Ser Val Asp His Lys Gly Lys Gln
1 5 10 15

Arg Lys Val Val Asp His Pro Lys Arg Gln Gln Phe Gly Ile Pro Met
20 25 30

Asp Arg Ile Gly Arg Asn Arg Leu Ser Asn Ser Arg Gly
35 40 45

<210> 2324
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T388M"

<400> 2324
Asp Asp Ile Ser Ser Gly Leu Lys Gly Tyr Val Lys Cys Asp Val Ala
1 5 10 15

Val Val Gly Lys Gly Asp Asn Ile Lys Met Met Pro His Lys Ala Asn
20 25 30

Glu Thr Asp Glu Asp Asp Ile Glu Gly Asn Leu Leu Leu Pro Glu Gly
35 40 45

Val Pro Pro Glu
50

<210> 2325
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2325
Lys Leu Glu Thr Met Val Lys Leu Asp Ala Thr Ser Glu Ala Val Val

1 5 10 15

Lys Val Asp Val Ala Glu Glu Glu Lys Lys Lys Lys Lys Lys Lys
20 25 30

Lys Gly Thr Ala Glu Glu Pro Glu Glu Glu Glu Pro Asp Glu Ser Met
35 40 45

Leu Asp Trp Trp
50

<210> 2326
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V431I"

<400> 2326
Val Ala Gln Asn Lys Lys Gln Phe Lys Ser Arg Glu Thr Leu Tyr Gly
1 5 10 15

Gln Glu Ile Asp Gln Ala Ser Leu Leu Ile Ile Ile Leu Lys Leu Ser
20 25 30

Ala Gly Asp Gln Val Trp Leu Glu Val Ser Lys Asp Trp Asn Gly Val
35 40 45

Tyr Val Ser Ala
50

<210> 2327
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2327
Ala Trp Ala Val His Ala Ala Gly Val Ser Lys Ser Asp Leu Leu Cys
1 5 10 15

Phe Leu Thr Ala Leu Met Leu Leu Gln Met Leu Trp Tyr Val Gly Arg
20 25 30

Ser Ser Ala His Arg Arg Leu Phe Arg Leu Lys Asp Thr His Ala Gly
35 40 45

Ala Gly Trp Leu Arg Gly Ser Ile Thr Leu Phe
50 55

<210> 2328
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R277I"

<400> 2328
Val Gln Asn Leu Glu Ala Glu Asn Tyr Asn Ile Glu Ser Ala Ile Ile
1 5 10 15

Ala Val Leu Arg Met Asn Gln Gly Lys Ile Ile Asn Asn Ala Glu Glu
20 25 30

Asn Leu Glu Pro Ser Gly Arg Val Leu Lys Gln Cys Gly Pro Leu Trp
35 40 45

Glu Glu Gly Gly
50

<210> 2329
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T909I"

<400> 2329
Ala Leu Ala Ser Ile Pro Pro Val Ala Glu Gly Lys Ala His Pro Pro
1 5 10 15

Thr Gln Ile Leu Asn Arg Glu Arg Glu Ile Ile Val Pro Val Glu Leu
20 25 30

Glu Pro Lys Arg Thr Ile Gln Ser Leu Lys Glu Lys Thr Glu Lys Val
35 40 45

Lys Asp Pro Lys
50

<210> 2330
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A153del"

<400> 2330
Val Ala Asp Glu Asp Asn Ser Glu Ile Ser Asp Ser Glu Asp Asp Ser
1 5 10 15

Cys Lys Ser Lys Thr Ala Ala Ala Ala Asp Val Asn Gly Phe Lys Pro
20 25 30

Leu Ser Gly Asn Glu Gln Leu Lys Asn Asn Gly Asn Ser Thr Ser Leu
35 40 45

Pro Leu Ser Arg Lys
50

<210> 2331
<211> 39
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.R44fs"

<400> 2331
Thr Ser Gly Met Asp Leu Leu His Pro Ser Val Gly Tyr Pro Gly Pro
1 5 10 15

Trp Ala Ser Cys Pro Ala Ala Thr Pro Gly Asn Ser Ala Gly Arg Gly
20 25 30

Arg Arg Ser Leu Gly Arg Ser
35

<210> 2332
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E122K"

<400> 2332
Gly Thr Ile Glu Tyr Thr Val Glu Ser Arg Asp Ser Leu Asn Ser Ile
1 5 10 15

Ala Leu Lys Phe Asp Thr Thr Pro Asn Lys Lys Leu Val Gln Leu Asn
20 25 30

Lys Leu Phe Ser Arg Ala Val Val Thr Gly Gln Val Leu Tyr Val Pro
35 40 45

Asp Pro Glu Tyr
50

<210> 2333
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R20fs"

<400> 2333
Met Ala Arg Arg Phe Gln Glu Glu Leu Ala Ala Phe Leu Phe Glu Tyr
1 5 10 15

Asp Thr Pro Ala Trp Cys Trp Cys Val Ile Arg Arg Trp Ala Leu Ser
20 25 30

Ser Asp

<210> 2334
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P142Q"

<400> 2334
Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu Cys Ser Ser Asp
1 5 10 15

Arg Gly Cys Lys Lys Gly Trp Met Asp Gln Gln Gln Ser Lys Gly Ile
20 25 30

Gln Thr Gly Arg Cys Val Val Tyr Glu Gly Asn Gln Lys Thr Cys Glu
35 40 45

Val Ser Ala Trp
50

<210> 2335
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Y408F"

<400> 2335
Met Gln Arg Met Ala Ser Val Arg Ala Val Pro Asn Pro Val Ile Asn
1 5 10 15

Pro Tyr Gln Pro Ala Pro Pro Ser Gly Phe Phe Phe Met Ala Ala Ile
20 25 30

Pro Gln Thr Gln Asn Arg Ala Ala Tyr Tyr Pro Pro Ser Gln Ile Ala
35 40 45

Gln Leu Arg Pro
50

<210> 2336
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R94C"

<400> 2336
Leu Asp Thr Met Asn Phe Asp Val Ile Lys Gly Lys Pro Val Arg Ile
1 5 10 15

Met Trp Ser Gln Arg Asp Pro Ser Leu Cys Cys Lys Ser Gly Val Gly
20 25 30

Asn Ile Phe Ile Lys Asn Leu Asp Lys Ser Ile Asp Asn Lys Ala Leu
35 40 45

Tyr Asp Thr Phe
50

<210> 2337
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E156fs"

<400> 2337
Asp Glu Asn Gly Ser Lys Gly Tyr Gly Phe Val His Phe Glu Thr Gln
1 5 10 15

Glu Ala Ala Glu Arg Ala Ile Glu Lys Asn Glu Trp Asn Ala Pro Lys
20 25 30

<210> 2338
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A181T"

<400> 2338
Glu Lys Met Asn Gly Met Leu Leu Asn Asp Arg Lys Val Phe Val Gly
1 5 10 15

Arg Phe Lys Ser Arg Lys Glu Arg Glu Thr Thr Glu Leu Gly Ala Arg
20 25 30

Ala Lys Glu Phe Thr Asn Val Tyr Ile Lys Asn Phe Gly Glu Asp Met
35 40 45

Asp Asp Glu Arg
50

<210> 2339
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<221> source
<223> /note="p.K254fs"

<400> 2339
Lys Ser Lys Gly Phe Gly Phe Val Ser Phe Glu Arg His Glu Asp Ala
1 5 10 15

Gln Lys Ala Val Asp Glu Met Asn Gly Asn Gly Ala Gln Trp Lys Thr
20 25 30

Asn Leu Cys Trp Ser Ser Ser Glu Lys Gly Gly Thr Ala Asp Gly Thr
35 40 45

<210> 2340
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K333fs"

<400> 2340
Leu Arg Lys Glu Phe Ser Pro Phe Gly Thr Ile Thr Ser Ala Lys Val
1 5 10 15

Met Met Glu Gly Gly Arg Ser Lys Gly Leu Val Leu Tyr Val Ser Pro
20 25 30

Pro Gln Lys Lys Pro Leu Lys Gln Leu Gln Lys
35 40

<210> 2341
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V325fs"

<400> 2341
Leu Asp Asp Gly Ile Asp Asp Glu Arg Leu Arg Lys Ala Phe Ser Pro

1 5 10 15

Phe Gly Thr Ile Thr Ser Ala Lys Val Gly Arg Trp Ser Gln Gln Arg
20 25 30

Val Trp Phe Cys Met Phe Leu Leu Pro Arg Arg Ser His
35 40 45

<210> 2342
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K333fs"

<400> 2342
Leu Arg Lys Ala Phe Ser Pro Phe Gly Thr Ile Thr Ser Ala Lys Val
1 5 10 15

Met Met Glu Gly Gly Arg Ser Lys Gly Leu Val Leu Tyr Val Ser Pro
20 25 30

Pro Gln Lys Lys Pro Leu Lys Gln Leu Gln Lys
35 40

<210> 2343
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E359K"

<400> 2343
Ala Val Glu Ser Thr Ser Gln Ala Gly Asp Arg Gly Ser Val Ser Ser
1 5 10 15

Tyr Asp Arg Gly Gln Pro Tyr Ala Thr Lys Lys Trp Ser Asp Asp Glu
20 25 30

Ser Gly Asn Pro Phe Gly Gly Ser Glu Thr Asn Gly Gly Ala Asn Pro
35 40 45

Phe Glu Asp Asp
50

<210> 2344
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q331H"

<400> 2344
Ala Asp Leu Asn Arg Thr Leu Ser Arg Arg Glu Lys Lys Lys Ala Thr
1 5 10 15

Asp Gly Val Thr Leu Thr Gly Ile Asn His His Thr Gly Asp Gln Ser
20 25 30

Leu Pro Ser Lys Pro Ser Ser Thr Leu Asn Val Pro Ser Asn Pro Ala
35 40 45

Gln Ser Ala Gln
50

<210> 2345
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T114P"

<400> 2345
Ser Ser Asp Lys Val Thr Val Asn Tyr Tyr Asp Glu Glu Gly Ser Ile
1 5 10 15

Pro Ile Asp Gln Ala Gly Leu Phe Leu Pro Pro Ala Ile Glu Ile Ser
20 25 30

Leu Asp Val Asp Ala Asp Arg Asp Gly Val Val Glu Lys Asn Asn Pro
35 40 45

Lys Lys Ala Ser
50

<210> 2346
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K302fs"

<400> 2346
Val Glu Cys Ile Ser Trp Ala Pro Glu Ser Ser Tyr Ser Ser Ile Ser
1 5 10 15

Glu Ala Thr Gly Ser Glu Thr Lys Lys Val Val Asn Leu Gly His Ser
20 25 30

Cys Cys Leu Asp Pro Glu Thr Arg Leu Leu Arg Cys Gly Met Ser Val
35 40 45

Leu Ala Cys Ala Leu
50

<210> 2347
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N280fs"

<400> 2347

Asp Ser Gly Ser Ser Gln His Leu Glu His Ile Pro Pro Lys Gly Ser
1 5 10 15

Ser Glu Leu Thr Thr His Asp Leu Lys Thr Leu Asp Leu Leu His Leu
20 25 30

<210> 2348
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A996T"

<400> 2348
Asp Ser Ala His Lys Met Leu Val Arg Glu Asn Gly Val His Ser Leu
1 5 10 15

Ile Ile Glu Pro Val Thr Ser Arg Asp Thr Thr Gly Ile Tyr Thr Cys
20 25 30

Ile Ala Thr Asn Arg Ala Gly Gln Asn Ser Phe Ser Leu Glu Leu Val
35 40 45

Val Ala Ala Lys
50

<210> 2349
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.1075_1076insEA"

<400> 2349
Lys Ala Val Ser Lys Thr Ser Arg Asp Gly Ala Glu Gln Gln Gly Pro
1 5 10 15

Glu Ala Thr Val Glu Glu Ala Glu Ala Glu Ala Glu Ala Ala Ala Phe

20 25 30

Gly Ser Glu Lys Pro Gln Ser Met Phe Glu Pro Pro Gln Val Ser Ser
35 40 45

Pro Val Gln Glu Lys Arg Asp Val Leu Pro
50 55

<210> 2350
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G1118fs"

<400> 2350
Val Gln Glu Lys Arg Asp Val Leu Pro Lys Ile Leu Pro Ala Glu Asp
1 5 10 15

Arg Ala Leu Arg Glu Arg Gly Pro Pro Pro Ala Thr Ala Ser Cys Ala
20 25 30

Ala Gln Trp Pro Asp
35

<210> 2351
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A299T"

<400> 2351
Lys Leu Glu Met Val His Lys Ser Arg Lys Asp His Ser Ser Gly Asn
1 5 10 15

Pro Gly Gln Gln Ala Gln Ala Pro Ser Thr Thr Ala Gly Pro Glu Ala
20 25 30

Asn Leu Asp Gln Pro Val Thr Met Ile Phe Met Gly Tyr Gln Asn Ile
35 40 45

Glu Asp Glu Glu
50

<210> 2352
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G101fs"

<400> 2352
Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys
1 5 10 15

Lys Ser Cys Arg Asn Gly Ser Trp Gly Val Pro Trp Met Thr Ser Met
20 25 30

<210> 2353
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K400fs"

<400> 2353
Asp Ser Val Gly Phe Asn Gly Lys Pro Glu Cys Tyr Tyr Phe Glu Asn
1 5 10 15

Pro Thr Asn Pro Glu Leu Cys Gln Lys Ser Arg Thr Ala Leu Ile Thr
20 25 30

His Thr Leu Cys Cys Trp Leu Thr Trp Ala Gln Val Ser Ala Phe
35 40 45

<210> 2354
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T417fs"

<400> 2354
Val Ser Ile Leu Ala Val Tyr Ser Lys Asp Asn Tyr Lys Arg Val Thr
1 5 10 15

Gly Thr Ser Leu Gly Gly Gly Thr Phe Leu Val Ser Ala Val Phe Leu
20 25 30

Leu Ala Val Pro Leu Leu Lys Lys Leu Leu Lys Trp His Leu Val Glu
35 40 45

Ile Ala Pro Lys Trp Ile Asn
50 55

<210> 2355
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G126A"

<400> 2355
Ala Ala Glu Glu Ala Arg Arg Asn Pro Thr Leu Gly Gly Leu Leu Gly
1 5 10 15

Arg Gln Arg Leu Leu Leu Arg Met Gly Ala Ala Gly Arg Leu Gly Ala
20 25 30

Pro Met Glu Arg His Gly Arg Ala Ser Ala Thr Ser Val Ser Ser Ala
35 40 45

Gly Glu Gln Ala
    50

<210> 2356
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R260I"

<400> 2356
Leu Glu Met Ala Ser Lys Gly Asp Ser Thr Gln Ala Asp Lys Leu Val
1   5   10   15

Arg Asp Ile Tyr Gly Gly Asp Tyr Glu Ile Ile Phe Gly Leu Pro Gly
            20   25   30

Trp Ala Val Ala Ser Ser Phe Gly Asn Met Ile Tyr Lys Glu Lys Arg
        35   40   45

Glu Ser Val Ser
    50

<210> 2357
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.H107Y"

<400> 2357
Gln Leu Ala Ala Glu Tyr Gly Leu Leu Gly Glu Lys Glu Leu Ser Gln
1   5   10   15

Glu Asn Gln Leu Val Glu Thr Gly Gly Tyr Tyr Val Gly Leu Pro Ser
            20   25   30

Val Ser Tyr Ala Ser Ser Gly Ala Ser Val Ser Leu Gln Leu Val Ala

35 40 45

Glu Met Ala Thr
50

<210> 2358
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C225fs"

<400> 2358
Ser Leu Asn Gly Phe Gly Thr Arg Ser Ser Asp Gly Asp Leu Cys Leu
1 5 10 15

Val Val Lys Glu Glu Pro Cys Phe Phe Ser Gly Lys Ser Glu Asp
20 25 30

<210> 2359
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P917T"

<400> 2359
Gln Tyr Val His Thr Ala Ser Ser Arg Arg Val Cys Asp Ser Ser Gly
1 5 10 15

Tyr Trp Thr Pro Glu Glu Ala Val Gly Thr Thr Pro Asp Val Asp Gln
20 25 30

Pro Cys Glu Pro Ser Leu Gln Ala Trp Ser Pro Glu Val His Leu Tyr
35 40 45

His Met Asn Met
50

<210> 2360
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.I1683fs"

<400> 2360
Asn Ser Val Glu Tyr Lys Cys Glu Gln Gly Tyr Gly Ile Gly Ala Val
1 5 10 15

Cys Ser Pro Leu Cys Val Ile Pro Pro Val Thr Pro
20 25

<210> 2361
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P1706H"

<400> 2361
Cys Val Ile Pro Pro Ser Asp Pro Val Met Leu Pro Glu Asn Ile Thr
1 5 10 15

Ala Asp Thr Leu Glu His Trp Met Glu His His Val Lys Val Gln Ser
20 25 30

Ile Val Cys Thr Gly Arg Arg Gln Trp His Pro Asp Pro Val Leu Val
35 40 45

His Cys Ile Gln
50

<210> 2362
<211> 37
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G84fs"

<400> 2362
Thr Asp Ala His Gly Asp Leu Leu Pro Leu Thr Asn Asp Asp Ser Leu
1 5 10 15

His Arg Ala Leu Ala Ser Gly Pro Pro Ala Thr Ala Pro Thr Gly Ala
20 25 30

Glu Ala Gly Arg Ser
35

<210> 2363
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A584T"

<400> 2363
Lys Tyr Asn Val Ala Tyr Ser Lys Lys Trp Asp Phe Thr Ala Leu Ile
1 5 10 15

Asp Phe Trp Asp Lys Val Leu Glu Glu Thr Thr Glu Ala Gln His Leu
20 25 30

Tyr Gln Ser Ile Leu Pro Asp Met Val Lys Ile Ala Leu Cys Leu Pro
35 40 45

Asn Ile Cys Thr
50

<210> 2364
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K461fs"

<400> 2364
Pro Ser Leu Lys Thr Val Lys Val Val Ile Phe Gln Pro Glu Leu Leu
1 5 10 15

Asn Ile Phe Tyr Asp Ser Met Lys Lys Glu Thr Ser Leu His His
20 25 30

<210> 2365
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K847fs"

<400> 2365
Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His Ile Gly Leu Ser Ala
1 5 10 15

Ala Tyr Leu Pro Arg Met Trp Val Glu Asn Ile Gln Lys Lys Lys Ala
20 25 30

Arg Leu Ala Cys Leu Ser Phe Asn Pro Ile Ser Met Ser Thr Ser Leu
35 40 45

Thr

<210> 2366
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A236del"

<400> 2366
Ser Ser Gln Gly Gln Arg Gly His Thr Ser Met Lys Ala Val Tyr Val
1 5 10 15

Glu Pro Ala Ala Ala Ala Ala Ala Ala Ile Ser Asp Asp Gln Ile Asp
20 25 30

Ile Ala Glu Val Glu Gln Tyr Gly Pro Gln Glu Asn Val His Met Phe
35 40 45

Val Asp Ser Asp Ser
50

<210> 2367
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T62I"

<400> 2367
Pro Ser Arg Ser Phe Ser Ser Ala His Arg His Leu Ser Arg Arg Asn
1 5 10 15

Gly Leu Ser Arg Leu Cys Gln Ser Arg Ile Ile Ala Leu Ser Glu Asp
20 25 30

Arg Trp Ser Ser Tyr Cys Leu Ser Ser Leu Ala Ala Gln Asn Ile Cys
35 40 45

Thr Ser Lys Leu
50

<210> 2368
<211> 35
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P395fs"

<400> 2368
Tyr Ser His Pro Gln Tyr Thr Ala Tyr Asn Glu Ala Trp Arg Phe Ser
1 5 10 15

Asn Pro Ala Leu Leu Met Pro Pro Pro Val Arg Pro Cys Arg Cys Cys
20 25 30

Arg Cys Leu
35

<210> 2369
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T424M"

<400> 2369
His Gly Gly Val Pro His Gln Pro Gln Thr Asp Tyr Ala Leu Ser Pro
1 5 10 15

Leu Thr Gly Gly Leu Glu Pro Thr Thr Met Met Val Ser Ala Ser Cys
20 25 30

Ser Gln Arg Leu Asp His Met Lys Ser Leu Asp Ser Leu Pro Thr Ser
35 40 45

Gln Ser Tyr Cys
50

<210> 2370
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S197L"

<400> 2370
Leu Glu Arg Lys Glu Ala Glu Glu Ser Glu Lys Lys Ala Lys His Ser
1 5 10 15

Ile Asp Gly Ile Leu Ser Glu Arg Ala Leu Leu Ala Pro Gln Ser Asp
20 25 30

Glu Gly Ser Asp Ile Asp Ser Glu Pro Asp Leu Pro Leu Lys Arg Lys
35 40 45

Gln Arg Arg Ser
50

<210> 2371
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P375fs"

<400> 2371
Gln Thr Ser Ser Tyr Ser Cys Met Leu Pro Thr Ser Pro Ser Val Asn
1 5 10 15

Gly Arg Ser Tyr Asp Thr Tyr Thr Pro His Ile Cys Arg His Thr
20 25 30

<210> 2372
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

<221> source
<223> /note="p.P55Q"

<400> 2372
Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser
1 5 10 15

Glu Thr Ala Phe Ile Arg Lys Leu His Gln Gln Thr Asp Asn Phe Ala
20 25 30

Gln Ser Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val
35 40 45

Pro Leu Cys Gly
50

<210> 2373
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E70K"

<400> 2373
Pro Gly Gly Arg Gly Lys Gln Asp Ile Gly Asp Ile Leu Gln Gln Ile
1 5 10 15

Met Thr Ile Thr Asp Gln Ser Leu Asp Lys Lys Ala Gln Ala Lys Lys
20 25 30

His Ala Leu Asn Cys His Arg Met Lys Pro Ala Leu Phe Ser Val Leu
35 40 45

Cys Glu Ile Lys
50

<210> 2374
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y262F"

<400> 2374
Leu Arg Ser Arg Phe Leu Asp Ala Arg Arg Lys Arg Arg Asn Phe Ser
1 5 10 15

Lys Gln Ala Thr Glu Val Leu Asn Glu Phe Phe Phe Tyr Ser His Leu
20 25 30

Ser Asn Pro Tyr Pro Ser Glu Glu Ala Lys Glu Glu Leu Ala Lys Lys
35 40 45

Cys Gly Ile Thr
50

<210> 2375
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.H729del"

<400> 2375
Lys Lys Asp Lys His Ser Gln Ser Pro Arg Ala Ala Gly Pro Arg Glu
1 5 10 15

Gly His Ser His Ser His His His His Arg Gly
20 25

<210> 2376
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L102Q"

<400> 2376
Asp Lys Leu Glu Glu Asp Ile Asn Ser Ser Met Thr Asn Ser Thr Ala
1 5 10 15

Ala Ser Arg Pro Pro Val Thr Leu Arg Gln Gln Val Val Pro Ala Thr
20 25 30

Gln Cys Gly Ser Leu Ile Gly Lys Gly Gly Cys Lys Ile Lys Glu Ile
35 40 45

Arg Glu Ser Thr
50

<210> 2377
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R230H"

<400> 2377
Ala Val Arg Ile Ala Arg Glu Ile Gly Tyr Pro Val Met Ile Lys Ala
1 5 10 15

Ser Ala Gly Gly Gly Gly Lys Gly Met His His Ile Ala Trp Asp Asp
20 25 30

Glu Glu Thr Arg Asp Gly Phe Arg Leu Ser Ser Gln Glu Ala Ala Ser
35 40 45

Ser Phe Gly Asp
50

<210> 2378
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V477M"

<400> 2378
Gln Val Ser Asp Val Asn Asp Asn Ala Pro Arg Phe Ser Gln Pro Val
1 5 10 15

Tyr Asp Val Tyr Val Thr Glu Asn Asn Met Met Pro Gly Ala Tyr Ile
20 25 30

Tyr Ala Val Ser Ala Thr Asp Arg Asp Glu Gly Ala Asn Ala Gln Leu
35 40 45

Ala Tyr Ser Ile
50

<210> 2379
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R587S"

<400> 2379
Ile Leu Ile Val Asp Gln Asn Asp Asn Ala Pro Ala Ile Val Ala Pro
1 5 10 15

Leu Pro Gly Arg Asn Gly Thr Pro Ala Ser Ser Glu Val Leu Pro Arg
20 25 30

Ser Ala Glu Pro Gly Tyr Leu Leu Thr Arg Val Ala Ala Val Asp Ala
35 40 45

Asp Asp Gly Glu
50

<210> 2380
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.V986L"

<400> 2380
Ser Asp Gly Arg Gln Ala Ala Asp Tyr Arg Ser Asn Leu His Val Pro
1 5 10 15

Gly Met Asp Ser Val Pro Asp Thr Glu Leu Leu Phe Glu Thr Pro Glu
20 25 30

Ala Gln Pro Gly Ala Glu Arg Ser Phe Ser Thr Phe Gly Lys Glu Lys
35 40 45

Ala Leu His Ser
50

<210> 2381
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.N118fs"

<400> 2381
Glu Val Phe Leu Glu Asn Pro Leu Glu Leu Phe Gln Val Glu Ile Glu
1 5 10 15

Val Leu Asp Ile Asn Asp Asn Pro Pro Leu Phe Pro Gly Ala Arg Pro
20 25 30

Asp Gly Gly Asn Leu
35

<210> 2382
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P225fs"

<400> 2382
Thr Ala Val Asp Gly Gly Gly Gly Gly Gly Val Gly Glu Gly Gly Gly
1 5 10 15

Gly Gly Gly Gly Ala Gly Leu Pro Pro Pro Ala Ala Ala His Arg His
20 25 30

Gly Pro Thr His His Pro Ser Ala Gly Leu Gln
35 40

<210> 2383
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T486M"

<400> 2383
Asp Asn Ala Pro Val Phe Thr Gln Ser Phe Val Thr Val Ser Ile Pro
1 5 10 15

Glu Asn Asn Ser Pro Gly Ile Gln Leu Met Met Lys Val Ser Ala Met
20 25 30

Asp Ala Asp Ser Gly Pro Asn Ala Lys Ile Asn Tyr Leu Leu Gly Pro
35 40 45

Asp Ala Pro Pro
50

<210> 2384
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1010I"

<400> 2384
Ser Ser Asp Pro Tyr Ser Val Ser Asp Cys Gly Tyr Pro Val Thr Thr
1 5 10 15

Phe Glu Val Pro Val Ser Val His Thr Ile Ile Pro Pro Met Lys Glu
20 25 30

Val Val Arg Ser Cys Thr Pro Met Lys Glu Ser Thr Thr Met Glu Ile
35 40 45

Trp Ile His Pro
50

<210> 2385
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1552I"

<400> 2385
Asp Asp Leu Ser Ala His Asn Pro Leu Tyr Lys Glu Asn Ile Ser Gln
1 5 10 15

Val Ser Thr Asn Ser Asp Ile Ser Gln Ile Ile Thr Asp Phe Val Asp
20 25 30

Pro Phe Ser Pro Lys Ile Gln Ala Lys Ser Lys Ser Leu Arg Gly Pro
35 40 45

Arg Glu Lys Ile
50

<210> 2386
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C1713F"

<400> 2386
Val Glu Leu Lys Ser Glu Pro Asn Val Ile Ser Ser Pro Ala Glu Cys
1 5 10 15

Ser Leu Glu Leu Ser Pro Ser Arg Pro Phe Phe Val Leu His Ser Ser
20 25 30

Leu Ser Arg Arg Glu Thr Pro Ile Cys Met Leu Pro Ile Glu Thr Glu
35 40 45

Arg Asn Ile Phe
50

<210> 2387
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E530K"

<400> 2387
Tyr Val Ser Ile Asn Pro Asn Ser Gly Asp Ile Tyr Ala Leu Arg Ser
1 5 10 15

Phe Asn His Glu Gln Thr Lys Ala Phe Lys Lys Phe Lys Val Leu Ala
20 25 30

Lys Asp Gly Gly Leu Pro Ser Leu Gln Ser Asn Ala Thr Val Arg Val
35 40 45

Ile Ile Leu Asp
50

<210> 2388
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R286C"

<400> 2388
Asn Ala Ser Asp Pro Asp Glu Gly Thr Asn Gly Gln Val Val Tyr Ser
1 5 10 15

Phe Tyr Gly Tyr Val Asn Asp Arg Thr Cys Cys Glu Leu Phe Gln Ile
20 25 30

Asp Pro His Ser Gly Leu Val Thr Val Thr Gly Ala Leu Asp Tyr Glu
35 40 45

Glu Gly His Val
50

<210> 2389
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A519T"

<400> 2389
Leu Val Glu Arg Arg Val Gly Glu Arg Ala Leu Ser Asn Tyr Val Ser
1 5 10 15

Val His Ala Glu Ser Gly Lys Val Tyr Thr Thr Leu Gln Pro Leu Asp
20 25 30

His Glu Glu Leu Glu Leu Leu Gln Phe Gln Val Ser Ala Arg Asp Ala
35 40 45

Gly Val Pro Pro
50

<210> 2390

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A736V"

<400> 2390
Ala Leu Ser Thr Val Ser Phe Ile Phe Leu Leu Thr Ile Ile Ile Leu
1 5 10 15

Ser Ile Ile Lys Cys Tyr Arg Tyr Thr Val Val Tyr Gly Thr Ala Cys
20 25 30

Cys Gly Gly Phe Cys Gly Val Arg Glu Arg Ser Pro Ala Glu Leu Tyr
35 40 45

Lys Gln Ala Asn
50

<210> 2391
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A742V"

<400> 2391
Thr Ala Leu Arg Cys Ser Ala Ala Pro Thr Glu Gly Ala Cys Gly Pro
1 5 10 15

Val Lys Pro Thr Leu Val Cys Ser Ser Val Val Val Gly Ser Trp Ser
20 25 30

Tyr Ser Gln Gln Arg Arg Gln Arg Val Cys Ser Gly Glu Gly Leu Pro
35 40 45

Lys Ala Asp Leu
50

<210> 2392
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K138N"

<400> 2392
Pro Leu Gln Val Phe His Val Asp Val Glu Val Lys Asp Ile Asn Asp
1 5 10 15

Asn Pro Pro Val Phe Pro Ala Thr Gln Asn Asn Asn Leu Phe Ile Ala
20 25 30

Glu Ser Arg Pro Leu Asp Ser Arg Phe Pro Leu Glu Gly Ala Ser Asp
35 40 45

Ala Asp Ile Gly
50

<210> 2393
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A156V"

<400> 2393
Arg Phe Ser Arg Gln Glu Gln Arg Leu Phe Ile Leu Glu Ser Arg Met
1 5 10 15

Pro Asp Ser Arg Phe Pro Leu Glu Gly Val Val Ser Asp Leu Asp Ile
20 25 30

Gly Ala Asn Ala Gln Leu Arg Tyr Arg Leu Asn Pro Asn Glu Tyr Phe
35 40 45

Asp Leu Asp Val
    50

<210> 2394
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.E190K"

<400> 2394
Asn Ala Leu Leu Ser Tyr Lys Leu Ser Ser Ser Glu Phe Phe Phe Leu
1   5   10   15

Asp Ile Gln Ala Asn Asp Glu Leu Ser Lys Lys Ser Leu Ser Leu Val
            20   25   30

Leu Gly Lys Ser Leu Asp Arg Glu Glu Thr Ala Glu Val Asn Leu Leu
        35   40   45

Leu Val Ala Thr
    50

<210> 2395
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A266T"

<400> 2395
Ala Phe Glu Arg Thr Ile Tyr Lys Val Arg Leu Leu Glu Asn Ala Pro
1   5   10   15

Asn Gly Thr Leu Val Val Thr Val Asn Thr Thr Thr Asp Leu Asp Glu
            20   25   30

Gly Val Asn Lys Asp Ile Ala Tyr Ser Phe Asn Thr Asp Met Ser Ala
35 40 45

Asp Ile Leu Ser
50

<210> 2396
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E271K"

<400> 2396
Ser Tyr Lys Val Val Leu Ser Glu Asn Val Gln Asn Asp Thr Arg Val
1 5 10 15

Ile Gln Leu Asn Ala Ser Asp Pro Asp Lys Lys Gly Leu Asn Gly Glu
20 25 30

Ile Ser Tyr Gly Ile Lys Met Ile Leu Pro Val Ser Glu Lys Cys Met
35 40 45

Phe Ser Ile Asn
50

<210> 2397
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N568K"

<400> 2397
Ser Ser Gln Val Thr Val Arg Val Val Val Leu Asp Asp Asn Asp Asn
1 5 10 15

Arg Pro Met Ile Leu Tyr Pro Leu Gln Lys Lys Gly Thr Leu Pro Cys

20 25 30

Asn Asp Leu Val Pro Arg Ser Ala Glu Ala Gly Tyr Leu Val Thr Lys
35 40 45

Val Val Ala Val
50

<210> 2398
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R289C"

<400> 2398
Val Ser Ala Trp Asp Leu Asp Ser Gly Thr Asn Ser Glu Leu Ser Tyr
1 5 10 15

Thr Phe Ser His Ala Ser Glu Asp Ile Cys Cys Lys Thr Phe Glu Ile
20 25 30

Asn Gln Lys Ser Gly Asp Ile Thr Leu Thr Ala Pro Leu Asp Phe Glu
35 40 45

Ala Ile Glu Ser
50

<210> 2399
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P221L"

<400> 2399
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg Leu
1 5 10 15

Thr Leu Thr Ala Leu Asp Gly Gly Ser Leu Leu Pro Arg Ser Gly Thr
20 25 30

Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala Pro Glu
35 40 45

Phe Glu Gln Pro
50

<210> 2400
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P255F"

<400> 2400
Leu Ile Met Asp Ile Asn Asp Asn Ala Pro Glu Phe Val His Thr Pro
1 5 10 15

Tyr Gly Val Gln Val Leu Glu Asn Ser Phe Phe Leu Asp Ser Pro Ile
20 25 30

Val Arg Val Leu Ala Arg Asp Ile Asp Ala Gly Asn Phe Gly Ser Val
35 40 45

Ser Tyr Gly Leu Phe
50

<210> 2401
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D51Y"

<400> 2401
Ala Gly Ser Glu Ala Val Arg Tyr Ser Ile Pro Glu Glu Thr Glu Ser
1 5 10 15

Gly Tyr Ser Val Ala Asn Leu Ala Lys Tyr Tyr Leu Gly Leu Gly Val
20 25 30

Gly Glu Leu Ala Thr Arg Gly Ala Arg Met His Tyr Lys Gly Asn Lys
35 40 45

Glu Leu Leu Gln
50

<210> 2402
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P649S"

<400> 2402
Arg Thr Ala Arg Leu Leu Ser Glu Arg Asp Ala Ala Lys His Arg Leu
1 5 10 15

Val Val Leu Val Lys Asp Asn Gly Glu Ser Ser Pro Arg Ser Ala Thr
20 25 30

Ala Thr Leu His Val Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu
35 40 45

Pro Leu Pro Glu
50

<210> 2403
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.D235N"

<400> 2403
Arg Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly
1 5 10 15

Thr Ala Gln Val Tyr Ile Glu Val Val Asn Asn Val Asn Asp Asn Ala
20 25 30

Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp Ser
35 40 45

Pro Ile Ser Phe
50

<210> 2404
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G599V"

<400> 2404
Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu Val Thr
1 5 10 15

Lys Val Val Ala Val Asp Arg Asp Ser Val Val Gln Asn Ala Trp Leu
20 25 30

Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val Gly
35 40 45

Leu His Thr Gly
50

<210> 2405
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V662M"

<400> 2405
Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln Pro
1 5 10 15

Pro Leu Ser Ala Thr Val Thr Leu Thr Met Met Ala Val Ala Asp Ser
20 25 30

Ile Pro Glu Val Leu Ala Asp Leu Gly Ser Leu Glu Pro Ser Asp Gly
35 40 45

Pro Tyr Asn Tyr
50

<210> 2406
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D664N"

<400> 2406
Arg Leu Leu Val Ala Val Arg Asp Gly Gly Gln Pro Pro Leu Ser Ala
1 5 10 15

Thr Ala Thr Leu His Leu Val Phe Ala Asn Asn Ser Leu Gln Glu Val
20 25 30

Leu Pro Asp Ile Thr Asp Arg Pro Asp Pro Ser Asp Leu Gln Ala Glu
35 40 45

Leu Gln Phe Tyr
50

<210> 2407
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

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<223> /note="p.P684H"

<400> 2407
Thr Val Thr Val Ala Val Ala Asp Arg Ile Pro Asp Ile Leu Ala Asp
1 5 10 15

Leu Gly Ser Ile Lys Thr Pro Ile Asp His His Glu Asp Leu Asp Leu
20 25 30

Thr Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu
35 40 45

Ala Phe Val Ile
50

<210> 2408
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.A70T"

<400> 2408
Ser Val Val Gly Asn Leu Ala Lys Asp Leu Gly Leu Ser Val Leu Asp
1 5 10 15

Val Ser Ala Arg Lys Leu Arg Val Ser Thr Thr Glu Lys Leu His Phe
20 25 30

Ser Val Asp Ala Glu Ser Gly Asp Leu Leu Val Lys Asn Arg Ile Asp
35 40 45

Arg Glu Gln Ile
50

<210> 2409
<211> 38
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.K12N"

<400> 2409
Met Ala Ala Leu Gln Lys Leu Pro His Cys Arg Asn Asn Leu Val Leu
1 5 10 15

Leu Cys Phe Leu Leu Ala Thr Leu Trp Glu Ala Arg Ala Gly Gln Ile
20 25 30

Arg Tyr Ser Val Arg Glu
35

<210> 2410
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S289L"

<400> 2410
Leu Thr Ala Thr Asp Pro Asp Glu Gly Ile Asn Gly Lys Leu Thr Tyr
1 5 10 15

Ser Phe Arg Asn Glu Glu Glu Lys Ile Leu Leu Glu Thr Phe Gln Leu
20 25 30

Asp Ser Asn Leu Gly Glu Ile Ser Thr Leu Gln Ser Leu Asp Tyr Glu
35 40 45

Glu Ser Arg Phe
50

<210> 2411
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R293C"

<400> 2411
Asp Pro Asp Glu Gly Ala Asn Gly Glu Val Thr Tyr Ser Phe His Asn
1 5 10 15

Val Asp His Arg Val Ala Gln Ile Phe Cys Cys Leu Asp Ser Tyr Thr
20 25 30

Gly Glu Ile Ser Asn Lys Glu Pro Leu Asp Phe Glu Glu Tyr Lys Met
35 40 45

Tyr Ser Met Glu
50

<210> 2412
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H63fs"

<400> 2412
Ser Cys Leu Val Lys Tyr Leu Glu Glu Asn Asn Thr Cys Pro Thr Cys
1 5 10 15

Arg Ile Val Ile His Gln Ser His Pro Cys Ser Thr Ser Val Met Thr
20 25 30

Glu Pro Cys Lys Ile Leu Phe Thr Asn Trp Tyr Gln Ala Ser Lys Lys
35 40 45

Arg Lys
50

<210> 2413

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P3946T"

<400> 2413
Pro Tyr Gln Thr Gln Pro Thr Phe Gln Ala Val Ala Thr Met Ser Phe
1 5 10 15

Thr Pro Gln Val Gln Pro Thr Pro Thr Thr Thr Gln Pro Ser Tyr Gln
20 25 30

Leu Pro Ser Gln Met Met Val Ile Gln Gln Lys Pro Arg Gln Thr Thr
35 40 45

Leu Tyr Leu Glu
50

<210> 2414
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R4133C"

<400> 2414
Val Lys Ala Glu Glu Asp Pro Met Glu Asp Pro Tyr Glu Leu Lys Leu
1 5 10 15

Leu Lys His Gln Ile Lys Gln Glu Phe Cys Cys Arg Gly Thr Glu Ser
20 25 30

Leu Asp His Leu Ala Gly Leu Ser His Tyr Tyr His Ala Asp Thr Ser
35 40 45

Tyr Arg His Phe
50

<210> 2415
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R271M"

<400> 2415
Leu Ala Arg Ile Tyr Ile Arg Arg Thr Leu Arg Asn Phe Ile Asn Asp
1 5 10 15

Glu Met Gln Ala Lys Gly Ile Pro Gln Met Met Ala Pro Pro Lys Arg
20 25 30

Lys Arg Lys Arg Val Lys Gln Arg Ile Asn Thr Tyr Val Phe Val Gly
35 40 45

Asn Gln Leu Ile
50

<210> 2416
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V281A"

<400> 2416
Arg Asn Phe Ile Asn Asp Glu Met Gln Ala Lys Gly Ile Pro Gln Arg
1 5 10 15

Ala Pro Pro Lys Arg Lys Arg Lys Arg Ala Ala Lys Gln Arg Ile Asn
20 25 30

Thr Tyr Val Phe Val Gly Asn Gln Leu Ile Pro Gln Pro Leu Asp Ser
35 40 45

Glu Glu Asp Glu
50

<210> 2417
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R135Q"

<400> 2417
Gly Glu His Ile Thr Asn His Arg Asn Pro Ser Asn Asn Arg Gln Ile
1 5 10 15

His Asn Gly Lys Lys Glu Glu Ala Ser Gln Gln Asn Leu Ser Thr Pro
20 25 30

Pro Leu Arg Cys Ser Ser Arg Gly Gln Ser Ile Thr Ser His His Ser
35 40 45

Ser Gly Pro Leu
50

<210> 2418
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A348V"

<400> 2418
Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val Ser Ile
1 5 10 15

Ile Asn Ile Tyr Lys Glu Gly Asn Leu Val Val Ile Gln Gln Ala Gly
20 25 30

Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro Leu
35 40 45

Leu Arg Arg Gly
50

<210> 2419
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R87H"

<400> 2419
Lys Ile Thr Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe
1 5 10 15

Ile Asp Leu Glu Ser Asp Asn Leu Cys His His Tyr Asp Phe Val Asp
20 25 30

Val Tyr Asn Gly His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly
35 40 45

Thr Phe Arg Pro
50

<210> 2420
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K64R"

<400> 2420
Asp Leu Thr Ala Pro Glu Thr Glu Lys Ala Ala Leu Ala Ile Gln Gly
1 5 10 15

Lys Phe Arg Arg Phe Gln Lys Arg Lys Arg Arg Asp Pro Ser Ser

20 25 30

<210> 2421
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S417L"

<400> 2421
Met Met Thr Leu Glu Asp His Tyr His Ser Asp Val Ala Tyr His Asn
1 5 10 15

Ser Leu His Ala Ala Asp Val Ala Gln Leu Leu Thr His Val Leu Leu
20 25 30

Ser Thr Pro Ala Leu Asp Ala Val Phe Thr Asp Leu Glu Ile Leu Ala
35 40 45

Ala Ile Phe Ala
50

<210> 2422
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E229K"

<400> 2422
Asn Val Tyr Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu
1 5 10 15

Ala Leu Lys Thr Val Tyr Lys Ser Gly Lys Lys Thr Ile Val Val Thr
20 25 30

Cys Ala Val Phe Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro
35 40 45

Gly Glu Val Lys
    50

<210> 2423
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.S650L"

<400> 2423
Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
1   5   10   15

Arg Ser Ser Glu Lys Gln Ala Leu Met Leu Leu Glu Leu Lys Ile Met
            20   25   30

Ser His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys
        35   40   45

Thr Lys Gly Gly
    50

<210> 2424
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.N56K"

<400> 2424
Pro Cys Ser Pro Thr Ser Pro Ala His Ser Leu Ser Arg Lys Ser Pro
1   5   10   15

Ile Met Tyr Pro Ser Thr Thr Met Ala Lys Lys Ala Pro Gly Leu Val
            20   25   30

Ser Cys Thr Phe Phe Leu Ala Val Asn Gly Leu Tyr Ser Ser Ser Asp
35 40 45

Asp Val Ile Glu
50

<210> 2425
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E500K"

<400> 2425
Leu Tyr Lys Gly Glu His Thr Leu Lys Gly Phe Ser Asp Phe Leu Glu
1 5 10 15

Ser His Ile Lys Thr Lys Ile Glu Asp Lys Lys Asp Glu Leu Leu Ser
20 25 30

Val Glu Gln Asn Glu Val Ile Glu Glu Glu Val Leu Ala Glu Glu Lys
35 40 45

Glu Val Pro Met
50

<210> 2426
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G793W"

<400> 2426
Thr Met Phe Ile Leu Asp Asp His Asp Ser Asp Leu Asp Leu Trp Pro
1 5 10 15

Trp Trp Gly Glu Pro Ile Tyr Arg Asn Trp Trp Gln Tyr Val Gly Lys
20 25 30

Thr Thr Ser Ser Ala Tyr Ser Tyr Ser Leu Glu Arg His Val Cys Leu
35 40 45

Gly Phe Val His
50

<210> 2427
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L1309F"

<400> 2427
Lys Asn Asp Asp Leu Asn Lys Pro Ile Asn Lys Gly Arg Lys Arg Ala
1 5 10 15

Ala Val Gly Gln Glu Ser Pro Gly Gly Phe Phe Glu Ala Gly Asn Ala
20 25 30

Lys Ala Pro Lys Leu Gln Asp Leu Ala Lys Lys Ala Ala Pro Ala Glu
35 40 45

Arg Gln Ile Asp
50

<210> 2428
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G191W"

<400> 2428
Glu Asp Pro Lys Glu Gln Val Lys Arg Tyr Gly Gly Phe Leu Arg Lys

1240

1 5 10 15

Tyr Pro Lys Arg Ser Ser Glu Val Ala Trp Trp Glu Gly Asp Gly Asp
20 25 30

Ser Met Gly His Glu Asp Leu Tyr Lys Arg Tyr Gly Gly Phe Leu Arg
35 40 45

Arg Ile Arg Pro
50

<210> 2429
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R565S"

<400> 2429
Arg Lys His Ser Leu Pro Gln Leu Leu Asp Ser Ser Ser Ala Ser Gln
1 5 10 15

Glu Tyr His Ile Val Lys Lys Ser Thr Ser Ser Ser Leu Ser Thr Thr
20 25 30

Gln Val Glu Ser Pro Trp Arg Leu Ile Arg Pro Ser Val Ile Ser Ile
35 40 45

Ile Gly Leu Tyr
50

<210> 2430
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R101fs"

<400> 2430
Asp Thr Glu Thr Val Gly Leu Ser Phe Gly Asn Ile Pro Val Phe Gly
1 5 10 15

Asp Tyr Gly Glu Lys Arg Arg Gly Gly Gln Glu Glu Glu Asn Pro Pro
20 25 30

Gly Ser Cys Ala Gly Cys Gly Leu His Leu Gly Asp Arg Ala Glu Glu
35 40 45

Glu Gln Pro Ser Arg Glu Glu Trp Glu Gly Pro Thr Ala Gly
50 55 60

<210> 2431
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G197fs"

<400> 2431
Ala Lys Trp Lys Asn Pro Asp Gly His Met Asp Gly Leu Thr Thr Asn
1 5 10 15

Gly Val Leu Val Met His Pro Arg Gly Ala Ser Pro Arg Ser Pro Ser
20 25 30

Pro Gly Ser Gly Ala Arg Ser Leu Ser Val Glu Met Cys Thr Pro Cys
35 40 45

Glu Lys Pro Gly Arg Pro Ser Asn Glu Glu Ser Trp Trp Lys Val Arg
50 55 60

Pro Thr Ser Cys Arg Thr Ala Pro Ser Leu Thr Cys Val Gly Pro Leu
65 70 75 80

Ser Ser Gly Glu Gln Gln Met Gly Phe Phe Ile Leu Gln Leu Arg Ser
85 90 95

Thr

<210> 2432
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I370fs"

<400> 2432
Gln Ser Lys Thr Lys Gln Asn Val Leu Ser Pro Glu Lys Glu Lys Gln
1 5 10 15

Met Ser Glu Pro Leu Asp Gln Lys Lys Leu Gly Gln Ile Ile Met Lys
20 25 30

Lys Met Arg Arg Pro Val Cys Tyr Lys
35 40

<210> 2433
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R118S"

<400> 2433
Thr Ser Gly Gly Asp Ala Gln Gly Met Asn Ala Ala Val Arg Ala Val
1 5 10 15

Val Arg Val Gly Ile Phe Thr Gly Ala Ser Ser Val Phe Phe Val His
20 25 30

Glu Gly Tyr Gln Gly Leu Val Asp Gly Gly Asp His Ile Lys Glu Ala
35 40 45

Thr Trp Glu Ser
50

<210> 2434
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M593fs"

<400> 2434
Ser Gly Thr Lys Arg Arg Val Phe Ile Ile Glu Thr Met Gly Gly Tyr
1 5 10 15

Cys Gly Tyr Leu Ala Asn Met Gly Gly Ser Arg Pro Glu Leu Met Pro
20 25 30

His Thr Phe Ser Lys Ser Pro Ser Thr Ser Gly Ile Cys Ser Pro Thr
35 40 45

Trp Ser Thr
50

<210> 2435
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R240H"

<400> 2435
Pro Ile Val Tyr Glu Leu Asp Lys Asn Leu Lys Pro Ile Lys Pro Met
1 5 10 15

Gln Phe Leu Gly Asp Glu Glu Thr Val His His Lys Ala Met Glu Ala
20 25 30

Val Ala Ala Gln Gly Lys Ala Lys Lys
35 40

<210> 2436

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F565C"

<400> 2436
Gln Ala Pro Ser Ser Thr Glu Ile Ser Leu Lys Leu His Ile Ala Gln
1 5 10 15

Pro Glu Asn Asn Thr His Val Ala Leu Cys Cys Lys Met Tyr Thr Ser
20 25 30

Ser Asp Cys Arg Tyr Glu Val Thr Val Lys Thr Ser Phe Ser Gln Ile
35 40 45

Leu Gly Gln Val
50

<210> 2437
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G426fs"

<400> 2437
Val Trp Leu Ser Ile Ile Ala Ala Arg Lys Gln Ser Val Glu Glu Ile
1 5 10 15

Val Arg Asp His Trp Ala Lys Phe Gly Pro Pro Leu Leu Leu Gln Val
20 25 30

<210> 2438
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I98V"

<400> 2438
Arg Thr Ala Ile Glu Ile Val Val Gln Met Ala Ala Ala Asn Gly Ile
1 5 10 15

Gly Arg Leu Ile Ile Gly Gln Asn Gly Val Val Leu Ser Thr Pro Ala
20 25 30

Val Ser Cys Ile Ile Arg Lys Ile Lys Ala Ala Gly Gly Ile Ile Leu
35 40 45

Thr Ala Ser His
50

<210> 2439
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R164fs"

<400> 2439
Lys Gly Cys Ala Ala Leu Ile His Val Pro Pro Leu Ser Arg Gly Leu
1 5 10 15

Pro Ala Ser Leu Leu Gly Arg Ala Leu Lys Ser His His Pro Gly Asn
20 25 30

Ala Gly Arg Gly Gly Lys Ala Gln Ala Gln Ser Pro Val Arg Arg Lys
35 40 45

Leu Asn His Gly Pro Ser Ser Gln Arg Glu Leu Thr Gly Gly Leu Leu
50 55 60

Leu
65

<210> 2440
<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V251fs"

<400> 2440
Leu Pro Cys Leu Pro Val Lys Leu Ser Pro Pro Leu Pro Pro Lys Lys
1 5 10 15

Val Met Ile Cys Met Pro Val Gly Gly Ala Arg Pro Leu Thr Gly Val
20 25 30

Leu His Ser Pro Glu Glu Trp Pro Ala Gly Cys Gly Pro Ala Pro Pro
35 40 45

His Cys Pro Ala Leu Pro Asp Pro Ala Pro Ala Ala Val Arg Gln Pro
50 55 60

Arg Pro Ala Pro Pro Leu His His Arg Leu Pro Pro His Ala Pro Leu
65 70 75 80

Gly Leu Gln Asn Asp Arg Arg Ala Gln Gln Asn Ala Gly His Asp His
85 90 95

Ala Glu Ala Gly Lys Leu
100

<210> 2441
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V251fs"

<400> 2441

Leu Pro Cys Leu Pro Val Lys Leu Ser Pro Pro Leu Pro Pro Lys Lys
1 5 10 15

Val Met Ile Cys Met Pro Val Gly Gly Gln Thr Ser His Trp Cys Pro
20 25 30

Thr Gln Pro Arg Arg Val Ala Ser Arg Val Trp Pro Ser Thr Thr Thr
35 40 45

Leu Ser Cys Pro Pro Arg Ser Ser Thr Ser Cys Ser Thr Ala Ala Thr
50 55 60

Ala Ser Thr Ser Pro Pro Pro Pro Ala Pro Ser Pro Cys Thr Pro Arg
65 70 75 80

Ala Ala Glu

<210> 2442
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S237fs"

<400> 2442
Ala Pro Val Pro Pro Pro Lys Pro Ala Ser Arg Asn Thr Thr Arg Glu
1 5 10 15

Ala Ala Gly Ser Ser His Ser Lys Lys Asn Asn Trp Leu
20 25

<210> 2443
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.S354fs"

<400> 2443
Asp Glu Arg Glu Lys Ser Thr Cys Ser Met Gly Ser Glu Leu Leu Pro
1 5 10 15

Met Ile Ser Pro Arg Ser Pro Ser Pro His Cys Leu Leu Ile Tyr Leu
20 25 30

Gln Ser Leu His Ala Pro Leu His Ser Leu Leu Arg Leu Phe Lys Leu
35 40 45

Cys Gln Lys Leu Ser Phe His His Pro
50 55

<210> 2444
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T35del"

<400> 2444
Ser Thr Ala Met Asp Thr Glu Pro Asn Pro Gly Thr Ser Ser Val Ser
1 5 10 15

Thr Thr Thr Ser Ser Thr Thr Thr Thr Ile Thr Thr Ser Ser Ser Arg
20 25 30

Met Gln Gln Pro Gln Ile Ser Val Tyr Ser Gly Ser Asp Arg His Ala
35 40 45

Val Gln Val Ile Gln
50

<210> 2445
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G173L"

<400> 2445
Leu Gly Ile Leu Gly Leu Gly Arg Ile Gly Arg Glu Val Ala Thr Arg
1 5 10 15

Met Gln Ser Phe Gly Met Lys Thr Ile Leu Leu Tyr Asp Pro Ile Ile
20 25 30

Ser Pro Glu Val Ser Ala Ser Phe Gly Val Gln Gln Leu Pro Leu Glu
35 40 45

Glu Ile Trp Pro Leu
50

<210> 2446
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I1681M"

<400> 2446
Lys Lys Arg Gly Arg Lys Pro Lys Lys Leu Gln Tyr Ala Lys Pro Glu
1 5 10 15

Asp Leu Glu Gln Asn Asn Val His Pro Met Met Arg Asp Glu Val Leu
20 25 30

Pro Ser Ser Thr Cys Asn Phe Leu Ser Glu Thr Asn Asn Val Lys Glu
35 40 45

Asp Leu Leu Gln
50

<210> 2447
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S32del"

<400> 2447
Pro Trp Pro Ala Asn Gln Pro Leu Pro Gly Gly Leu Leu Pro Arg Pro
1 5 10 15

Leu Ser Leu Ala Pro Ser Ser Ser Ser Cys Cys Ser Pro Pro Cys Ser
20 25 30

Gln Asp Gly Arg Met Ala Ala Gln Gly Ala Pro Arg Phe Leu Leu Thr
35 40 45

Phe Asp Phe Asp Glu
50

<210> 2448
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V22F"

<400> 2448
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
1 5 10 15

Cys Glu Ala Ser Thr Phe Phe Val Leu Leu Asn Ser Thr Asp Ser Ser
20 25 30

Pro Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln
35 40 45

<210> 2449
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.S519L"

<400> 2449
Ser Glu Thr Gln Ser Ser Pro Thr Lys Gly Val Leu Met Tyr Gln Pro
1 5 10 15

Ser Ser Val Arg Val Pro Ser Val Thr Leu Leu Val Asp Pro Ala Ala
20 25 30

Ile Pro Pro Ser Leu Thr Asp Tyr Ser Val Pro Phe His His Thr Pro
35 40 45

Ile Ser Ser Met
50

<210> 2450
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D460N"

<400> 2450
Gly Gly Asp Pro Ser Glu Asn Lys Lys Lys Val Glu Val Ile Asp Leu
1 5 10 15

Thr Ile Glu Ser Ser Ser Asp Glu Glu Asn Asn Leu Pro Pro Thr Lys
20 25 30

Lys His Cys Ser Val Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser
35 40 45

Lys Gly Val Leu
50

<210> 2451
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.H116fs"

<400> 2451
Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala Pro Gly Thr Leu Leu Gly
1 5 10 15

Pro Lys Arg Glu Val Asp Met His Pro Leu Cys Pro Ser Leu Cys Thr
20 25 30

Leu Met Ser Pro
35

<210> 2452
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R225L"

<400> 2452
Asn Asp Lys Ser Leu Arg Gln Phe Arg Tyr Thr Phe Gln Ala Cys Leu
1 5 10 15

Tyr Glu Leu Leu Lys Arg Leu Cys Asn Leu Leu Ala Val Leu Leu Phe
20 25 30

Val Ala Val Ala Gly Leu Thr Phe Phe Ala Leu Ser Phe Gly Phe Tyr
35 40 45

Tyr Glu Tyr Gly
50

<210> 2453
<211> 49
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P787fs"

<400> 2453
Val Thr Val Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr
1 5 10 15

Val Leu Thr Pro Phe Ser Gly Pro Pro Leu Leu Lys Leu Thr Trp Ile
20 25 30

Met Trp Ser Leu Lys Ser Thr Asp Thr Cys Arg Arg Ser Ser Gly Ala
35 40 45

Gly

<210> 2454
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V183G"

<400> 2454
Asn Ala Gln Lys Arg Lys Ser Leu Tyr Lys Gln Ile Gly Leu Tyr Pro
1 5 10 15

Val Leu Val Ile Asp Ser Ser Gly Tyr Gly Gly Asn Pro Asn Tyr Thr
20 25 30

Gly Arg Ile Arg Leu Asp Ile Gln Gly Thr Gly Gln Leu Leu Phe Ser
35 40 45

Val Val Ile Asn
50

<210> 2455
<211> 35
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A346fs"

<400> 2455
Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile Gln Leu Lys Trp
1 5 10 15

Lys Arg Pro Pro Glu Asn Glu Ala Pro Gln Cys Pro Ser Cys Met Pro
20 25 30

Ser Gly Thr
35

<210> 2456
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F1473L"

<400> 2456
Glu Glu Leu Asn Gly Tyr Ile Trp His Leu Ile His Ala Pro Pro Glu
1 5 10 15

Val Ala Glu Cys Asp Leu Val Tyr Thr Leu Leu Phe His Pro Leu Pro
20 25 30

Arg Asp Glu Lys Ala Met Gly Thr Ser Pro Ala Pro Lys Ser Ser Asp
35 40 45

Gly Thr Trp Ala
50

<210> 2457
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R287fs"

<400> 2457
Pro Leu Asp Phe Ser Lys Asp Thr Ser Gly Lys Pro Val Ala Arg Ser
1 5 10 15

Lys Thr Met Pro Pro Gln Val Pro Pro Ala Pro Met Pro Pro Ala Met
20 25 30

Ala Thr Glu Arg Met Arg Arg Leu Ala Arg Thr Ala Gly Phe Leu Gln
35 40 45

Pro Arg Trp Ala Pro Gly Pro Thr Leu Leu Pro Met Ala Met Ser Cys
50 55 60

Leu Arg Ser Gln Lys Arg Glu Met Arg Arg Leu Leu His Phe Ala Thr
65 70 75 80

Cys Trp Ile Ser Phe Asp Leu Ala Leu Thr Ser Lys Thr Thr Ser Ser
85 90 95

Leu Ala Met Ser Gly Val Leu Ser Pro Leu Ala Gln Ser Thr Ser Gly
100 105 110

Met Arg Ser Thr
115

<210> 2458
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N345K"

<400> 2458
Gly Glu Thr Ser Thr Lys Ser Leu Trp Val Ile Asn Ser Ala Leu Arg

1 5 10 15

Ile Lys Ile Leu Cys Ala Thr Tyr Val Lys Lys Val Asn Ile Arg Asp
20 25 30

Ile Asp Lys Ile Tyr Val Arg Thr Gly Ile Tyr His Gly Gly Glu Pro
35 40 45

Leu Cys Asp Asn
50

<210> 2459
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D350G"

<400> 2459
Lys Ser Leu Trp Val Ile Asn Ser Ala Leu Arg Ile Lys Ile Leu Cys
1 5 10 15

Ala Thr Tyr Val Asn Val Asn Ile Arg Gly Gly Ile Asp Lys Ile Tyr
20 25 30

Val Arg Thr Gly Ile Tyr His Gly Gly Glu Pro Leu Cys Asp Asn Val
35 40 45

Asn Thr Gln Arg
50

<210> 2460
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R38H"

<400> 2460
Ile His Leu Met Pro Pro Arg Ile Leu Val Glu Cys Leu Leu Pro Asn
1 5 10 15

Gly Met Ile Val Thr Leu Glu Cys Leu His His Glu Ala Thr Leu Ile
20 25 30

Thr Ile Lys His Glu Leu Phe Lys Glu Ala Arg Lys Tyr Pro Leu His
35 40 45

Gln Leu Leu Gln
50

<210> 2461
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E39K"

<400> 2461
His Leu Met Pro Pro Arg Ile Leu Val Glu Cys Leu Leu Pro Asn Gly
1 5 10 15

Met Ile Val Thr Leu Glu Cys Leu Arg Lys Lys Ala Thr Leu Ile Thr
20 25 30

Ile Lys His Glu Leu Phe Lys Glu Ala Arg Lys Tyr Pro Leu His Gln
35 40 45

Leu Leu Gln Asp
50

<210> 2462
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C420R"

<400> 2462
Asp Leu Pro Arg Ala Ala Arg Leu Cys Leu Ser Ile Cys Ser Val Lys
1 5 10 15

Gly Arg Lys Gly Ala Lys Glu Glu His Arg Arg Pro Leu Ala Trp Gly
20 25 30

Asn Ile Asn Leu Phe Asp Tyr Thr Asp Thr Leu Val Ser Gly Lys Met
35 40 45

Ala Leu Asn Leu
50

<210> 2463
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.PVPHGLEDL447del"

<400> 2463
Leu Ala Trp Gly Asn Ile Asn Leu Phe Asp Tyr Thr Asp Thr Leu Val
1 5 10 15

Ser Gly Lys Met Ala Leu Asn Leu Trp Leu Asn Pro Ile Gly Val Thr
20 25 30

Gly Ser Asn Pro Asn Lys Glu Thr Pro Cys Leu Glu Leu Glu Phe Asp
35 40 45

Trp Phe Ser Ser Val Val Lys Phe Pro Asp Met Ser Val Ile Glu Glu
50 55 60

His Ala Asn Trp Ser Val Ser Arg Glu Ala Gly Phe Ser
65 70 75

<210> 2464
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E453K"

<400> 2464
Asn Leu Phe Asp Tyr Thr Asp Thr Leu Val Ser Gly Lys Met Ala Leu
1 5 10 15

Asn Leu Trp Pro Val Pro His Gly Leu Lys Lys Asp Leu Leu Asn Pro
20 25 30

Ile Gly Val Thr Gly Ser Asn Pro Asn Lys Glu Thr Pro Cys Leu Glu
35 40 45

Leu Glu Phe Asp
50

<210> 2465
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L455fs"

<400> 2465
Asp Tyr Thr Asp Thr Leu Val Ser Gly Lys Met Ala Leu Asn Leu Trp
1 5 10 15

Pro Val Pro His Gly Leu Glu Asp Leu Ala Glu Pro Tyr Trp Cys Tyr
20 25 30

Trp Ile Lys Ser Lys
35

<210> 2466
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E542K"

<400> 2466
Leu Ala Arg Asp Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys
1 5 10 15

Ala Ile Ser Thr Arg Asp Pro Leu Ser Lys Lys Ile Thr Glu Gln Glu
20 25 30

Lys Asp Phe Leu Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu
35 40 45

Ile Leu Pro Lys
50

<210> 2467
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E545K"

<400> 2467
Asp Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys Ala Ile Ser
1 5 10 15

Thr Arg Asp Pro Leu Ser Glu Ile Thr Lys Lys Gln Glu Lys Asp Phe
20 25 30

Leu Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu Ile Leu Pro
35 40 45

Lys Leu Leu Leu
50

<210> 2468
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E545A"

<400> 2468
Asp Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys Ala Ile Ser
1 5 10 15

Thr Arg Asp Pro Leu Ser Glu Ile Thr Ala Ala Gln Glu Lys Asp Phe
20 25 30

Leu Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu Ile Leu Pro
35 40 45

Lys Leu Leu Leu
50

<210> 2469
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E545G"

<400> 2469
Asp Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys Ala Ile Ser
1 5 10 15

Thr Arg Asp Pro Leu Ser Glu Ile Thr Gly Gly Gln Glu Lys Asp Phe
20 25 30

Leu Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu Ile Leu Pro
35 40 45

Lys Leu Leu Leu
50

<210> 2470
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q546K"

<400> 2470
Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys Ala Ile Ser Thr
1 5 10 15

Arg Asp Pro Leu Ser Glu Ile Thr Glu Lys Lys Glu Lys Asp Phe Leu
20 25 30

Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu Ile Leu Pro Lys
35 40 45

Leu Leu Leu Ser
50

<210> 2471
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q546P"

<400> 2471
Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys Ala Ile Ser Thr
1 5 10 15

Arg Asp Pro Leu Ser Glu Ile Thr Glu Pro Pro Glu Lys Asp Phe Leu
20 25 30

Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu Ile Leu Pro Lys
35 40 45

Leu Leu Leu Ser
50

<210> 2472
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q546R"

<400> 2472
Asn Glu Leu Arg Glu Asn Asp Lys Glu Gln Leu Lys Ala Ile Ser Thr
1 5 10 15

Arg Asp Pro Leu Ser Glu Ile Thr Glu Arg Arg Glu Lys Asp Phe Leu
20 25 30

Trp Ser His Arg His Tyr Cys Val Thr Ile Pro Glu Ile Leu Pro Lys
35 40 45

Leu Leu Leu Ser
50

<210> 2473
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.M1V"

<400> 2473
Val Val Pro Pro Arg Pro Ser Ser Gly Glu Leu Trp Gly Ile His Leu
1 5 10 15

Met Pro Pro Arg Ile Leu Val Glu Cys Leu Leu
20 25

<210> 2474

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E726K"

<400> 2474
His Leu Asn Arg Gln Val Glu Ala Met Glu Lys Leu Ile Asn Leu Thr
1 5 10 15

Asp Ile Leu Lys Gln Glu Lys Lys Asp Lys Lys Thr Gln Lys Val Gln
20 25 30

Met Lys Phe Leu Val Glu Gln Met Arg Arg Pro Asp Phe Met Asp Ala
35 40 45

Leu Gln Gly Phe
50

<210> 2475
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R88Q"

<400> 2475
Gln Asp Glu Ser Ser Tyr Ile Phe Val Ser Val Thr Gln Glu Ala Glu
1 5 10 15

Arg Glu Glu Phe Phe Asp Glu Thr Arg Gln Gln Leu Cys Asp Leu Arg
20 25 30

Leu Phe Gln Pro Phe Leu Lys Val Ile Glu Pro Val Gly Asn Arg Glu
35 40 45

Glu Lys Ile Leu
50

<210> 2476
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R93Q"

<400> 2476
Tyr Ile Phe Val Ser Val Thr Gln Glu Ala Glu Arg Glu Glu Phe Phe
1 5 10 15

Asp Glu Thr Arg Arg Leu Cys Asp Leu Gln Gln Leu Phe Gln Pro Phe
20 25 30

Leu Lys Val Ile Glu Pro Val Gly Asn Arg Glu Glu Lys Ile Leu Asn
35 40 45

Arg Glu Ile Gly
50

<210> 2477
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M1004I"

<400> 2477
Arg Phe Gln Glu Met Cys Tyr Lys Ala Tyr Leu Ala Ile Arg Gln His
1 5 10 15

Ala Asn Leu Phe Ile Asn Leu Phe Ser Ile Ile Met Leu Gly Ser Gly
20 25 30

Met Pro Glu Leu Gln Ser Phe Asp Asp Ile Ala Tyr Ile Arg Lys Thr
35 40 45

Leu Ala Leu Asp
    50

<210> 2478
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.M1043V"

<400> 2478
Asp Ile Ala Tyr Ile Arg Lys Thr Leu Ala Leu Asp Lys Thr Glu Gln
1   5   10   15

Glu Ala Leu Glu Tyr Phe Met Lys Gln Val Val Asn Asp Ala His His
            20   25   30

Gly Gly Trp Thr Thr Lys Met Asp Trp Ile Phe His Thr Ile Lys Gln
        35   40   45

His Ala Leu Asn
    50

<210> 2479
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.M1043I"

<400> 2479
Asp Ile Ala Tyr Ile Arg Lys Thr Leu Ala Leu Asp Lys Thr Glu Gln
1   5   10   15

Glu Ala Leu Glu Tyr Phe Met Lys Gln Ile Ile Asn Asp Ala His His
            20   25   30

Gly Gly Trp Thr Thr Lys Met Asp Trp Ile Phe His Thr Ile Lys Gln
35 40 45

His Ala Leu Asn
50

<210> 2480
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N1044Y"

<400> 2480
Ile Ala Tyr Ile Arg Lys Thr Leu Ala Leu Asp Lys Thr Glu Gln Glu
1 5 10 15

Ala Leu Glu Tyr Phe Met Lys Gln Met Tyr Tyr Asp Ala His His Gly
20 25 30

Gly Trp Thr Thr Lys Met Asp Trp Ile Phe His Thr Ile Lys Gln His
35 40 45

Ala Leu Asn
50

<210> 2481
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N1044K"

<400> 2481
Ile Ala Tyr Ile Arg Lys Thr Leu Ala Leu Asp Lys Thr Glu Gln Glu
1 5 10 15

Ala Leu Glu Tyr Phe Met Lys Gln Met Lys Lys Asp Ala His His Gly

20 25 30

Gly Trp Thr Thr Lys Met Asp Trp Ile Phe His Thr Ile Lys Gln His
35 40 45

Ala Leu Asn
50

<210> 2482
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H1047R"

<400> 2482
Ile Arg Lys Thr Leu Ala Leu Asp Lys Thr Glu Gln Glu Ala Leu Glu
1 5 10 15

Tyr Phe Met Lys Gln Met Asn Asp Ala Arg Arg His Gly Gly Trp Thr
20 25 30

Thr Lys Met Asp Trp Ile Phe His Thr Ile Lys Gln His Ala Leu Asn
35 40 45

<210> 2483
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H1047L"

<400> 2483
Ile Arg Lys Thr Leu Ala Leu Asp Lys Thr Glu Gln Glu Ala Leu Glu
1 5 10 15

Tyr Phe Met Lys Gln Met Asn Asp Ala Leu Leu His Gly Gly Trp Thr
20 25 30

Thr Lys Met Asp Trp Ile Phe His Thr Ile Lys Gln His Ala Leu Asn
35 40 45

<210> 2484
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G106V"

<400> 2484
Glu Phe Phe Asp Glu Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln
1 5 10 15

Pro Phe Leu Lys Val Ile Glu Pro Val Val Val Asn Arg Glu Glu Lys
20 25 30

Ile Leu Asn Arg Glu Ile Gly Phe Ala Ile Gly Met Pro Val Cys Glu
35 40 45

Phe Asp Met Val
50

<210> 2485
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R108H"

<400> 2485
Phe Asp Glu Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln Pro Phe
1 5 10 15

Leu Lys Val Ile Glu Pro Val Gly Asn His His Glu Glu Lys Ile Leu
20 25 30

Asn Arg Glu Ile Gly Phe Ala Ile Gly Met Pro Val Cys Glu Phe Asp
35 40 45

Met Val Lys Asp
50

<210> 2486
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E110del"

<400> 2486
Glu Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln Pro Phe Leu Lys
1 5 10 15

Val Ile Glu Pro Val Gly Asn Arg Glu Lys Ile Leu Asn Arg Glu Ile
20 25 30

Gly Phe Ala Ile Gly Met Pro Val Cys Glu Phe Asp Met Val Lys Asp
35 40 45

Pro Glu Val Gln Asp
50

<210> 2487
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K111E"

<400> 2487
Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln Pro Phe Leu Lys Val
1 5 10 15

Ile Glu Pro Val Gly Asn Arg Glu Glu Glu Ile Leu Asn Arg Glu
20 25 30

Ile Gly Phe Ala Ile Gly Met Pro Val Cys Glu Phe Asp Met Val Lys
35 40 45

Asp Pro Glu Val
50

<210> 2488
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K111del"

<400> 2488
Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln Pro Phe Leu Lys Val
1 5 10 15

Ile Glu Pro Val Gly Asn Arg Glu Glu Ile Leu Asn Arg Glu Ile Gly
20 25 30

Phe Ala Ile Gly Met Pro Val Cys Glu Phe Asp Met Val Lys Asp Pro
35 40 45

Glu Val Gln Asp Phe
50

<210> 2489
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C381R"

<400> 2489
Cys Phe Ala Leu Tyr Ala Val Ile Glu Lys Ala Lys Lys Ala Arg Ser

1 5 10 15

Thr Lys Lys Lys Ser Lys Lys Ala Asp Arg Arg Pro Ile Ala Trp Ala
20 25 30

Asn Leu Met Leu Phe Asp Tyr Lys Asp Gln Leu Lys Thr Gly Glu Arg
35 40 45

Cys Leu Tyr Met
50

<210> 2490
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V165I"

<400> 2490
Arg His Pro Pro Ser Glu Glu Ser Gln Ala Phe Gln Arg Gln Leu Thr
1 5 10 15

Ala Leu Ile Gly Tyr Asp Val Thr Asp Ile Ile Ser Asn Val His Asp
20 25 30

Asp Glu Leu Glu Phe Thr Arg Arg Gly Leu Val Thr Pro Arg Met Ala
35 40 45

Glu Val Ala Ser
50

<210> 2491
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G376R"

<400> 2491
Ala Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly
1 5 10 15

Asp Tyr Thr Leu Thr Leu Arg Lys Gly Arg Arg Asn Asn Lys Leu Ile
20 25 30

Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr
35 40 45

Phe Ser Ser Val
50

<210> 2492
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K379N"

<400> 2492
Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr Thr
1 5 10 15

Leu Thr Leu Arg Lys Gly Gly Asn Asn Asn Asn Leu Ile Lys Ile Phe
20 25 30

His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser
35 40 45

Val Val Glu Leu
50

<210> 2493
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.KPDL567del"

<400> 2493
Arg Arg Arg Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg
1 5 10 15

Glu Ile Asp Lys Arg Met Asn Ser Ile Ile Gln Leu Arg Lys Thr Arg
20 25 30

Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys Lys
35 40 45

Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr
50 55 60

<210> 2494
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L371R"

<400> 2494
Leu Leu Ser Thr Ser Ser Leu Ala Ser His Asp Ser Thr Leu Ser Leu
1 5 10 15

Ala Ser Ser Gln Ala Ser Gly Pro Ala Arg Arg Ser Arg His Leu Leu
20 25 30

Thr Ser Phe Val Ser Gly Leu Ser Asp Gly Met Asp Ser Gly Tyr Val
35 40 45

Glu Asp Ser Glu
50

<210> 2495
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.S291fs"

<400> 2495
Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro
1 5 10 15

Pro Ser His Arg Pro Leu Lys Ser Pro Pro Glu Arg Asp Pro Val Leu
20 25 30

Cys Leu Lys Gly Leu Thr Asn Gly Gln Pro Ser Gln Asp
35 40 45

<210> 2496
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L164F"

<400> 2496
Leu Gln Glu Glu Leu Ala Arg Ser Phe Phe Trp Gln Val Leu Glu Ala
1 5 10 15

Val Arg His Cys His Asn Cys Gly Val Phe Phe His Arg Asp Ile Lys
20 25 30

Asp Glu Asn Ile Leu Ile Asp Leu Asn Arg Gly Glu Leu Lys Leu Ile
35 40 45

Asp Phe Gly Ser
50

<210> 2497
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L184F"

<400> 2497
His Asn Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu
1   5   10   15

Ile Asp Leu Asn Arg Gly Glu Leu Lys Phe Phe Ile Asp Phe Gly Ser
            20   25   30

Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg
        35   40   45

Val Tyr Ser Pro
    50

<210> 2498
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R219K"

<400> 2498
Ile Val Thr Arg Asn Val Phe Ser His Arg Leu Ser Val Tyr Arg Lys
1   5   10   15

Tyr Asp Leu Lys Gly Ser Thr Val Ala Lys Lys Glu Ala Ser Asp Lys
            20   25   30

Glu Lys Ala Lys Glu Leu Pro Thr Leu Lys Asp Asn Asp Phe Ile Asn
        35   40   45

Glu Gly Gln Lys
    50

<210> 2499
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R204H"

<400> 2499
Asn Thr Leu Leu Pro Gln Phe Leu Gly Met Tyr Arg Val Ser Val Asp
1 5 10 15

Asn Glu Asp Ser Tyr Met Leu Val Met His His Asn Met Phe Ser His
20 25 30

Arg Leu Pro Val His Arg Lys Tyr Asp Leu Lys Gly Ser Leu Val Ser
35 40 45

Arg Glu Ala Ser
50

<210> 2500
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P295fs"

<400> 2500
Pro Pro Gly Lys Pro Ser Thr Glu Ala Arg Ser Ala Ala Ser Asn Thr
1 5 10 15

Gly Thr Pro Asp Gly Pro Glu Ala Pro Gln Ala Gln Met Pro Pro Pro
20 25 30

Met Pro Ala Leu Gly Ser Ser Gly Pro His Pro Pro Val Pro Pro Thr
35 40 45

His Pro Asn Met Glu Gly Leu Cys Leu Pro Arg Ala Cys Leu Ser Gly
50 55 60

Ala Cys Arg Thr Leu Pro Glu Thr Leu Arg Thr Ala Pro Arg Lys Ser
65 70 75 80

Ser Leu Met Pro Thr Lys Ala Ser Arg Thr Val Arg Arg Ser Ser Pro
85 90 95

Arg Arg

<210> 2501
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V699M"

<400> 2501
Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys
1 5 10 15

Asn Glu Tyr Met Pro Ser Arg Ile Ile Met Met Tyr Arg Asp Gly Val
20 25 30

Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe
35 40 45

Leu Asp Cys Leu
50

<210> 2502
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T938M"

<400> 2502
Val Glu Asn Ser Ala Ser Arg Ala Asn Leu Ser Leu Arg Val Thr Ala
1 5 10 15

Glu Glu Pro Ile Cys Gly Leu Arg Ala Met Met Pro Ser Pro Glu Ala
20 25 30

Arg Val Leu Gln Gly Val Leu Val Arg Tyr Ser Pro Val Val Glu Ala
35 40 45

Gly Ser Asp Met
50

<210> 2503
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y486F"

<400> 2503
Lys Leu Ile Arg Tyr Val Thr Thr Phe Asp Phe Phe Leu Ala Ala Cys
1 5 10 15

Glu Ile Ile Phe Cys Phe Phe Ile Phe Phe Phe Tyr Val Val Glu Glu
20 25 30

Ile Leu Glu Ile Arg Ile His Lys Leu His Tyr Phe Arg Ser Phe Trp
35 40 45

Asn Cys Leu Asp
50

<210> 2504
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F1856L"

<400> 2504
Pro Pro Val Ala Ser Leu Ser Pro Thr Ser Gly Ser Ile Gly Gly Gly

1 5 10 15

Thr Thr Leu Val Ile Thr Gly Asn Gly Leu Leu Tyr Pro Gly Asn Thr
20 25 30

Thr Val Thr Ile Gly Asp Glu Pro Cys Gln Ile Ile Ser Ile Asn Pro
35 40 45

Asn Glu Val Tyr
50

<210> 2505
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.K76fs"

<400> 2505
Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu Gly Ala Glu Asn
1 5 10 15

Leu Arg Lys Val Thr Thr Asp Lys Lys Val Trp Leu Met
20 25

<210> 2506
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W230fs"

<400> 2506
Phe Leu Gln Arg Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala
1 5 10 15

Phe Val Ser Leu Gly Ala Pro Trp Gly Ala Trp Pro Arg Pro Cys Ala
20 25 30

Ser Trp Leu Gln Glu Thr Thr Thr Gly Ser Gln Ser Ser Gly Pro
35 40 45

<210> 2507
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L53fs"

<400> 2507
Lys Met Ile Lys Cys Val Ile Pro Gly Ser Asp Pro Phe Leu Glu Tyr
1 5 10 15

Asn Asn Tyr Gly Cys Tyr Cys Gly Leu Trp Gly Ala Gln Ala Pro Pro
20 25 30

Trp Met Asn Trp Thr Ser Ala Ala Arg His Met Thr Thr Ala Met Thr
35 40 45

Arg Pro Arg Ser Trp Thr Ala Val Asn Phe Cys Trp Thr Thr Arg Thr
50 55 60

Pro Thr Pro Ile His Thr Arg Ala Leu Ala Arg Gln Ser Pro Val Ala
65 70 75 80

Ala Lys Thr Lys Ser Val Arg Pro Ser Phe Ala Thr Ala Thr Ala Thr
85 90 95

Leu Pro Ser Ala Phe Gln Lys Leu His Ile Thr Arg His Thr Arg Thr
100 105 110

Trp Thr Pro Arg Ser Ile Val Arg Val Glu Tyr His Leu Ser Lys Ala
115 120 125

Ser Pro Leu Ser Ala Ser Ser His Thr Val Leu Ser Asn Lys Ala Pro
130 135 140

Cys
145

<210> 2508
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R201Q"

<400> 2508
Gly Pro Asp Leu Cys Cys Arg Glu His Asp Arg Cys Pro Gln Asn Ile
1 5 10 15

Ser Pro Leu Gln Tyr Asn Tyr Gly Ile Gln Gln Asn Tyr Arg Phe His
20 25 30

Thr Ile Ser His Cys Asp Cys Asp Thr Arg Phe Gln Gln Cys Leu Gln
35 40 45

Asn Gln His Asp
50

<210> 2509
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K184fs"

<400> 2509
Phe Glu Ser Thr Gly Val Leu Leu Glu His Leu Lys Ser His Ala Gly
1 5 10 15

Lys Ser Ser Gly Gly Val Lys Glu Lys Ser Thr Ser Ala Asn Ile Val
20 25 30

Ile Ala Gly Ser Thr Pro Glu Arg Met Ser Gly Asp Thr Trp Trp Cys
35 40 45

Thr Leu Glu Glu Arg Thr Ser Ser Val Ser Ile Val His Arg Asp Leu
50 55 60

Gly Glu Arg Ile Thr
65

<210> 2510
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P10fs"

<400> 2510
Met Thr Thr Phe Phe Thr Ser Val Pro Pro Gly Phe Lys Met Gln Ser
1 5 10 15

Arg Arg Arg Lys Trp Ala Gly Asn
20

<210> 2511
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R201fs"

<400> 2511
Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala
1 5 10 15

Ala Ile Tyr Arg Arg His Arg Gly Gly Leu Cys His Leu Arg Val Trp
20 25 30

Arg Gln Pro His Gln Pro Leu Leu Gly Asp Gln Arg His Thr Leu Leu
35 40 45

His

<210> 2512
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E499fs"

<400> 2512
Lys Gly Arg Val Leu Val Lys Gly Lys Lys Leu Pro Ala Ala Arg Ser
1 5 10 15

Glu Asp Gly Arg Ala Leu Ser Asp Arg Arg Arg Arg Arg Arg Met Thr
20 25 30

Arg Arg Lys Lys Arg Arg Trp Arg Leu Gln Arg Arg Gly Gly Trp Pro
35 40 45

Ser Arg Ser Pro Arg Ser Cys Arg Pro Trp Leu Cys Thr Ala Thr Pro
50 55 60

Pro Ala
65

<210> 2513
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G439C"

<400> 2513
Asn Thr Val Gly Ser Leu Leu His Phe Leu Thr Lys Leu Pro Ala Ser
1 5 10 15

Glu Thr Ala His Gly Arg Ile Ser Val Cys Cys Pro Cys Leu Lys Gln
20 25 30

Cys Val Arg Asp Thr Val Cys Glu Tyr Arg Ala Thr Leu Gln Arg Thr
35 40 45

Ser Ile Ser Gln
50

<210> 2514
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G564C"

<400> 2514
Leu Met Glu Gln Glu Gln Thr Ile Tyr Arg Arg Val Leu Pro Val Asp
1 5 10 15

Tyr Leu Cys Phe Leu Thr Arg Asp Leu Cys Cys Thr Pro Glu Cys Gln
20 25 30

Ser Ser Leu Pro Cys Leu Lys Ala Ser Ile Ser Ala Ser Ile Leu Thr
35 40 45

Thr Gln Asn Gly
50

<210> 2515
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M564I"

<400> 2515
Val Lys Gly Lys Lys Leu Pro Ser Asp Pro Asp Val Leu Glu Gly Glu
1 5 10 15

Val Thr Asp Glu Asp Glu Glu Ala Glu Ile Ile Ser Arg Arg Met Ser
20 25 30

Val Asp Tyr Asn Gly Glu Gln Lys Gln Ile Arg Leu Cys Arg Glu Leu
35 40 45

Ser Asp Leu Val
50

<210> 2516
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1386Q"

<400> 2516
Gln Asp Ala Arg Arg Arg Gln Glu Gln Ile Gln Ala Met Pro Leu Ala
1 5 10 15

Asp Ser Gln Ala Val Arg Glu Gln Leu Gln Gln Gln Glu Gln Ala Leu
20 25 30

Leu Glu Glu Ile Glu Arg His Gly Glu Lys Val Glu Glu Cys Gln Arg
35 40 45

Phe Ala Lys Gln
50

<210> 2517
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R110L"

<400> 2517

Val Asp Arg Cys Leu Phe Tyr Tyr Lys Asp Glu Lys Glu Glu Ser Ile
1 5 10 15

Leu Gly Ser Ile Pro Leu Leu Ser Phe Leu Leu Val Ala Ala Val Gln
20 25 30

Pro Ser Asp Asn Ile Ser Arg Lys His Thr Phe Lys Ala Glu His Ala
35 40 45

Gly Val Arg Thr
50

<210> 2518
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V328fs"

<400> 2518
Thr Asn Pro Asp Lys Ile Ala Gln Arg Lys Ser Ser Met Asn Gln Leu
1 5 10 15

Gln Gln Trp Val Asn Leu Arg Arg Gly Tyr Pro Arg Leu Lys Thr Phe
20 25 30

Gly Val Pro Leu Gly Ser Ile Leu Cys Leu Ala Gly Ser Leu Ser Thr
35 40 45

Met Ala Pro Thr Pro Pro Ser Thr Pro Met Ile Ile Ser Thr Thr Arg
50 55 60

Gln Glu Cys Gly Arg Arg Ala Ser Val Pro Cys Arg Pro Met Ile Gly
65 70 75 80

Ser Ala Arg Pro Gly Pro Trp Arg Thr Ser Ala Met Pro Ser Ala Met
85 90 95

Gly Val Ala Leu Pro Thr Ser Cys Glu Ser Gly Arg Ser Pro Pro Ala
100 105 110

Thr Gly Gly Arg Met Pro Pro Ser Gly Ser Gln Ala Pro Pro Gly Ser

115 120 125

Gln Ser Ile Met Met Ser Trp Met Pro Pro Leu Ala Pro Cys Ala Ala
130 135 140

Cys Pro Cys Ser Pro Ala Pro Thr Leu Cys Pro Ala His Pro Ala Arg
145 150 155 160

Ala Pro Thr Ala Val Pro Ala Phe Thr Pro Leu Ser Ala His Pro Val
165 170 175

Pro Val Leu Ser Gly Cys His Leu Ala Val Arg Thr Ser Met Leu Thr
180 185 190

Leu Leu Pro Met
195

<210> 2519
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S146P"

<400> 2519
Thr Ala Leu Leu Glu Ala Asn Ser Thr Pro Ala Pro Ala Gly Ala Thr
1 5 10 15

Val Pro Pro Arg Ser Arg Arg Val Cys Pro Pro Lys Val Arg Cys Val
20 25 30

Thr Arg Ser Trp Ser Pro Cys Lys Val Glu Arg Arg Ile Trp Val Arg
35 40 45

Val Tyr Ser Pro
50

<210> 2520
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E384K"

<400> 2520
Ala Ile Ile Phe Leu Gln Asn Ser Phe Cys Ser Leu Asn Thr His Arg
1 5 10 15

Thr Pro Arg Thr Ala Gln Glu Val Ala Lys Lys Leu Ile Asp Gln His
20 25 30

Glu Thr Met Met Lys Leu Val Leu Glu Asp Pro Leu Leu Val Ser Leu
35 40 45

Arg Leu Glu Gly
50

<210> 2521
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A895V"

<400> 2521
Arg Ile Ile His Asn Trp Asp Leu Thr Lys Arg Pro Ile Cys Arg Gln
1 5 10 15

Ala Leu Lys Phe Leu Thr Gln Ile Arg Val Val Gln Pro Leu Ile Asn
20 25 30

Leu Gln Met Val Asn Ala Ser Leu Tyr Glu His Val Glu Arg Met His
35 40 45

Leu Ile Gly Arg
50

<210> 2522
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S459L"

<400> 2522
Asp Gln Ser Phe Arg Thr Gly Ser Pro Gly Asp Ala Pro Glu Arg Pro
1 5 10 15

Pro Leu Cys Asp Phe Ser Glu Gly Leu Leu Leu Ala Pro Met Asp Phe
20 25 30

Tyr Arg Phe Thr Val Glu Ser Pro Ser Thr Val Thr Ser Gly Gly Gly
35 40 45

His His Asp Pro
50

<210> 2523
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T254fs"

<400> 2523
Gln Pro Ser Ala Asp Arg Ala Ser Ser Leu Ser Arg Pro Trp Glu Lys
1 5 10 15

Thr Asp Lys Gly Ala Thr Tyr Thr Pro Arg His Pro Arg Ser
20 25 30

<210> 2524
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.E351Q"

<400> 2524
Gly Glu Met Gln Ala Ser Gly Pro Pro Ala Pro Gly Thr Val Gln Val
1 5 10 15

Ser Val Asn Gly Met Asp Asp Ser Pro Gln Gln Pro Ala Lys Pro Ser
20 25 30

Gln Ala Glu Gly Thr Pro Gly Thr Pro Pro Lys Asp Ala Thr Thr Ser
35 40 45

Thr Ala Leu Pro
50

<210> 2525
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R306W"

<400> 2525
Leu Glu Thr Leu Val Leu Ser Arg Ser Leu Thr Gln Glu Leu Gln Gly
1 5 10 15

Thr Val Glu Ala Leu Glu Ser Ser Val Trp Trp Gly Leu Pro Ala Gly
20 25 30

Ala Gln Glu Lys Val Ala Glu Val Arg Arg Ser Val Asp Ala Leu Gln
35 40 45

Thr Ala Phe Ala
50

<210> 2526
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D233G"

<400> 2526
Lys Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu
1 5 10 15

Ser Lys Lys Gly His Ser Phe Glu Val Gly Gly Val Trp Ser Ile Gly
20 25 30

Cys Ile Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu Thr Ser
35 40 45

Cys Leu Lys Glu
50

<210> 2527
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P296fs"

<400> 2527
Gly Trp Thr Pro Glu Gly Gly Cys Gly Phe Cys Asn Gln Asp Arg Arg
1 5 10 15

Thr Leu Pro Gly Gly Gln Pro Pro Pro Pro Gly Val Ser Gly Arg Val
20 25 30

Cys Gly Thr Ala Tyr Ser Val Ser Ala Pro Leu Pro Ala Ala Ala Ala
35 40 45

Thr Pro Gly Leu Ser Pro Arg Gln Gly His Pro Phe Pro Ala Gln Gln
50 55 60

Arg Gly Leu Pro
65

<210> 2528
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R297fs"

<400> 2528
Gly Trp Thr Pro Glu Gly Gly Cys Gly Phe Cys Asn Gln Asp Arg Arg
1 5 10 15

Thr Leu Pro Gly Gly Gln Pro Pro Pro Gly Cys Phe Trp Pro Cys Leu
20 25 30

Trp Asn Ser Leu Leu Arg Phe Cys Pro Ala Ser Cys Ser Gly Cys Tyr
35 40 45

Ser Trp Thr Ile Pro Pro Thr Gly Ser Pro Phe Ser Cys Thr Thr Thr
50 55 60

Arg Ser Ser Met Asn Pro Thr Ser Leu Thr Pro Gly Arg Ser Ser Arg
65 70 75 80

Thr Thr Ser Gln Leu
85

<210> 2529
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E77K"

<400> 2529
Phe Pro Ser Pro Gly Pro Val Ala Leu Gly Ser Ala Ala Pro Phe Leu
1 5 10 15

Pro Leu Pro Gly Val Pro Ser Gly Leu Lys Lys Phe Leu Val Gln Ile
20 25 30

Asp Gln Ile Leu Ile His Gln Lys Ala Glu Arg Val Glu Thr Phe Leu
35 40 45

Gly Trp Glu Thr
50

<210> 2530
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P1016fs"

<400> 2530
Leu Thr Pro Pro Gly Gln Ser Pro Gly Ser Ala Pro Ile Ile Ile Asn
1 5 10 15

Ile Asn Arg Ala Gln Leu Thr Asn Pro Arg
20 25

<210> 2531
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1295K"

<400> 2531
Ala Leu Glu Cys Lys Glu Ala Phe Ala Glu Leu Gln Thr Asp Ile His
1 5 10 15

Glu Leu Thr Asn Asp Leu Asp Gly Ala Lys Ser Ile Pro Phe Leu Asp
20 25 30

Tyr Arg Thr Tyr Ala Met Arg Val Leu Phe Pro Gly Ile Glu Asp His
35 40 45

Pro Val Leu Lys
50

<210> 2532
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P464fs"

<400> 2532
Tyr Asn Gly Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu
1 5 10 15

Lys Lys Ile Arg Ala Asp Gly Pro Pro Pro Met Val Gly Ser Ser Thr
20 25 30

Arg Trp Ser Leu Cys Ser Arg Thr Glu Ala Pro Ser Ser Gly Thr Trp
35 40 45

Pro Ser Pro Leu Ile Ser Ala Thr Cys Thr Ser Cys Leu Arg Asp Arg
50 55 60

Ser Pro Gly Ser Pro Trp Ser His Val Ser Ser Ile Arg Leu Val Gly
65 70 75 80

Ser Ala

<210> 2533
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.P58S"

<400> 2533
Leu Thr His Leu Ala Val His Arg Val Thr Gly Glu Val Phe Val Gly
1 5 10 15

Ala Val Asn Arg Val Phe Lys Leu Ala Ser Ser Asn Leu Thr Glu Leu
20 25 30

Arg Ala His Val Thr Gly Pro Val Glu Asp Asn Ala Arg Cys Tyr Pro
35 40 45

Pro Pro Ser Met
50

<210> 2534
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S462L"

<400> 2534
Ile Tyr Ile Tyr Leu Thr Ala Gly Lys Glu Val Arg Arg Ile Arg Val
1 5 10 15

Ala Asn Cys Asn Lys His Lys Ser Cys Leu Leu Glu Cys Leu Thr Ala
20 25 30

Thr Asp Pro His Cys Gly Trp Cys His Ser Leu Gln Arg Cys Thr Phe
35 40 45

Gln Gly Asp Cys
50

<210> 2535
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R819C"

<400> 2535
Asn Ile Asn Val Ser Glu Tyr Cys Val Ala Thr Tyr Cys Gly Phe Leu
1 5 10 15

Ala Pro Ser Leu Lys Ser Ser Lys Val Cys Cys Thr Asn Val Thr Val
20 25 30

Lys Leu Arg Val Gln Asp Thr Tyr Leu Asp Cys Gly Thr Leu Gln Tyr
35 40 45

Arg Glu Asp Pro
50

<210> 2536
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 2536
Gly Leu Gln Cys Ala Gly Gly Ala Gly Arg Gly Asp Leu Tyr Ser Arg
1 5 10 15

Leu Val Ser Val Phe Pro Ala Arg Glu Leu Leu Leu Phe Ala Val Phe
20 25 30

Glu Arg Pro Gln Gly Ser Pro Ala Ala Arg Ala Ala Pro Ala Ala Leu
35 40 45

Cys Ala Phe Arg
50

<210> 2537
<211> 85
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 2537
Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser
1 5 10 15

Ala Arg Leu Gly Gly Pro Cys Pro Pro Ala Val Thr Arg Ala Ser Ala
20 25 30

Pro Arg Ala Thr Ala Ala Ala Gly Ala Trp Arg Gly Arg Arg Pro Pro
35 40 45

Thr Ala Arg Ser Ser Ala Thr Thr Arg Gly Pro Pro Ser Ser Thr Ser
50 55 60

Arg Ala Val Gly Arg Pro Pro Cys Trp Arg Gly Pro Gly Ser Thr Thr
65 70 75 80

His Thr Ser Arg Pro
85

<210> 2538
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K651R"

<400> 2538
Ala Lys Arg Ile Lys Gln Leu His His Glu Ala Gln Gln Ser Glu Gly
1 5 10 15

Glu Gln Asn Tyr Arg Lys Phe Arg Ala Arg Arg Ile Cys Pro Gly Glu
20 25 30

Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met
35 40 45

Phe Ala Glu Met
    50

<210> 2539
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.G174W"

<400> 2539
Asn Leu Glu Lys Leu Leu Val Phe Thr Ala Ala Gly Val Lys Pro Gln
1   5   10   15

Gly Lys Val Ala Gly Phe Asp Leu Asp Trp Trp Thr Leu Ile Thr Thr
            20   25   30

Arg Ser Gly Lys Val Phe Pro Thr Gly Pro Ser Asp Trp Arg Ile Leu
        35   40   45

Tyr Pro Glu Ile
    50

<210> 2540
<211> 52
<212> PRT
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<223> /note="p.T37M"

<400> 2540
Gly Ala Val Ala Gly Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe
1   5   10   15

Ser Asp Asp Ser Pro Trp Ser Gly Ile Met Met Glu Arg Pro Leu His
            20   25   30

Ile Leu Pro Trp Ser Pro Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr

35 40 45

Thr Asn Glu Asn
50

<210> 2541
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L223P"

<400> 2541
Leu Asp Leu Tyr Val Asn Ile Ala Lys Gln Asp Ile Met Leu Ser Leu
1 5 10 15

Ala Asn Leu Val Arg Leu Asn Gln Ala Pro Pro Phe Pro Pro Ser Lys
20 25 30

Arg Lys Met Glu Ser Leu Tyr Gln Cys Gly Phe Asp Asp Thr Val Lys
35 40 45

Phe Leu Leu Lys
50

<210> 2542
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P1199fs"

<400> 2542
Leu Ala Tyr Val Cys Cys Val Arg Gln Leu Glu Val Val Lys Ser Ser
1 5 10 15

Asp Tyr Cys Glu Tyr Leu Arg Pro Pro Ser Thr Ala Thr Ala Pro Trp
20 25 30

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Thr Ser Ala Ser Ser Thr Arg Ser Ala Lys Trp Ala Thr Ser Thr Gly
        35                  40                  45

Ala Arg Cys Leu Thr Ser Gly Ala Ala Ala Ala Cys Trp Arg Arg Cys
    50                  55                  60

Ser Ala Thr Ser Arg Gly Arg Ala Arg Ser Pro Arg Val Arg Ser Ser
65                  70                  75                  80

Pro Val Pro Thr Pro Pro Ser Arg Thr Leu Pro Lys Leu Cys Leu Ala
                85                  90                  95

Leu Ser Pro Pro Ser Pro Pro Trp Trp Met Thr Asn Leu Thr Thr Arg
            100                 105                 110

Arg Ser Thr Arg Arg Ser Cys Trp Thr Ser Pro Gly Met His Thr Gln
        115                 120                 125

Thr Ser Arg Ala Pro Gln Pro Ser Arg Ala Gln Thr Trp Arg Thr Ser
    130                 135                 140

Pro His Cys Gly Ile Asp Thr Pro Val Trp Leu Ser Gln Asn Cys Leu
145                 150                 155                 160

Arg Ala Pro Leu Thr Arg Thr Gly Arg Gly Leu Cys
                165                 170
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<210> 2543
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="p.R73C"

<400> 2543

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Pro Arg Ala Leu Pro Pro Thr Leu Phe Leu Pro His Phe Leu Gly Gly
1               5                   10                  15

Asp Gly Pro Cys Leu Thr Pro Gln Pro Cys Cys Ala Pro Ala Ala Leu
            20                  25                  30
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Pro Asn Arg Ser Leu Ala Val Ala Gly Gly Thr Pro Arg Ala Ala Pro
35 40 45

Lys Lys Arg Arg
50

<210> 2544
<211> 31
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I301fs"

<400> 2544
Arg His Val Pro Lys His Leu Pro Pro Ala Leu Tyr Lys Leu His Leu
1 5 10 15

Lys Asn Asn Lys Leu Glu Lys Ile Pro Arg Gly Pro Ser Ala Ser
20 25 30

<210> 2545
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A150V"

<400> 2545
Gln Leu Gln His Leu Cys Val Ala His Asn Lys Leu Ser Val Ala Pro
1 5 10 15

Gln Phe Leu Pro Arg Ser Leu Arg Val Val Val Asp Leu Ala Ala Asn
20 25 30

Gln Val Met Glu Ile Phe Pro Leu Thr Phe Gly Glu Lys Pro Ala Leu
35 40 45

Arg Ser Val Tyr
50

<210> 2546
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S162fs"

<400> 2546
Thr Ala Thr Ala Lys Pro Asn Thr Thr Ser Ser Gln Asn Gly Ala Glu
1 5 10 15

Asp Thr Thr Asn Ser Gly Gly Lys Ser Gln Pro Gln Cys Asp His Arg
20 25 30

Pro His Ile His
35

<210> 2547
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G75W"

<400> 2547
Ser Ala Pro Val Pro Ile Ala Ala His Ala Ser Val Ala Gly His Leu
1 5 10 15

Ser Thr Ser Thr Thr Val Ser Ser Ser Trp Trp Ala Gln Asn Ser Asp
20 25 30

Ser Thr Lys Lys Thr Leu Val Thr Leu Ile Ala Asn Asn Asn Ala Gly
35 40 45

Asn Pro Leu Val

50

<210> 2548
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E603D"

<400> 2548
Pro Phe Gln Ser His Phe Cys Val Val Ser Lys Pro Lys Asp Cys Ile
1 5 10 15

Phe Pro Tyr Ala Phe Lys Glu Val Ile Asp Asp Lys Lys Asn Val Lys
20 25 30

Val Glu Val Ala Ala Thr Glu Arg Thr Leu Leu Gly Phe Phe Leu Ala
35 40 45

Lys Val His Lys
50

<210> 2549
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V411L"

<400> 2549
Glu Ile Gly Phe Gln Lys Asp Ser Gln Gly Glu Tyr Lys Ala Pro Gln
1 5 10 15

Cys Ile His Met Asp Cys Leu Arg Trp Leu Leu Lys Arg Asp Ser Tyr
20 25 30

Leu Pro Val Gly Ser His Asn Leu Lys Ala Ala Ala Lys Ala Lys Leu
35 40 45

Gly Tyr Asp Pro
50

<210> 2550
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S459F"

<400> 2550
Tyr Asp Pro Val Glu Leu Asp Pro Glu Asp Met Cys Arg Met Ala Thr
1 5 10 15

Glu Gln Pro Gln Thr Leu Ala Thr Tyr Phe Phe Val Ser Asp Ala Val
20 25 30

Ala Thr Tyr Tyr Leu Tyr Met Lys Tyr Val His Pro Phe Ile Phe Ala
35 40 45

Leu Cys Thr Ile
50

<210> 2551
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R573L"

<400> 2551
Glu Ser Gly Val Phe Arg Ser Asp Ile Pro Cys Arg Phe Arg Met Asn
1 5 10 15

Pro Ala Ala Phe Asp Phe Leu Leu Gln Leu Leu Val Glu Lys Thr Leu
20 25 30

Arg His Ala Leu Glu Glu Glu Glu Lys Val Pro Val Glu Gln Val Thr
35 40 45

Asn Phe Glu Glu
50

<210> 2552
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P286R"

<400> 2552
Asp Asp Leu Val Glu Arg Pro Asp Pro Val Val Leu Ala Phe Asp Ile
1 5 10 15

Glu Thr Thr Lys Leu Pro Leu Lys Phe Arg Arg Asp Ala Glu Thr Asp
20 25 30

Gln Ile Met Met Ile Ser Tyr Met Ile Asp Gly Gln Gly Tyr Leu Ile
35 40 45

Thr Asn Arg Glu
50

<210> 2553
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P97fs"

<400> 2553
Glu Glu Thr Ser Ala Glu Glu Ala Val Ser Trp Gln Glu Arg Arg Met
1 5 10 15

Ala Ala Ala Pro Pro Gly Cys Thr Pro Gln Leu Cys Trp Thr
20 25 30

<210> 2554
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R860Q"

<400> 2554
Asn Ala Val Pro Phe Lys Ser Ala Arg Lys Ala Val Asp Glu Glu Glu
1 5 10 15

Glu Ala Val Glu Glu Arg Arg Asn Met Gln Gln Thr Ile Trp Val Thr
20 25 30

Gly Arg Lys Gly Leu Thr Glu Arg Glu Ala Ala Ala Leu Ile Val Glu
35 40 45

Glu Ala Arg Met
50

<210> 2555
<211> 41
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.K332Q"

<400> 2555
Ile Phe Ser Val Glu Ser Thr Gly Val Leu Pro Pro Asp Val Leu Val
1 5 10 15

Ser Glu Ala Ile Lys Val Leu Met Gly Gln Gln Cys Arg Arg Phe Leu
20 25 30

Asp Glu Leu Asp Ala Val Gln Met Asp

35 40

<210> 2556
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L372F"

<400> 2556
Gly Asp Asn Lys Val Asp Asp Arg Asp Tyr Tyr Gly Asn Lys Arg Leu
1 5 10 15

Glu Leu Ala Gly Gln Leu Leu Ser Leu Phe Phe Phe Glu Asp Leu Phe
20 25 30

Lys Lys Phe Asn Ser Glu Met Lys Lys Ile Ala Asp Gln Val Ile Pro
35 40 45

Lys Gln Arg Ala
50

<210> 2557
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P231T"

<400> 2557
Gly Arg Arg Asn Leu Gln Pro Arg Pro Ser Ala Phe Lys Pro Leu Ser
1 5 10 15

Lys Asn Gly Ala Val Ala Ser Phe Val Thr Thr Arg Pro Gly Pro Leu
20 25 30

Lys Pro Ser Leu Gly Pro Trp Ser Leu Ser Phe Cys Asp Asp Ala Trp
35 40 45

Pro Ser Val Leu
    50

<210> 2558
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

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<223> /note="p.P242H"

<400> 2558
Phe Lys Pro Leu Ser Lys Asn Gly Ala Val Ala Ser Phe Val Pro Arg
1   5   10   15

Pro Gly Pro Leu Lys Pro Ser Leu Gly His His Trp Ser Leu Ser Phe
            20   25   30

Cys Asp Asp Ala Trp Pro Ser Val Leu Val Gln Pro Ala Pro Ser Ala
        35   40   45

Ile Trp Asp Phe
    50

<210> 2559
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.R306Q"

<400> 2559
Trp Val Gly Cys His Pro Asn Gly Met Lys Ile Phe Phe Tyr Asp Ser
1   5   10   15

Glu Asn Pro Pro Ala Ser Glu Val Leu Gln Gln Ile Gln Asn Ile Leu
            20   25   30

Thr Glu Glu Pro Lys Val Thr Gln Val Tyr Ala Glu Asn Gly Thr Val
35 40 45

Leu Gln Gly Ser
50

<210> 2560
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K750fs"

<400> 2560
Val Ala Ser Ser Pro Asn Gly Lys Glu Ser Asp Leu Arg Arg Ser Glu
1 5 10 15

Val Pro Cys Ala Pro Met Pro Lys Lys Leu Ile Ser His Leu Met Lys
20 25 30

Trp Ala His Pro
35

<210> 2561
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R508C"

<400> 2561
Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu Lys Ser
1 5 10 15

Leu His Glu Lys Leu Lys Gln Asp Lys Cys Cys Phe Ser Thr Phe Leu
20 25 30

Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro Gly
35 40 45

Asp Trp Thr Leu
50

<210> 2562
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K507E"

<400> 2562
Glu Glu Gln Asn Thr Gly Ile Ser Gln Asp Glu Ile Leu Thr Asn Lys
1 5 10 15

Gln Lys Gln Ile Glu Val Ala Glu Lys Glu Glu Met Asn Ser Glu Leu
20 25 30

Ser Leu Ser His Lys Lys Glu Glu Asp Leu Leu Arg Glu Asn Ser Met
35 40 45

Leu Gln Glu Glu
50

<210> 2563
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V166M"

<400> 2563
Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
1 5 10 15

Leu Ile Val Met Leu Arg Asp Thr Asp Met Met Asn Lys Lys Asp Lys

20 25 30

Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
35 40 45

Val Val Lys Leu
50

<210> 2564
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V288M"

<400> 2564
Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu
1 5 10 15

Gly Val His Glu Gln Lys Gln Gln Val Met Met Lys Phe Leu Ile Lys
20 25 30

Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
35 40 45

Ile Leu Ala Val
50

<210> 2565
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R303I"

<400> 2565
Leu Gly Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
1 5 10 15

Lys Lys Ala Asn Leu Asn Ala Leu Asp Ile Ile Tyr Gly Arg Thr Ala
20 25 30

Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu
35 40 45

Leu Glu Gln Asn
50

<210> 2566
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K674N"

<400> 2566
Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
1 5 10 15

Met Lys His Gln Ser Gln Leu Arg Glu Asn Asn Lys Tyr Leu Glu Asp
20 25 30

Ile Glu Ser Val Lys Lys Arg Asn Asp Asn Leu Leu Lys Ala Leu Gln
35 40 45

Leu Asn Glu Leu
50

<210> 2567
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S112G"

<400> 2567
Asp Asp Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys
1 5 10 15

Cys His Cys Phe Pro Cys Cys Arg Gly Gly Gly Ser Lys Ser Lys Val
20 25 30

Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr
35 40 45

His Val Arg Gly
50

<210> 2568
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D51N"

<400> 2568
Lys Trp Cys Arg His Cys Phe Pro Trp Cys Arg Gly Ser Gly Lys Ser
1 5 10 15

Asn Val Gly Thr Ser Gly Asp His Asp Asn Asn Ser Ala Met Lys Thr
20 25 30

Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Trp Cys
35 40 45

Arg Gly Ser Ser
50

<210> 2569
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R136H"

<400> 2569
Gly Ser Gly Lys Ser Lys Val Gly Pro Trp Gly Asp Tyr Asp Asp Ser
1 5 10 15

Ala Phe Met Glu Pro Arg Tyr His Val His His Arg Glu Asp Leu Asp
20 25 30

Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu
35 40 45

Ile Val Met Leu
50

<210> 2570
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T239A"

<400> 2570
Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp Val Gly Leu Ala Met Gly
1 5 10 15

Lys Leu Tyr Gly Asn Asp Phe Ser Gln Ala Ala Thr Ile Ser Arg Phe
20 25 30

Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys Lys Leu Lys Pro Leu
35 40 45

Leu Glu Lys Trp
50

<210> 2571
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T239S"

<400> 2571
Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp Val Gly Leu Ala Met Gly
1 5 10 15

Lys Leu Tyr Gly Asn Asp Phe Ser Gln Ser Ser Thr Ile Ser Arg Phe
            20 25 30

Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys Lys Leu Lys Pro Leu
        35 40 45

Leu Glu Lys Trp
    50

<210> 2572
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.D321Y"

<400> 2572
Gly Gly Gly Gly Gly Ala Gly Pro Gly Leu Asn Ser His Asp Pro His
1 5 10 15

Ser Asp Glu Asp Thr Pro Thr Ser Asp Tyr Tyr Leu Glu Gln Phe Ala
            20 25 30

Lys Gln Phe Lys Gln Arg Arg Ile Lys Leu Gly Phe Thr Gln Ala Asp
        35 40 45

Val Gly Leu Ala
    50

<210> 2573
<211> 93
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P135fs"

<400> 2573
Ala Phe Pro Ala Leu Asp Gly Gly Asp Ala Leu Ser Cys Thr Ser Ala
1 5 10 15

Ser Pro Ala Pro Ser Ser Ala Pro Pro Ala Leu Pro Arg Arg Ser Pro
20 25 30

Arg Pro Gln Pro Leu Arg Trp Thr Ser Ser His Cys Cys Arg Ser Ser
35 40 45

Ser Trp Pro His Pro Thr Gln His Gln Ala Leu Thr Pro Arg Arg Lys
50 55 60

Gly Pro Pro Gly Ala Arg Gln Ala Ser Asp Leu Lys Val Asn Gly Leu
65 70 75 80

Val Leu Arg Arg Thr Ala Pro Lys Thr Arg Arg Leu Pro
85 90

<210> 2574
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S382R"

<400> 2574
Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln Ala Glu
1 5 10 15

Asp Ser Lys Ser Ser His Ser His Thr Arg Arg Lys Lys His Lys Lys
20 25 30

Lys Thr His His Cys Ser Glu Glu Lys Glu Asp Glu Asp Tyr Met Pro
35 40 45

Ile Lys Asn Thr
    50

<210> 2575
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="p.P454fs"

<400> 2575
Gly Glu Ser Trp Glu Leu Met Asp Ser Ala Gly Asn Lys Leu Ile Ala
1   5   10   15

Pro Ala Val Cys Phe Val Ile Pro Pro Gln Thr Leu Arg Pro Trp Leu
            20   25   30

Trp Leu Thr Ala Trp Ala Ala Ser Thr Gly Ala Cys Gly Arg Arg Gln
        35   40   45

Leu Gly Ala Asn Ala Arg Cys Ser Ser Gly Met Arg Cys
    50   55   60

<210> 2576
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.H326Y"

<400> 2576
Asp Trp Lys Glu Tyr Leu Asn Leu Leu Ile Cys Glu Glu Ser His Leu
1   5   10   15

Lys Tyr Met Glu Asp Tyr His Gln Phe Tyr Tyr Glu Asp Val Lys Asp
            20   25   30

Ala Gln Glu Leu Leu Arg Lys Val Asp Ser Asp Leu Asn Gln Lys Tyr
35 40 45

Gly Pro Asp Phe
50

<210> 2577
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R311W"

<400> 2577
Ile His Leu His Val Asn Leu Val Arg Gln Glu Met Phe Pro His Asp
1 5 10 15

Pro Ala Glu Ala Leu Cys Arg Ala Phe Trp Trp Val Thr Asp Glu Arg
20 25 30

Phe Val Gln Lys Ala Ala Arg Glu Ser Leu Arg Cys Gly Thr Thr Gly
35 40 45

Val Val Thr Phe
50

<210> 2578
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P226fs"

<400> 2578
Asn Ser Arg Thr Leu Thr Arg Ala Ala Ser Leu Arg Gly Gly Val Gly
1 5 10 15

Ala Pro Gly Ser Pro Ser Thr Pro Pro His Ala Ser Leu Pro Arg Arg

20 25 30

Arg Phe Pro Met Ser Ala Trp Ser Ser Glu Arg Leu Lys Val His Ser
35 40 45

Arg Lys Trp Thr Tyr Arg
50

<210> 2579
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 2579
Leu Ser Ser Arg Glu Lys Ile Ser Leu Gln Asp Leu Ser Lys Glu Arg
1 5 10 15

Arg Pro Gly Gly Ala Gly Gly Pro Pro Ser Arg Thr Arg Met Arg Gly
20 25 30

Lys Lys Val Pro Pro Asn His Pro Leu Gln Asn Pro Glu Pro Ser Met
35 40 45

Ala Ser Pro Pro Arg Arg Thr Pro Ala Leu Arg Val Pro Cys Ser Leu
50 55 60

Lys Arg Pro Pro Ser Pro Gly Ala Leu Ala Ser
65 70 75

<210> 2580
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.P179R"

<400> 2580
Cys Tyr Pro Arg Val Ser Ser Ala Val Lys Ala Glu Leu Arg Gln Tyr
1 5 10 15

Phe Arg Asn Leu Cys Ser Asp Asp Thr Arg Arg Met Val Arg Arg Ala
20 25 30

Ala Ala Ser Lys Leu Gly Glu Phe Ala Lys Val Leu Glu Leu Asp Asn
35 40 45

Val Lys Ser Glu
50

<210> 2581
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R183W"

<400> 2581
Val Ser Ser Ala Val Lys Ala Glu Leu Arg Gln Tyr Phe Arg Asn Leu
1 5 10 15

Cys Ser Asp Asp Thr Pro Met Val Arg Trp Trp Ala Ala Ala Ser Lys
20 25 30

Leu Gly Glu Phe Ala Lys Val Leu Glu Leu Asp Asn Val Lys Ser Glu
35 40 45

Ile Ile Pro Met
50

<210> 2582
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S219L"

<400> 2582
Lys Val Leu Glu Leu Asp Asn Val Lys Ser Glu Ile Ile Pro Met Phe
1 5 10 15

Ser Asn Leu Ala Ser Asp Glu Gln Asp Leu Leu Val Arg Leu Leu Ala
20 25 30

Val Glu Ala Cys Val Asn Ile Ala Gln Leu Leu Pro Gln Glu Asp Leu
35 40 45

Glu Ala Leu Val
50

<210> 2583
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S256F"

<400> 2583
Ile Ala Gln Leu Leu Pro Gln Glu Asp Leu Glu Ala Leu Val Met Pro
1 5 10 15

Thr Leu Arg Gln Ala Ala Glu Asp Lys Phe Phe Trp Arg Val Arg Tyr
20 25 30

Met Val Ala Asp Lys Phe Thr Glu Leu Gln Lys Ala Val Gly Pro Glu
35 40 45

Ile Thr Lys Thr
50

<210> 2584
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.P326L"

<400> 2584
Ser Lys Gly Thr Ile Arg Leu Cys Asp Met Arg Ala Ser Ala Leu Cys
1 5 10 15

Asp Arg His Thr Lys Phe Phe Glu Glu Leu Leu Glu Asp Pro Ser Asn
20 25 30

Arg Ser Phe Phe Ser Glu Ile Ile Ser Ser Ile Ser Asp Val Lys Phe
35 40 45

Ser His Ser Gly
50

<210> 2585
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

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<223> /note="p.T389fs"

<400> 2585
Arg Lys Val Gln Lys Glu Gly Lys Ile Ser Tyr Ala Asp Phe Val Trp
1 5 10 15

Phe Leu Ile Ser Glu Glu Asp Lys Lys His Arg Pro Ala Ser Ser Thr
20 25 30

Gly Ser Ala Ala Trp Thr Trp Thr Gly Thr Ala Pro Cys Pro Cys Ser
35 40 45

Ser Ser Ser Thr Ser Thr Arg Ser Ser Ala Glu Gly Trp Thr Ala Trp
50 55 60

Pro Ser Arg Pro Cys Pro Ser Arg Thr Ala Ser Ala Arg Cys Trp Thr
65 70 75 80

Trp Ser Ser Arg Gly Leu Lys Gly Arg Ser Arg Cys Arg Thr

85 90

<210> 2586
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F310L"

<400> 2586
Glu Leu Arg Arg Ser Ser Phe Leu Gln Asn Val Ala Leu Leu Glu Glu
1 5 10 15

Glu Ala Asp Ile Asn Gln Leu Thr Glu Leu Leu Phe Ser Tyr Glu His
20 25 30

Phe Tyr Val Ile Tyr Cys Lys Phe Trp Glu Leu Asp Thr Asp His Asp
35 40 45

Leu Leu Ile Asp
50

<210> 2587
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S259Y"

<400> 2587
Gly Phe Ala Leu Pro Leu Lys Glu Glu His Lys Ile Phe Leu Leu Lys
1 5 10 15

Val Leu Leu Pro Leu His Lys Val Lys Tyr Tyr Leu Ser Val Tyr His
20 25 30

Pro Gln Leu Ala Tyr Cys Val Val Gln Phe Leu Glu Lys Asp Ser Thr
35 40 45

Leu Thr Glu Pro
50

<210> 2588
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L597F"

<400> 2588
Asp Ser Val Pro Leu Ile Ser Asp Ala Val Glu Asn Met Asp Ser Thr
1 5 10 15

Leu His Tyr Ile His Ser Asp Ser Asp Phe Phe Ser Asn Asn Ser Ser
20 25 30

Phe Ser Pro Asp Glu Glu Arg Arg Thr Lys Val Gln Asp Val Val Pro
35 40 45

Gln Ala Leu Leu
50

<210> 2589
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R301C"

<400> 2589
Leu Val His Glu Gly Tyr Lys Phe Met Phe Asp Glu Lys Leu Val Thr
1 5 10 15

Val Trp Ser Ala Pro Asn Tyr Cys Tyr Cys Cys Cys Gly Asn Ile Ala
20 25 30

Ser Ile Met Val Phe Lys Asp Val Asn Thr Arg Glu Pro Lys Leu Phe
35 40 45

Arg Ala Val Pro
50

<210> 2590
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R265L"

<400> 2590
Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn Glu Thr Val Leu
1 5 10 15

Glu Met Glu Glu Gln Leu Val Tyr Leu Leu Leu Asp Ser Phe Gly Leu
20 25 30

Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro Met Ala Gly
35 40 45

Ile Ser His Thr
50

<210> 2591
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A268T"

<400> 2591
Gln Pro Glu Phe Ser Glu Ala Ala Gln Thr Pro Leu Trp Lys Pro Gln
1 5 10 15

Ser Ser Glu Pro Lys Arg Asp Ser Ser Thr Thr Phe Pro Lys Lys Ala
20 25 30

Ser Gln Pro Pro Leu Ser Asp Phe Pro Lys Lys Pro Pro Gln Pro Glu
35 40 45

Leu Gly Asp Leu
50

<210> 2592
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C84S"

<400> 2592
Lys Leu Gln Val Leu Asp Leu Gln Asp Val Cys Glu Asn Phe Trp Met
1 5 10 15

Val Trp Ser Glu Ala Met Ala His Gly Ser Ser Phe Leu Asn Ala Lys
20 25 30

Arg Asn Lys Thr Pro Val Gln Asp Cys Pro Arg Met Arg Glu Arg Gln
35 40 45

Pro Leu Thr Val
50

<210> 2593
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R104Q"

<400> 2593
Ala Met Ala His Gly Cys Phe Leu Asn Ala Lys Arg Asn Lys Thr Pro

1 5 10 15

Val Gln Asp Cys Pro Arg Met Arg Glu Gln Gln Gln Pro Leu Thr Val
20 25 30

Phe Val Glu Leu Trp Leu Lys Asn Arg Thr Leu Asp Glu Tyr Leu Thr
35 40 45

Cys Leu Leu Leu
50

<210> 2594
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R248H"

<400> 2594
Leu Thr Gln Phe Thr Pro Tyr Leu Gly His Met Arg Asn Leu Gln Lys
1 5 10 15

Leu Ile Leu Ser His Met Asp Val Ser His His Tyr Val Ser Pro Glu
20 25 30

Gln Lys Lys Glu Ile Val Thr Gln Phe Thr Thr Gln Phe Leu Lys Leu
35 40 45

Arg Cys Leu Gln
50

<210> 2595
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I448V"

<400> 2595
Ala Leu Cys Trp Gly Arg Phe Ala Glu Leu Gly Ala Glu Leu Met Lys
1 5 10 15

Thr Pro Arg Asp Leu Arg Gln Pro Lys Val Val Ile Val Phe Cys Thr
20 25 30

Val Pro Cys Pro Arg Cys Gly Ile Arg Ala Ser Tyr Asp Leu Glu Pro
35 40 45

Ser His Cys Leu
50

<210> 2596
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R319H"

<400> 2596
Leu Glu Met Val Val Met Thr Asp Cys Leu Leu Ser Glu Ser Asp Leu
1 5 10 15

Lys His Leu Ser Trp Cys Pro Ser Ile His His Gln Leu Lys Glu Leu
20 25 30

Asp Leu Arg Gly Val Thr Leu Thr His Phe Ser Pro Glu Pro Leu Thr
35 40 45

Gly Leu Leu Glu
50

<210> 2597
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R274fs"

<400> 2597
Lys Pro Gln Gly Pro Pro Pro Pro Gly Lys Pro Gln Gly Pro Pro Ala
1 5 10 15

Gln Gly Gly Ser Lys Ser Gln Ser Ala Asp Leu Leu Gln Glu Ser His
20 25 30

Lys Asp His Pro Asn Lys Lys Ala Thr Ile Leu Lys Val Pro His Leu
35 40 45

Gln Gln Glu Ala Ile Pro Ser Ser Leu Arg His Leu Leu Leu Asp Ser
50 55 60

Pro Arg Asp His His Ala Leu Leu Lys Gly Ala Asp Leu Pro Asp Leu
65 70 75 80

Pro Ser Asp Ser Leu Pro Ser His Leu Gly Phe Asn Asp Arg Lys
85 90 95

<210> 2598
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S588C"

<400> 2598
Pro Tyr Pro Leu Lys Lys Gln Asn Gly Lys Ile Lys Tyr Glu Cys Asn
1 5 10 15

Val Cys Ala Lys Thr Phe Gly Gln Leu Cys Cys Asn Leu Lys Val His
20 25 30

Leu Arg Val His Ser Gly Glu Arg Pro Phe Lys Cys Gln Thr Cys Asn
35 40 45

Lys Gly Phe Thr
50

<210> 2599
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1036L"

<400> 2599
His Leu Cys Asn Arg Cys Phe Gly Gln Gln Thr Asn Leu Asp Arg His
1 5 10 15

Leu Lys Lys His Glu His Glu Asn Ala Leu Leu Val Ser Gln His Pro
20 25 30

Gly Val Leu Thr Asn His Leu Gly Thr Ser Ala Ser Ser Pro Thr Ser
35 40 45

Glu Ser Asp Asn
50

<210> 2600
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E271Q"

<400> 2600
Arg Arg His Lys Lys Tyr Thr Cys Gly Ser Val Gly Ala Ala Leu Tyr
1 5 10 15

Glu Gly Leu Ala Glu Glu Leu Lys Pro Gln Gln Gly Leu Gly Gly Gly
20 25 30

Ser Gly Gln Ala His Glu Cys Lys Asp Cys Glu Arg Met Phe Pro Asn
35 40 45

Lys Tyr Ser Leu

50

<210> 2601
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.*802K"

<400> 2601
Asp Ser Val Gly Thr Glu Asp Cys Arg Ile Asn Ser Ala Val Tyr Ser
1 5 10 15

Ala Asp Glu Ser Leu Ser Ala His Lys Lys Lys Lys Glu Lys Lys Gln
20 25 30

Ala Ile Leu Asp Glu Asn Ala Asn Gly Lys Ile His Ile Thr Ser Tyr
35 40 45

Leu Leu
50

<210> 2602
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M387L"

<400> 2602
Gly Gln Glu Leu Gly Ile Arg Ser Ser Ile Glu Pro Ala Glu Ser Leu
1 5 10 15

Gly Gln Ala Val Asn Cys Trp Ser Gly Leu Leu Gly Met Ser Met Ala
20 25 30

Arg Asn Trp Ala Ser Ser Gly Ala Ala Ser Gly Arg Lys Ser Ser Trp
35 40 45

Gln Gly Glu Asn
    50

<210> 2603
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.D201Y"

<400> 2603
Leu Arg Leu Ser Gln Asn His Ile Ser Arg Ile Pro Pro Gly Val Phe
1   5   10   15

Ser Lys Leu Glu Asn Leu Leu Leu Leu Tyr Tyr Leu Gln His Asn Arg
            20   25   30

Leu Ser Asp Gly Val Phe Lys Pro Asp Thr Phe His Gly Leu Lys Asn
        35   40   45

Leu Met Gln Leu
    50

<210> 2604
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.F469L"

<400> 2604
Ser Lys Asp Gly Thr Lys Ile Pro Met Phe Ile Val His Lys Lys Gly
1   5   10   15

Ile Lys Leu Asp Gly Ser His Pro Ala Leu Leu Leu Tyr Gly Tyr Gly
            20   25   30

Gly Phe Asn Ile Ser Ile Thr Pro Asn Tyr Ser Val Ser Arg Leu Ile
35 40 45

Phe Val Arg His
50

<210> 2605
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V731I"

<400> 2605
Ala Lys Glu Ile Ile Lys Ile Pro Asp Gln Pro Asp Thr Leu Cys Phe
1 5 10 15

Gln Ile Arg Gly Ala Ala Pro Pro Tyr Ile Ile Tyr Ala Val Gly Arg
20 25 30

Gly Ser Glu Ala Met Ala Ala Gly Leu Cys Ala Gly Gln Cys Ile Leu
35 40 45

Lys Val Asn Gly
50

<210> 2606
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1246K"

<400> 2606
Cys Leu Glu His Leu Phe Asn Gln Val Asp Ser Ile Asn Ala Leu Leu
1 5 10 15

Lys Gly Pro Val Met Ser Arg Ala Phe Lys Lys Glu Thr Lys His Phe
20 25 30

Pro Met Asn His Ser Leu Gln Glu Phe Lys Gln Lys Glu Glu Cys Thr
35 40 45

Ile Arg Gly Arg
50

<210> 2607
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R363Q"

<400> 2607
Trp Phe Val Cys Met Ala Lys Thr Pro Glu Glu Lys His Glu Trp Phe
1 5 10 15

Glu Ala Ile Leu Lys Glu Arg Glu Arg Gln Gln Lys Gly Leu Lys Leu
20 25 30

Gly Met Glu Gln Asp Thr Trp Val Met Ile Ser Glu Gln Gly Glu Lys
35 40 45

Leu Tyr Lys Met
50

<210> 2608
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.R562fs"

<400> 2608
Cys Asp Asn Gly Phe Met His His Val Leu Glu Lys Ser Glu Phe Lys

1 5 10 15

Asp Glu Pro Leu Leu Phe Arg Phe Phe Phe Gly
20 25

<210> 2609
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N675H"

<400> 2609
Pro Thr Thr Pro Glu Glu Pro Thr Pro Thr Thr Pro Glu Glu Pro Ala
1 5 10 15

Pro Thr Thr Pro Lys Ala Ala Ala Pro His His Thr Pro Lys Glu Pro
20 25 30

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro
35 40 45

Ala Pro Thr Thr
50

<210> 2610
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1289Q"

<400> 2610
Leu Phe Trp Val Gln Ile Val Leu Trp Arg Gln Gly Phe Tyr Tyr Pro
1 5 10 15

Leu Gly Ile Val Arg Glu Val Leu Pro Gln Gln Ala Ser Thr Trp Glu
20 25 30

Gln Gly Leu Arg Ile Leu Gly Leu Glu Tyr Ser Leu Arg Val Pro Pro
35 40 45

Ser Asp Gln Ala
50

<210> 2611
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R407Q"

<400> 2611
Cys Pro Leu Asp Ala Leu Asn Thr Thr Lys Pro Lys Ser Leu Ala Val
1 5 10 15

Lys Lys Ala Lys Trp His Leu Gly Ile Gln Gln Ser Gln Ser Lys Pro
20 25 30

Tyr Asp Ile Met Ala Glu Val Tyr Arg Ala Met Lys Gln Leu Asp Phe
35 40 45

Glu Trp Lys Val
50

<210> 2612
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P104H"

<400> 2612
Pro Thr Val Phe Arg Trp Thr Gly Gly Gly Lys Glu Val Tyr Leu Ser
1 5 10 15

Gly Ser Phe Asn Asn Trp Ser Lys Leu His His Leu Thr Arg Ser His
20 25 30

Asn Asn Phe Val Ala Ile Leu Asp Leu Pro Glu Gly Glu His Gln Tyr
35 40 45

Lys Phe Phe Val
50

<210> 2613
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S309L"

<400> 2613
Glu Arg Leu Lys Val Val Asp Val Ile Gly Thr Lys Val Tyr Asn Asp
1 5 10 15

Gly Glu Gln Ile Ile Ala Gln Gly Asp Leu Leu Ala Asp Ser Phe Phe
20 25 30

Ile Val Glu Ser Gly Glu Val Lys Ile Thr Met Lys Arg Lys Gly Lys
35 40 45

Ser Glu Val Glu
50

<210> 2614
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.G432fs"

<400> 2614

Phe Leu Thr His Leu Ile Cys Thr Phe Gln Thr Lys Asp His Leu Phe
1 5 10 15

Phe Val Met Glu Phe Leu Asn Gly Gly Thr
20 25

<210> 2615
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q157fs"

<400> 2615
Ser Ser Gly Glu Ala Pro Lys Asp Asn Glu Glu Arg Val Phe Arg Glu
1 5 10 15

Arg Met Arg Pro Arg Lys Arg Gln Gly Gly Arg Gln Ala Gln Gly Pro
20 25 30

Ser Gly Gln Arg Pro Gln Val His Gly His Leu Ser Ser Ala Ala His
35 40 45

Leu Leu Leu Pro Leu Gln Arg Leu His Leu Gly Cys His Arg Lys Ala
50 55 60

Gly Ile Pro Val Ser Ser Leu His Leu Arg Gly Pro Gln Ala Val Pro
65 70 75 80

Arg Ala His Asn His Lys Val Cys Trp Val Lys Glu Ala Gly Asp Pro
85 90 95

Arg Pro Gly Gly Leu Pro Ala Val Gln Arg Gln His Ala Pro Gln Val
100 105 110

Arg Tyr Pro Gln Leu Gln Gly Pro Tyr Leu Leu Arg Ser Leu Trp Val
115 120 125

Pro Ala Leu Gly Thr Leu Ala Ala Gly Phe Ala Val
130 135 140

<210> 2616

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R345C"

<400> 2616
Ser Ser Ser Pro Ile Pro Ser Pro Ser Pro Ser Pro Thr Asp Pro Lys
1 5 10 15

Arg Cys Phe Phe Gly Ala Ser Pro Gly Cys Cys Leu His Ile Ser Asp
20 25 30

Phe Ser Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys Val Met
35 40 45

Leu Ala Glu Arg
50

<210> 2617
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R480C"

<400> 2617
Ile Val Gly Ser Ser Asp Asn Pro Asp Gln Asn Thr Glu Asp Tyr Leu
1 5 10 15

Phe Gln Val Ile Leu Glu Lys Gln Ile Cys Cys Ile Pro Arg Ser Leu
20 25 30

Ser Val Lys Ala Ala Ser Val Leu Lys Ser Phe Leu Asn Lys Asp Pro
35 40 45

Lys Glu Arg Leu
50

<210> 2618
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A324V"

<400> 2618
Gly Met Asn Val His His Arg Cys Gln Thr Lys Val Ala Asn Leu Cys
1 5 10 15

Gly Ile Asn Gln Lys Leu Met Ala Glu Val Val Leu Ala Met Ile Glu
20 25 30

Ser Thr Gln Gln Ala Arg Cys Leu Arg Asp Thr Glu Gln Ile Phe Arg
35 40 45

Glu Gly Pro Val
50

<210> 2619
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q3568E"

<400> 2619
Asp Thr Ser Thr Gly His Lys Asn Lys Glu Phe Val Ala Arg Ile Lys
1 5 10 15

Ser Lys Leu Asp Gln Gly Gly Val Ile Glu Glu Asp Phe Ile Asn Ala
20 25 30

Leu Asp Gln Leu Ser Asn Pro Glu Leu Leu Phe Lys Asp Trp Ser Asn
35 40 45

Asp Val Arg Ala
    50

<210> 2620
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.K122N"

<400> 2620
Asn Ile Leu Lys Ala Asn Ala Ser Ile Cys Phe Ala Val Pro Asp Pro
1   5   10   15

Leu Met Pro Asp Pro Ser Lys Gln Pro Asn Asn Asn Gln Leu Asn Pro
            20   25   30

Ile Gly Ser Leu Gln Glu Leu Ala Ile His His Gly Trp Arg Leu Pro
        35   40   45

Glu Tyr Thr Leu
    50

<210> 2621
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S28fs"

<400> 2621
Ser Ser Arg Cys Leu Leu Leu Arg Arg Lys Met Ala Glu Asn Ala Ala
1   5   10   15

Glu Ser Thr Glu Val Asn Ser Pro Pro Pro Ser Pro Pro Ser Pro Ser
            20   25   30

Ser Leu Leu Ser Pro Cys Asn Ala Ser Ile Met Cys Pro Leu Asn Pro
35 40 45

Ala Ala Gln Asp Gly Ala Arg Cys Pro Ser Cys
50 55

<210> 2622
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<400> 2622
Ser Ser Arg Cys Leu Leu Leu Arg Arg Lys Met Ala Glu Asn Ala Ala
1 5 10 15

Glu Ser Thr Glu Val Asn Ser Pro Pro Pro Pro Gln Pro Pro Gln Pro
20 25 30

Val Val Pro Ala Lys Pro Val Gln Cys Val His His Val Ser Thr Gln
35 40 45

Pro Ser Cys Pro
50

<210> 2623
<211> 52
<212> PRT
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<400> 2623
Thr Val Arg Phe Ala Leu Arg Arg Met Glu Glu Leu Gly Leu His Pro
1 5 10 15

Ala Asp His Arg Val Tyr Phe Gly Gln Val Val Leu Gly Met Cys Asp

20 25 30

Gln Ile Ser Phe Pro Leu Gly Gln Ala Gly Tyr Pro Val Tyr Lys Tyr
35 40 45

Val Pro Tyr Gly
50

<210> 2624
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V297I"

<400> 2624
Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys
1 5 10 15

Trp Ala Pro Phe Tyr Gly Phe Thr Ile Ile Ile Arg Asp Phe Phe Pro
20 25 30

Thr Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val Val
35 40 45

Glu Cys Ile Ala
50

<210> 2625
<211> 34
<212> PRT
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<400> 2625
Ser Pro Tyr Ser Gly Ser Ala Met Gln Glu Gly Leu Ser Pro Asn His
1 5 10 15

Leu Lys Lys Ala Lys Leu Met Phe Phe Ile Pro Val Ile Pro Ala Pro
20 25 30

Ile Cys

<210> 2626
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V225D"

<400> 2626
Pro Arg Glu Ser Tyr Arg Glu Asn Lys Arg Lys Gln Lys Leu Pro Gln
1 5 10 15

Gln Gln Gln Gln Ser Phe Gln Gln Leu Asp Asp Ser Ala Arg Lys Glu
20 25 30

Gln Lys Arg Glu Glu Arg Arg Gln Leu Lys Gln Gln Leu Glu Asp Met
35 40 45

Gln Lys Gln Leu
50

<210> 2627
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R289W"

<400> 2627
Ser Thr Ser Val Leu Pro His Thr Gly Tyr Ile Tyr His Ser Asp Ile
1 5 10 15

Val Gln Ser Leu Pro Pro Asp Leu Arg Trp Trp Lys Ala Ala Arg Leu
20 25 30

Val Ala Ala Lys Cys Thr Leu Ala Ala Arg Val Asp Ser Phe His Glu
35 40 45

Ser Thr Glu Gly
50

<210> 2628
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R763L"

<400> 2628
Lys Cys Pro His Ser Thr Pro Leu Trp Leu Leu Leu Ser Arg Leu Glu
1 5 10 15

Glu Lys Ile Gly Gln Leu Thr Arg Ala Leu Leu Ala Ile Leu Glu Lys
20 25 30

Ser Arg Leu Lys Asn Pro Lys Asn Pro Gly Leu Trp Leu Glu Ser Val
35 40 45

Arg Leu Glu Tyr
50

<210> 2629
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P1883T"

<400> 2629

Ser Ala Ser Ile Pro Ile Leu Ala Ser Ala Leu Ala Ser Thr Ser Ala
1 5 10 15

Pro Thr Pro Ala Pro Ala Ala Ser Ser Thr Thr Ala Ala Pro Val Ile
20 25 30

Thr Ala Pro Thr Ile Pro Ala Ser Ala Pro Thr Ala Ser Val Pro Leu
35 40 45

Ala Pro Ala Ser
50

<210> 2630
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A196V"

<400> 2630
Asp Val Thr Ala Val Glu Gln Pro Ile Val Pro Arg Pro Ala Pro Arg
1 5 10 15

Pro Thr Asp Tyr Leu Ser Trp Gly Thr Val Val Ser Pro Tyr Ser Ala
20 25 30

Met Ala Thr Tyr Ser Ala Thr Cys Ala Asn Asn Ser Pro Ala Gln Gly
35 40 45

Ile Asn Met Ala
50

<210> 2631
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D107N"

<400> 2631
Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His Pro
1 5 10 15

Gln Tyr Asp Arg Lys Thr Leu Asn Asn Asn Asn Ile Met Leu Ile Lys
20 25 30

Leu Ser Ser Arg Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu
35 40 45

Pro Thr Ala Pro
50

<210> 2632
<211> 30
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L680fs"

<400> 2632
Leu Pro Gln Gly His Gln Val Ser Arg Leu Val Ile Ser Ile Arg Leu
1 5 10 15

Pro Gln His Leu Gly Leu Arg Pro Pro Trp Pro Ser Trp Ser
20 25 30

<210> 2633
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E39Q"

<400> 2633
Thr Val Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser
1 5 10 15

Trp Gly Ala Gln Ile Ile Gly Gly His Gln Gln Val Thr Pro His Ser
20 25 30

Arg Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
35 40 45

Gly Phe Leu Leu
50

<210> 2634
<211> 37
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G256fs"

<400> 2634
Asn Val Leu Ser Arg Leu Ser Leu Met Ala Met Pro Asn Gly Phe His
1 5 10 15

Glu Asp Gly Pro Gln Gly Pro Gly Gly Met Arg Met Met Met Arg Arg
20 25 30

Thr Arg Thr Ser Cys
35

<210> 2635
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T563P"

<400> 2635
Pro Glu Ile Ala Phe Trp Gly Ser Asn Ala Gly Val Lys Thr Thr Arg
1 5 10 15

Leu Glu Ala His Ser Glu Met Gly Ser Pro Pro Glu Ile Leu Glu Lys
20 25 30

Glu Thr Pro Glu Asn Leu Ser Asn Gly Thr Ser Ser Asn Val Glu Ala
35 40 45

Ala Lys Arg Leu
50

<210> 2636
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R397C"

<400> 2636
Phe Gln Leu Ser Gly Gln Lys Leu Phe Ile Pro Gln Ile Thr Thr Lys
1 5 10 15

His Ser Gly Leu Tyr Ala Cys Ser Val Cys Cys Asn Ser Ala Thr Gly
20 25 30

Lys Glu Ser Ser Lys Ser Met Thr Val Lys Val Ser Gly Lys Arg Ile
35 40 45

Pro Val Ser Leu
50

<210> 2637
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R320C"

<400> 2637

Leu Ile Leu Pro Ser Val Thr Arg Asn Glu Thr Gly Pro Tyr Gln Cys
1 5 10 15

Glu Ile Arg Asp Gln Tyr Gly Gly Ile Cys Cys Ser Tyr Pro Val Thr
20 25 30

Leu Asn Val Leu Tyr Gly Pro Asp Leu Pro Arg Ile Tyr Pro Ser Phe
35 40 45

Thr Tyr Tyr Arg
50

<210> 2638
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E404K"

<400> 2638
Leu Phe Ile Pro Gln Ile Thr Arg Asn His Ser Gly Leu Tyr Ala Cys
1 5 10 15

Ser Val His Asn Ser Ala Thr Gly Lys Lys Lys Ile Ser Lys Ser Met
20 25 30

Thr Val Lys Val Ser Gly Pro Cys His Gly Asp Leu Thr Glu Ser Gln
35 40 45

Ser

<210> 2639
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A5V"

<400> 2639
Met Ala Ala Ala Val Val Val Val Glu Phe Gln Arg Ala Gln Ser Leu
1 5 10 15

Leu Ser Thr Asp Arg Glu Ala Ser Ile Asp Ile Leu His Ser Ile
20 25 30

<210> 2640
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R201Q"

<400> 2640
Ser Met Glu Lys Lys Glu Arg Val Glu Phe Ile Leu Glu Gln Met Arg
1 5 10 15

Leu Cys Leu Ala Val Lys Asp Tyr Ile Gln Gln Thr Gln Ile Ile Ser
20 25 30

Lys Lys Ile Asn Thr Lys Phe Phe Gln Glu Glu Asn Thr Glu Lys Leu
35 40 45

Lys Leu Lys Tyr
50

<210> 2641
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R231W"

<400> 2641
Ile Ala Lys Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu
1 5 10 15

Ile Asp Glu Lys Glu Tyr Ile Ser Leu Trp Trp Leu Ile Ile Ser Glu
20 25 30

Leu Arg Asn Gln Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile
35 40 45

Glu Lys Ile Lys
50

<210> 2642
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N495D"

<400> 2642
Gly Gly Arg Trp Phe Pro Glu Gly Pro Thr His Met Leu Pro Leu Leu
1 5 10 15

Met Arg Ala Leu Pro Gly Val Asp Pro Asp Asp Asp Phe Ser Lys Cys
20 25 30

Met Ile Thr Phe Gln Phe Ile Ala Thr Phe Ser Thr Leu Val Pro Leu
35 40 45

Val Asp Cys Ser
50

<210> 2643
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V145I"

<400> 2643
Ile Arg Glu Leu Val Ser Arg Leu Gln Glu Arg Asn Val Gln Val Phe
1 5 10 15

Leu Ile Ser Gly Gly Phe Arg Ser Ile Ile Ile Glu His Val Ala Ser
20 25 30

Lys Leu Asn Ile Pro Ala Thr Asn Val Phe Ala Asn Arg Leu Lys Phe
35 40 45

Tyr Phe Asn Gly
50

<210> 2644
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P689H"

<400> 2644
Leu Arg Thr Glu Tyr Asp Pro His Thr His Val Tyr Tyr Thr Thr Ala
1 5 10 15

Glu Pro Arg Ser Glu Ile Ser Val Gln His His Val Thr Val Thr Gln
20 25 30

Asp Thr Leu Ser Cys Gln Ser Pro Glu Ser Thr Ser Ser Thr Arg Asp
35 40 45

Leu Leu Ser Gln
50

<210> 2645
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.P1307fs"

<400> 2645
Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro Gly Arg Gln
1 5 10 15

Gly Gln Gln Pro Arg Arg Asp Pro Pro Glu Lys Ala Cys Gly His Pro
20 25 30

Pro Thr Asp Arg Ala Glu Thr Leu Leu Lys Phe Leu Leu Lys Gly Ile
35 40 45

Leu Ala Leu Ala Ile Gly Pro Ala Gly Ala Leu Ala Gly Pro Val Leu
50 55 60

Thr Thr Leu Gly Thr Gln Arg Pro Leu Pro Trp Ala Ala Pro Cys Pro
65 70 75 80

Ala Thr Ala Ser Pro Ser Pro Leu
85

<210> 2646
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.F588fs"

<400> 2646
Lys Lys Phe Cys Cys Phe Pro Phe Gly Ser Val Pro Asp Glu His Gly
1 5 10 15

Thr Asp Ile His Pro Ile Ser Leu Phe Leu Glu Thr Ile Leu Ala Pro
20 25 30

Phe Ser Gln Gly Val Ser Pro Ser Ile Leu
35 40

<210> 2647
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R130G"

<400> 2647
Cys Glu Asp Leu Asp Gln Trp Leu Ser Glu Asp Asp Asn His Val Ala
1 5 10 15

Ala Ile His Cys Lys Ala Gly Lys Gly Gly Gly Thr Gly Val Met Ile
20 25 30

Cys Ala Tyr Leu Leu His Arg Gly Lys Phe Leu Lys Ala Gln Glu Ala
35 40 45

Leu Asp Phe Tyr
50

<210> 2648
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R130Q"

<400> 2648
Cys Glu Asp Leu Asp Gln Trp Leu Ser Glu Asp Asp Asn His Val Ala
1 5 10 15

Ala Ile His Cys Lys Ala Gly Lys Gly Gln Gln Thr Gly Val Met Ile
20 25 30

Cys Ala Tyr Leu Leu His Arg Gly Lys Phe Leu Lys Ala Gln Glu Ala
35 40 45

Leu Asp Phe Tyr
50

<210> 2649
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R130P"

<400> 2649
Cys Glu Asp Leu Asp Gln Trp Leu Ser Glu Asp Asp Asn His Val Ala
1 5 10 15

Ala Ile His Cys Lys Ala Gly Lys Gly Pro Pro Thr Gly Val Met Ile
20 25 30

Cys Ala Tyr Leu Leu His Arg Gly Lys Phe Leu Lys Ala Gln Glu Ala
35 40 45

Leu Asp Phe Tyr
50

<210> 2650
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R130L"

<400> 2650
Cys Glu Asp Leu Asp Gln Trp Leu Ser Glu Asp Asp Asn His Val Ala
1 5 10 15

Ala Ile His Cys Lys Ala Gly Lys Gly Leu Leu Thr Gly Val Met Ile
20 25 30

Cys Ala Tyr Leu Leu His Arg Gly Lys Phe Leu Lys Ala Gln Glu Ala
35 40 45

Leu Asp Phe Tyr
50

<210> 2651
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C136Y"

<400> 2651
Trp Leu Ser Glu Asp Asp Asn His Val Ala Ala Ile His Cys Lys Ala
1 5 10 15

Gly Lys Gly Arg Thr Gly Val Met Ile Tyr Tyr Ala Tyr Leu Leu His
20 25 30

Arg Gly Lys Phe Leu Lys Ala Gln Glu Ala Leu Asp Phe Tyr Gly Glu
35 40 45

Val Arg Thr Arg
50

<210> 2652
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S170N"

<400> 2652
Phe Leu Lys Ala Gln Glu Ala Leu Asp Phe Tyr Gly Glu Val Arg Thr
1 5 10 15

Arg Asp Lys Lys Gly Val Thr Ile Pro Asn Asn Gln Arg Arg Tyr Val
20 25 30

Tyr Tyr Tyr Ser Tyr Leu Leu Lys Asn His Leu Asp Tyr Arg Pro Val
35 40 45

Ala Leu Leu Phe
    50

<210> 2653
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R173H"

<400> 2653
Ala Gln Glu Ala Leu Asp Phe Tyr Gly Glu Val Arg Thr Arg Asp Lys
1   5   10   15

Lys Gly Val Thr Ile Pro Ser Gln Arg His His Tyr Val Tyr Tyr Tyr
            20   25   30

Ser Tyr Leu Leu Lys Asn His Leu Asp Tyr Arg Pro Val Ala Leu Leu
        35   40   45

Phe His Lys Met
    50

<210> 2654
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R234L"

<400> 2654
Gly Thr Cys Asn Pro Gln Phe Val Val Cys Gln Leu Lys Val Lys Ile
1   5   10   15

Tyr Ser Ser Asn Ser Gly Pro Thr Arg Leu Leu Glu Asp Lys Phe Met
            20   25   30

Tyr Phe Glu Phe Pro Gln Pro Leu Pro Val Cys Gly Asp Ile Lys Val

35 40 45

Glu Phe Phe His
50

<210> 2655
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L265fs"

<400> 2655
Glu Phe Pro Gln Pro Leu Pro Val Cys Gly Asp Ile Lys Val Glu Phe
1 5 10 15

Phe His Lys Gln Asn Lys Met Leu Lys Arg Thr Lys Cys Phe Thr Phe
20 25 30

Gly

<210> 2656
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T277I"

<400> 2656
Asp Ile Lys Val Glu Phe Phe His Lys Gln Asn Lys Met Leu Lys Lys
1 5 10 15

Asp Lys Met Phe His Phe Trp Val Asn Ile Ile Phe Phe Ile Pro Gly
20 25 30

Pro Glu Glu Thr Ser Glu Lys Val Glu Asn Gly Ser Leu Cys Asp Gln
35 40 45

Glu Ile Asp Ser
50

<210> 2657
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E40A"

<400> 2657
Gly Tyr Pro Thr Asn Ser Asp Phe Glu Leu Lys Thr Ala Glu Leu Pro
1 5 10 15

Pro Leu Lys Asn Gly Glu Val Leu Leu Ala Ala Ala Leu Phe Leu Thr
20 25 30

Val Asp Pro Tyr Met Arg Val Ala Ala Lys Arg Leu Lys Glu Gly Asp
35 40 45

Thr Met Met Gly
50

<210> 2658
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L22V"

<400> 2658
Met Glu Thr Arg Gln Val Ser Arg Ser Pro Arg Val Arg Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Val Val Val Val Pro Trp Gly Val Arg Thr Ala
20 25 30

Ser Gly Val Ala Leu Pro Pro Val Gly Val Leu Ser Leu Arg Pro Pro
35 40 45

<210> 2659
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R430W"

<400> 2659
Ala Val Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Phe Ser Asn Glu
1 5 10 15

Gln Gln Phe Asp Pro Leu Trp Lys Arg Trp Trp Asn Val Glu Cys Leu
20 25 30

Gln Pro Leu Thr His Leu Lys Arg Arg Leu Ser Tyr Ser Asp Ser Asp
35 40 45

Leu Lys Arg Ala
50

<210> 2660
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G503V"

<400> 2660
Ile Ile Arg Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys Thr
1 5 10 15

Ile Gln Met Val Arg Ser Gln Arg Ser Val Val Met Val Gln Thr Glu
20 25 30

Ala Gln Tyr Arg Phe Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr
35 40 45

Leu Gln Arg Arg
50

<210> 2661
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E76K"

<400> 2661
Val Thr His Ile Lys Ile Gln Asn Thr Gly Asp Tyr Tyr Asp Leu Tyr
1 5 10 15

Gly Gly Glu Lys Phe Ala Thr Leu Ala Lys Lys Leu Val Gln Tyr Tyr
20 25 30

Met Glu His His Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile Glu
35 40 45

Leu Lys Tyr Pro
50

<210> 2662
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R765Q"

<400> 2662
Pro Pro Thr Phe Ser Asp Lys Arg Glu Gln Ile Ser Glu Asn Pro Thr
1 5 10 15

Glu Ala Thr Asp Ile Gly Phe Gly Asn Gln Gln Cys Gly Lys Pro Lys

20 25 30

Gly Pro Arg Asp Pro Pro Ser Glu Trp Thr
35 40

<210> 2663
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S887L"

<400> 2663
Ser Tyr Gln His Lys Phe Gln Leu Gln Met Arg Ala Arg Gln Ser Asn
1 5 10 15

Gln Asp Ala Gln Asp Ile Glu Arg Ala Leu Leu Phe Arg Ser Leu Asn
20 25 30

Leu Gln Ala Glu Ser Val Arg Gly Phe Asn Met Gly Arg Ala Ile Ser
35 40 45

Thr Gly Ser Leu
50

<210> 2664
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E2067K"

<400> 2664
Tyr Ile Gln Glu Asp Asp Ile Tyr Asp Asp Ser Gln Glu Ala Glu Val
1 5 10 15

Ile Gln Ser Leu Leu Asp Val Val Asp Lys Lys Glu Ala Gln Asn Leu
20 25 30

Leu Asn Glu Asn Asn Ala Ala Gly Tyr Ser Cys Gly Pro Gly Thr Leu
35 40 45

Lys Met Asn Gly
50

<210> 2665
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E716del"

<400> 2665
Gln Tyr His His Lys Lys Thr Phe Ser Asp Ala Thr Met Leu Ile His
1 5 10 15

Ser Ser Glu Ser Glu Glu Glu Glu Glu Ala Pro Glu Ser Val Pro Gln
20 25 30

Ile Pro Met Leu Arg Glu Lys Met Glu Tyr Ser Ala Gln Leu Gln Ala
35 40 45

Ala Leu Ala Arg Ile
50

<210> 2666
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E286K"

<400> 2666
Thr His Asn Lys Ser Thr Ile Leu Val Glu Leu Ile Asn Lys Glu Glu
1 5 10 15

Thr Ala Leu Phe His Thr Asp Asp Ile Lys Lys Asn Ala Lys Tyr Ile
20 25 30

Ser Arg Leu Phe Ala Thr Arg His Lys Phe Tyr Lys Gln Asn Lys Ile
35 40 45

Cys Thr Glu Gln
50

<210> 2667
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 2667
Thr Tyr Ala Val Val Gln Lys Arg Gly Ala Pro Ala Gly Ala Gly Ser
1 5 10 15

Gly Thr Gln Thr Gly Thr Gly Thr Gly Ala Arg Ser Ala Glu Glu Ala
20 25 30

Pro Leu Tyr Ser Lys Val Thr Pro Arg Ala Gln Arg Pro Gly Ala His
35 40 45

Ala Glu Asp Ala Arg Gly Thr Leu
50 55

<210> 2668
<211> 31
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2668

Asn Leu Trp Lys Ala Cys Val Glu His His Thr Phe Phe Arg Leu Asp
1 5 10 15

Arg Pro Leu Pro Pro Gln Lys Asn Phe Leu His Ile Ile Leu His
20 25 30

<210> 2669
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q726H"

<400> 2669
Ser Leu Thr Pro Gly Arg Leu Tyr Thr Val Thr Ile Thr Thr Arg Ser
1 5 10 15

Gly Lys Tyr Glu Asn His Ser Phe Ser His His Glu Arg Thr Val Pro
20 25 30

Asp Lys Val Gln Gly Val Ser Val Ser Asn Ser Ala Arg Ser Asp Tyr
35 40 45

Leu Arg Val Ser
50

<210> 2670
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.D1560N"

<400> 2670
Glu Asn Pro Asn Ser Asn Ser Lys Ser Phe Asn Ile Lys Leu Gly Ala
1 5 10 15

Glu Met Glu Ser Leu Gly Gly Lys Cys Asn Asn Pro Thr Gln Gln Lys

20 25 30

Phe Cys Asp Gly Pro Leu Lys Pro His Thr Ala Tyr Arg Ile Ser Ile
35 40 45

Arg Ala Phe Thr
50

<210> 2671
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.Q895H"

<400> 2671
Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr Val Val Lys
1 5 10 15

Leu Arg Arg Gln Arg Cys Leu Met Val His His Val Glu Ala Gln Tyr
20 25 30

Ile Leu Ile His Gln Ala Leu Val Glu Tyr Asn Gln Phe Gly Glu Thr
35 40 45

Glu Val Asn Leu
50

<210> 2672
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1174Q"

<400> 2672
Pro Arg Trp Ser Thr Pro Glu Glu Leu Glu Leu Asp Glu Leu Leu Glu
1 5 10 15

Ala Ile Glu Gln Gly Gly Glu Glu Gln Gln Arg Arg Arg Arg Gln
20 25 30

Ala Glu Arg Leu Lys Pro Tyr Val Ala Ala Gln Leu Asp Val Leu Pro
35 40 45

Glu Thr Phe Thr
50

<210> 2673
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G334W"

<400> 2673
His Asp Glu Ser Leu Val Gly Pro Val Asp Pro Ser Ser Gly Gln Gln
1 5 10 15

Ser Arg Asp Thr Glu Val Leu Leu Val Trp Trp Leu Glu Pro Gly Thr
20 25 30

Arg Tyr Asn Ala Thr Val Tyr Ser Gln Ala Ala Asn Gly Thr Glu Gly
35 40 45

Gln Pro Gln Ala
50

<210> 2674
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R928L"

<400> 2674
Ser Trp Asp Thr Ala Lys Glu Asp Glu Asn Arg Asn Lys Asn Arg Tyr
1 5 10 15

Gly Asn Ile Ile Ser Tyr Asp His Ser Leu Leu Val Arg Leu Leu Val
20 25 30

Leu Asp Gly Asp Pro His Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Asp
35 40 45

Gly Tyr His Arg
50

<210> 2675
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2675
Trp Pro Asp His Gly Val Pro Cys Tyr Ala Thr Gly Leu Leu Gly Phe
1 5 10 15

Val Arg Gln Val Lys Phe Leu Asn Pro Arg Lys Leu Gly Pro
20 25 30

<210> 2676
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P559S"

<400> 2676
Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu Arg Asn Glu
1 5 10 15

Thr Tyr His Val Phe Ser Asn Leu His Ser Ser Gly Thr Thr Tyr Leu
20 25 30

Phe Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala Ala Leu
35 40 45

Thr Glu Ile Thr
50

<210> 2677
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D1434N"

<400> 2677
Phe Phe Ala Ala Lys Thr Leu Arg Asn Tyr Lys Pro Asn Met Val Glu
1 5 10 15

Thr Met Asp Gln Tyr His Phe Cys Tyr Asn Asn Val Ala Leu Glu Tyr
20 25 30

Leu Glu Gly Leu Glu Ser Arg
35

<210> 2678
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S396L"

<400> 2678
Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr Pro Ala
1 5 10 15

Arg Pro Pro Ile Pro Val Thr Ile Pro Leu Leu Val Gly Val Val Asn

20 25 30

Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys Lys
35 40 45

Glu Lys Glu Glu
50

<210> 2679
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A358T"

<400> 2679
Leu Asp Pro Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala
1 5 10 15

Ser Val Val Val Val Gly Val Ile Ala Thr Thr Leu Leu Phe Cys Leu
20 25 30

Leu Val Val Val Val Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala
35 40 45

Gln Gln Met Thr
50

<210> 2680
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S84fs"

<400> 2680
Pro Val Asn Asp Ser His Gly Arg Ala Pro Glu Glu Gly Asp Ala Glu
1 5 10 15

Val Met Gln Leu Gly Ser Ser Ser Pro Leu Leu Pro Ala Gly Phe Ser
20 25 30

Pro Pro Arg Pro Pro Ala Pro Ser His Pro Arg Pro Ser Cys Arg Arg
35 40 45

Cys Pro Pro Glu Ala Cys Pro Arg Thr Leu Pro Thr Ser Lys Ala Pro
50 55 60

Pro Ser Leu Thr Arg Cys Gly Ser Gly Thr Arg Thr Ser Cys Gly Cys
65 70 75 80

Pro Ser Arg Arg Pro Gly Pro Ser Ser Ala Arg Gly Gly Val Cys Pro
85 90 95

Ala Thr Ala Thr Arg Gly Ala Ser Ser Ser Ala Pro Ser Ala Cys Gly
100 105 110

Arg Ala Arg Cys Ser Val Arg Ser Ala Arg Ala Arg
115 120

<210> 2681
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T1312M"

<400> 2681
Ile Pro Lys Val Asp Leu Arg Val Trp Gln Asp Cys Cys Ala Asp Cys
1 5 10 15

Arg Ser Arg Gly Gln Phe Arg Ala Val Met Met Gln Glu Ser Gln Lys
20 25 30

Lys Arg Ser Ala Gln Tyr Ser Tyr Pro Val Asp Lys Asp Met Glu Leu
35 40 45

Ser His Leu Arg
50

<210> 2682
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1456T"

<400> 2682
Cys Pro Pro Ala Pro Cys Pro Ser Pro Glu Leu Val Lys Gly Thr Cys
1 5 10 15

Cys Pro Val Cys Arg Asp Arg Gly Met Thr Thr Ser Asp Ser Pro Glu
20 25 30

Lys Arg

<210> 2683
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q150fs"

<400> 2683
Gly Pro Gln Pro Leu Arg Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro
1 5 10 15

Met Gly Pro Ala Phe Asn Met Pro Pro Arg Val Leu Ala Thr His Pro
20 25 30

Gln Ala Thr
35

<210> 2684
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G148A"

<400> 2684
Asn Arg Leu Thr Ala Lys Gly Ala Glu Glu Thr Leu Gly Pro Gln Lys
1 5 10 15

Arg Lys Lys Pro Ser Glu Glu Glu Thr Ala Ala Thr Lys Arg Ser Lys
20 25 30

Met Ser Lys Glu Gln Thr Arg Pro Ser Cys Ser Ala Gly Ala Ser Thr
35 40 45

Ser Thr Ala Met
50

<210> 2685
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S226L"

<400> 2685
Ala His Cys Gly Leu Val Gly Phe Lys Pro Ser Tyr Gly Leu Val Ser
1 5 10 15

Arg His Gly Leu Ile Pro Leu Val Asn Leu Leu Met Asp Val Pro Gly
20 25 30

Ile Leu Thr Arg Cys Val Asp Asp Ala Ala Ile Val Leu Gly Ala Leu
35 40 45

Ala Gly Pro Asp
50

<210> 2686

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R401L"

<400> 2686
Asp Asp Arg Lys Glu Gly Ala Val Leu Ala Lys Lys Val Asn Trp Ile
1 5 10 15

Gly Cys Gln Gly Ser Glu Pro His Phe Leu Leu Gly Phe Pro Cys Ser
20 25 30

Leu Trp Val Leu Phe His Phe Leu Thr Val Gln Ala Ala Arg Gln Asn
35 40 45

Val Asp His Ser
50

<210> 2687
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R683L"

<400> 2687
Ser Leu Asp Met Ser Leu Cys Val Val Leu Tyr Val Ala Ser Ser Leu
1 5 10 15

Phe Leu Met Val Met Tyr Phe Phe Phe Leu Leu Val Arg Ser Arg Arg
20 25 30

Trp Lys Val Lys His His His Pro Ala Val
35 40

<210> 2688
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S588N"

<400> 2688
Met Pro Asn Gln Gln Gln Ala Ala Tyr Gln Gly Met Ile Gly Val Gln
1 5 10 15

Gln Pro Gln Asn Gln Gly Leu Leu Ser Asn Asn Gln Arg Ser Ser Met
20 25 30

Gly Gly Gln Met Gln Gly Leu Val Val Gln Tyr Thr Pro Leu Pro Ser
35 40 45

Tyr Gln Val Pro
50

<210> 2689
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S592G"

<400> 2689
Gln Gln Ala Ala Tyr Gln Gly Met Ile Gly Val Gln Gln Pro Gln Asn
1 5 10 15

Gln Gly Leu Leu Ser Ser Gln Arg Ser Gly Gly Met Gly Gly Gln Met
20 25 30

Gln Gly Leu Val Val Gln Tyr Thr Pro Leu Pro Ser Tyr Gln Val Pro
35 40 45

Val Gly Ser Asp
50

<210> 2690
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R206W"

<400> 2690
Glu Phe Ile Asn Asp Asn Asn Asn Gln Phe Lys Lys Phe Pro Gln Met
1 5 10 15

Thr Ser Tyr His Arg Met Leu Leu His Trp Trp Val Ala Ala Tyr Phe
20 25 30

Gly Met Asp His Asn Val Asp Gln Thr Gly Lys Ala Val Ile Ile Asn
35 40 45

Lys Thr Ser Asn
50

<210> 2691
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S596L"

<400> 2691
Ser Leu Tyr Glu Ala Lys Asn Leu Phe Ala Ala Gln Thr Lys Ala Gln
1 5 10 15

Ser Leu Ala Ala Glu Ile Asp Thr Ala Leu Leu Arg Asp Glu Leu Met
20 25 30

Glu Ala Leu Lys Glu Gln Glu Glu Ile Asn Phe Arg Leu Arg Gln Tyr
35 40 45

Met Asp Lys Ile
    50

<210> 2692
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R170H"

<400> 2692
Trp Tyr Lys Leu His Ser Lys Pro Gly Lys Lys Glu Lys Glu Arg Gly
1   5   10   15

Glu Ile Glu Val Thr Ile Gln Phe Thr His His Asn Asn Leu Ser Ala
            20   25   30

Ser Met Phe Asp Leu Ser Met Lys Asp Lys Pro Arg Ser Pro Phe Ser
        35   40   45

Lys Ile Arg Asp
    50

<210> 2693
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R167L"

<400> 2693
Glu His Gly Ile Arg Phe Phe Glu Thr Ser Ala Lys Ser Ser Met Asn
1   5   10   15

Val Asp Glu Ala Phe Ser Ser Leu Ala Leu Leu Asp Ile Leu Leu Lys
            20   25   30

Ser Gly Gly Arg Arg Ser Gly Asn Gly Asn Lys Pro Pro Ser Thr Asp

35 40 45

Leu Lys Thr Cys
50

<210> 2694
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R79W"

<400> 2694
Tyr Glu Ile Val Arg Leu Gln Leu Trp Asp Ile Ala Gly Gln Glu Arg
1 5 10 15

Phe Thr Ser Met Thr Arg Leu Tyr Tyr Trp Trp Asp Ala Ser Ala Cys
20 25 30

Val Ile Met Phe Asp Val Thr Asn Ala Thr Thr Phe Ser Asn Ser Gln
35 40 45

Arg Trp Lys Gln
50

<210> 2695
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G20W"

<400> 2695
Met Ala Lys Thr Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp
1 5 10 15

Ser Gly Val Trp Trp Lys Thr Cys Val Leu Phe Arg Phe Ser Glu Asp
20 25 30

Ala Phe Asn Ser Thr Phe Ile Ser Thr Ile Gly Ile Asp Phe
35 40 45

<210> 2696
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K928fs"

<400> 2696
Leu Glu Glu Glu Ser Ala Gln Leu Lys Glu Met Cys Arg Arg Glu Leu
1 5 10 15

Asp Lys Ala Glu Ser Glu Ile Lys Lys Lys Gln Phe Tyr His Trp
20 25 30

<210> 2697
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K928fs"

<400> 2697
Leu Glu Glu Glu Ser Ala Gln Leu Lys Glu Met Cys Arg Arg Glu Leu
1 5 10 15

Asp Lys Ala Glu Ser Glu Ile Lys Lys Thr Val Leu Ser Leu Val Thr
20 25 30

Ile Ser Arg Phe Val Leu Ser
35

<210> 2698
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N207D"

<400> 2698
Pro Ala Ser Ala Asp Asp Phe Leu Pro Thr Leu Ile Tyr Ile Val Leu
1 5 10 15

Lys Gly Asn Pro Pro Arg Leu Gln Ser Asp Asp Ile Gln Tyr Ile Thr
20 25 30

Arg Phe Cys Asn Pro Ser Arg Leu Met Thr Gly Glu Asp Gly Tyr Tyr
35 40 45

Phe Thr Asn Leu
50

<210> 2699
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P34R"

<400> 2699
Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
1 5 10 15

Thr Asn Ala Phe Pro Gly Glu Tyr Ile Arg Arg Thr Val Phe Asp Asn
20 25 30

Tyr Ser Ala Asn Val Met Val Asp Gly Lys Pro Val Asn Leu Gly Leu
35 40 45

Trp Asp Thr Ala
50

<210> 2700
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A159V"

<400> 2700
Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala Met Ala Lys Glu Ile
1 5 10 15

Gly Ala Val Lys Tyr Leu Glu Cys Ser Val Val Leu Thr Gln Arg Gly
20 25 30

Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val Leu Cys Pro Pro
35 40 45

Pro Val Lys Lys
50

<210> 2701
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P29S"

<400> 2701
Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu
1 5 10 15

Leu Ile Ser Tyr Thr Thr Asn Ala Phe Ser Ser Gly Glu Tyr Ile Pro
20 25 30

Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly Lys Pro
35 40 45

Val Asn Leu Gly

50

<210> 2702
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D69Y"

<400> 2702
Thr Ile Ile Glu Cys Leu Lys Tyr Ile Cys Thr Gly Asp Phe Pro Pro
1 5 10 15

Gly Thr Lys Gly Asn Thr Phe Val His Tyr Tyr Pro Lys Val Ala Gln
20 25 30

Glu Thr Asp Val Arg Ala Gln Ile Arg Leu Gln Phe Arg Asp Val Asn
35 40 45

Gly Glu Leu Ile
50

<210> 2703
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.T316fs"

<400> 2703
Arg Asp Phe Thr Asn Ile Tyr Trp Ser Gln Asn Arg Pro Asp Val Lys
1 5 10 15

Lys Gln Lys Leu Gln Asn Asp Lys Lys Leu
20 25

<210> 2704
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D167N"

<400> 2704
Val Gln Ile Pro Glu Cys Phe Gly Gly Val Ala Gly Glu Ala Val Phe
1 5 10 15

Ile Asp Thr Glu Gly Ser Phe Met Val Asn Asn Arg Val Val Asp Leu
20 25 30

Ala Thr Ala Cys Ile Gln His Leu Gln Leu Ile Ala Glu Lys His Lys
35 40 45

Gly Glu Glu His
50

<210> 2705
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y224H"

<400> 2705
Phe Thr Leu Asp Asn Ile Leu Ser His Ile Tyr Tyr Phe Arg Cys Arg
1 5 10 15

Asp Tyr Thr Glu Leu Leu Ala Gln Val His His Leu Leu Pro Asp Phe
20 25 30

Leu Ser Glu His Ser Lys Val Arg Leu Val Ile Val Asp Gly Ile Ala
35 40 45

Phe Pro Phe Arg
50

<210> 2706
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S257L"

<400> 2706
Tyr Ser Thr Pro His Ala Phe Thr Phe Asn Thr Ser Ser Pro Ser Ser
1 5 10 15

Glu Gly Ser Leu Ser Gln Arg Gln Arg Leu Leu Thr Ser Thr Pro Asn
20 25 30

Val His Met Val Ser Thr Thr Leu Pro Val Asp Ser Arg Met Ile Glu
35 40 45

Asp Ala Ile Arg
50

<210> 2707
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R398C"

<400> 2707
Leu Thr Glu Arg Glu Pro Ser Ser Ser Ser Leu Cys Ser Ile Asp Glu
1 5 10 15

Glu His Leu Thr Asp Ile Glu Ile Val Cys Cys Arg Val Phe Ser Ser
20 25 30

Lys Arg Ser Asn Val Asn Phe Val Thr Glu Ile Phe Arg Gln Ala Phe
35 40 45

Leu Leu Pro Ile
50

<210> 2708
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T379fs"

<400> 2708
Arg Ser Asp Ser Ala Pro Pro Thr Pro Val Asn Arg Leu Ser Met Pro
1 5 10 15

Gln Ser Ala Ala Val Ser Thr Thr Pro His Ile Thr Gly Gly Thr Gly
20 25 30

Leu Leu Leu
35

<210> 2709
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R381Q"

<400> 2709
Ser Lys Ser Ala Thr Phe Pro Ser Glu Lys Ala Arg His Leu Leu Asp
1 5 10 15

Asp Ser Val Leu Glu Ser Arg Ser Pro Gln Gln Arg Gly Leu Ala Leu
20 25 30

Thr Ser Ser Ser Ala Val Thr Asn Gly Leu Ser Leu Gly Ser Ser Glu
35 40 45

Ser Ser Glu Phe

50

<210> 2710
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M900I"

<400> 2710
His Ser Asp Leu Leu Gln Tyr Arg Lys Leu Ser Gln Ser Tyr Tyr Pro
1 5 10 15

Leu Leu Glu Cys Leu Thr Gln Asp His Ile Ile Ser Phe Ile Ile Asn
20 25 30

Leu Glu Pro Pro Val Leu Met Tyr Val Leu Thr Ser Ile Ser Glu Gly
35 40 45

Leu Thr Thr Leu
50

<210> 2711
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1231C"

<400> 2711
Val Glu Ser Lys Glu Trp Lys Glu Arg Gly Ile Gly Asn Val Lys Ile
1 5 10 15

Leu Arg His Lys Thr Ser Gly Lys Ile Cys Cys Leu Leu Met Arg Arg
20 25 30

Glu Gln Val Leu Lys Ile Cys Ala Asn His Tyr Ile Ser Pro Asp Met
35 40 45

Lys Leu Thr Pro
50

<210> 2712
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L386W"

<400> 2712
Glu Ala Thr Pro Glu Lys Glu Ser Leu Ala Glu Ser Ala Ala Ala Tyr
1 5 10 15

Thr Lys Ala Thr Ala Arg Lys Cys Leu Trp Trp Glu Lys Val Glu Val
20 25 30

Ile Thr Gly Glu Glu Ala Glu Ser Asn Val Leu Gln Met Gln Cys Lys
35 40 45

Leu Phe Val Phe
50

<210> 2713
<211> 52
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<400> 2713
Gln Trp Gly Leu Cys Ile Phe Asp Asp Ile Ile Glu His Cys Ser Pro
1 5 10 15

Thr Ser Phe Lys Tyr Val Glu Tyr Phe Trp Trp Trp Pro Met Leu Leu
20 25 30

Asn Met Arg Asp Asn Asn Pro Glu Val Arg Gln Ala Ala Ala Tyr Gly
35 40 45

Leu Gly Val Met
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<210> 2714
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I984L"

<400> 2714
Leu Val Lys Val Ile Lys Cys Ala Asn Ser Lys Thr Lys Lys Asn Val
1 5 10 15

Ile Ala Thr Glu Asn Cys Ile Ser Ala Leu Leu Gly Lys Ile Leu Lys
20 25 30

Phe Lys Pro Asn Cys Val Asn Val Asp Glu Val Leu Pro His Trp Leu
35 40 45

Ser Trp Leu Pro
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<210> 2715
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.R356L"

<400> 2715
Leu Pro Gly Lys Phe Lys Asn Leu Phe Arg Lys Phe Glu Asn Leu Thr
1 5 10 15

Asp Pro Cys Arg Asn His Lys Ser Tyr Leu Leu Glu Val Ile Ser Lys
20 25 30

Met Lys Pro Pro Val Ile Pro Phe Val Pro Leu Ile Leu Lys Asp Leu
35 40 45

Thr Phe Leu His
50

<210> 2716
<211> 32
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.R6C"

<400> 2716
Met Ala Cys Gly Phe Cys Cys Arg Ala Ile Ala Cys Gln Leu Ser Arg
1 5 10 15

Val Leu Asn Leu Pro Pro Glu Asn Leu Ile Thr Ser Ile Ser Ala Val
20 25 30

<210> 2717
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2717
Val Ser Thr Gln Pro Ala Pro Arg Ser Ile Phe Arg Arg Val Leu Ser
1 5 10 15

Ala Pro Pro Lys Glu Ser Arg Thr Ser His His Leu Arg Leu Ser Lys
20 25 30

Ala Leu Trp Gly Arg His Lys Asn Pro Pro Pro Glu Pro Asp Pro Glu

35 40 45

Pro Glu Gln Glu
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<210> 2718
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2718
Leu Ala Ala Leu Arg Gln Gly Pro Glu Gly Leu Val Gly Ala Asp Lys
1 5 10 15

Pro Ile Ser Tyr Arg Thr Lys Pro Pro Thr Thr Ser Ile His Arg Glu
20 25 30

Leu Leu Gly Val Cys Ser Asp Pro Tyr Thr Leu Ala Gln Gln Leu Thr
35 40 45

His Val Glu Leu
50

<210> 2719
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2719
Ala Thr Leu Leu Ala Leu Cys Val Gln His Ser Ala Arg Glu Leu Glu
1 5 10 15

Leu Gly His Leu Pro Arg Leu Leu Gly Cys Cys Leu Ala Arg Leu Ile
20 25 30

Lys Glu Ala Val Trp Glu Lys Ile Lys Glu Ile Gly Asp Arg Gln Pro
35 40 45

Glu Asn His Pro
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<210> 2720
<211> 37
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 2720
Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser
1 5 10 15

Asn Gly Leu Pro Glu Val Glu Asn Leu Asn Asp Thr Lys Lys Phe Ile
20 25 30

Leu Lys Ile Lys Ile
35

<210> 2721
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 2721
Asn Leu Lys Leu Lys Leu His Ser Phe Glu Ser His Lys Asp Glu Ile
1 5 10 15

Phe Gln Val Gln Trp Ser Pro His Asn Lys Lys Thr Ile Leu Ala Ser
20 25 30

Ser Gly Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly
35 40 45

Glu Glu Gln Ser
50

<210> 2722
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2722
Gln Lys Leu Met Ile Trp Asp Thr Arg Ser Asn Thr Thr Ser Lys Pro
1 5 10 15

Ser His Leu Val Asp Ala His Thr Ala Lys Lys Val Asn Cys Leu Ser
20 25 30

Phe Asn Pro Tyr Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp Lys
35 40 45

Thr Val Ala Leu
50

<210> 2723
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E313K"

<400> 2723
Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg
1 5 10 15

Asn Leu Lys Leu Lys Leu His Thr Phe Lys Lys Ser His Lys Asp Glu
20 25 30

Ile Phe Gln Val His Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser
35 40 45

Ser Gly Thr Asp
50

<210> 2724
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A340T"

<400> 2724
Asn Thr Tyr Ile Pro Leu Ile Ser Leu Pro Leu Val Pro Gly Phe Pro
1 5 10 15

Tyr Pro Thr Ala Ala Thr Thr Ala Ala Thr Thr Phe Arg Gly Ala His
20 25 30

Leu Arg Gly Arg Gly Arg Thr Val Tyr Gly Ala Val Arg Ala Val Pro
35 40 45

Pro Thr Ala Ile
50

<210> 2725
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E127K"

<400> 2725
Val Ser Lys Gly Thr Val Glu Gly Asn Tyr Val Ser Leu Thr Arg Ile

1 5 10 15

Leu Lys Cys Ser Glu Gln Ser Leu Ile Lys Lys Phe Phe Asn Lys Met
20 25 30

Lys Lys Trp Glu Asp Met Ala Asn Leu Pro Pro His Phe Arg Glu Arg
35 40 45

Thr Glu Arg Leu
50

<210> 2726
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.AAAAAAA286del"

<400> 2726
Leu Thr Ser Thr Ser Leu Asp Pro Tyr Asp Arg His Leu Leu Pro Thr
1 5 10 15

Ser Gly Ala Ala Ala Thr Ala Ala Ala Val Thr Ala Ala Ser Thr Ser
20 25 30

Tyr Tyr Gly Arg Asp Arg Ser Pro Leu Arg Arg Ala Thr Ala Pro Val
35 40 45

Pro Thr Val Gly Glu Gly Tyr Gly Tyr Gly His Glu Ser Glu Leu Ser
50 55 60

Gln Ala Ser Ala Ala Ala Arg
65 70

<210> 2727
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2727
Phe Arg Glu Lys Asn Val Pro Thr Thr Lys Gly Ala Pro Lys Asn Thr
1 5 10 15

Thr Lys Ser Trp Gln Gly Arg Ile Leu Trp Trp Glu Asn Glu Glu Glu
20 25 30

Glu Asp Leu Ala Glu Ser Gly Arg Leu Phe Val Arg Asn Leu Pro Tyr
35 40 45

Thr Ser Thr Glu
50

<210> 2728
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P644A"

<400> 2728
Thr Thr Ser Pro Lys Pro Leu Val Gln Gln Pro Ile Leu Pro Val Val
1 5 10 15

Lys Gln Ser Val Lys Glu Arg Leu Gly Ala Ala Val Pro Ser Ser Thr
20 25 30

Ile Glu Pro Ala Glu Ala Gln Ser Ala Ser Ser Asp Leu Pro Gln Asn
35 40 45

Val Thr Lys Leu
50

<210> 2729
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T353I"

<400> 2729
Glu Arg Thr Asp Ala Ser Ser Ala Ser Ser Phe Leu Asp Ser Asp Glu
1 5 10 15

Leu Glu Arg Thr Gly Ile Asp Leu Gly Ile Ile Thr Gly Arg Leu Gln
20 25 30

Leu Met Ala Arg Leu Ala Glu Gly Thr Gly Leu Gln Ile Pro Pro Ala
35 40 45

Ala Gln Gln Ala
50

<210> 2730
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
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<400> 2730
His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp Pro
1 5 10 15

Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Val Ile Pro Thr Val Ser
20 25 30

Thr Pro Pro Pro Phe Gln Gly Arg Pro Ile Thr Pro Val Tyr Thr Val
35 40 45

Ala Pro Asn Val Gln Arg Ile Pro Thr Ala Gly Ile Tyr Gly Ala Ser
50 55 60

Tyr Val Pro Phe Ala Ala Pro Ala
65 70

<210> 2731
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V675G"

<400> 2731
Arg Gln Asp Gly Glu Ser Lys Thr Ile Met Leu Lys Arg Ile Tyr Arg
1 5 10 15

Ser Thr Pro Pro Glu Val Ile Val Glu Gly Gly Leu Glu Pro Tyr Val
20 25 30

Arg Leu Thr Thr Ala Asn Val Arg Ile Ile Lys Asn Arg Thr Gly Pro
35 40 45

Met Gly His Thr
50

<210> 2732
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R96fs"

<400> 2732
Ser Tyr Gly Ala Arg Asp Gly Pro His Gly Asp Tyr Arg Gly Gly Glu
1 5 10 15

Gly Pro Gly His Asp Phe Arg Gly Gly Arg Phe Phe Val Phe
20 25 30

<210> 2733
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P112Q"

<400> 2733
His Asp Cys Ser Val Leu Arg Gly Ile Gly Tyr Tyr Leu Glu Ser Leu
1 5 10 15

Leu Cys Leu Ala Pro Phe Met Lys His Gln Gln Leu Lys Ile Val Leu
20 25 30

Arg Gly Val Thr Asn Asp Gln Val Asp Pro Ser Val Asp Val Leu Lys
35 40 45

Ala Thr Ala Leu
50

<210> 2734
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A198V"

<400> 2734
Leu Leu Gln Phe Asn Ile Phe Ile Ser Leu Val Glu Pro Gly Pro Val
1 5 10 15

Val Thr Glu Phe Glu Gly Lys Leu Leu Val Val Gln Val Ser Met Ala
20 25 30

Glu Phe Pro Gly Thr Asp Pro Glu Thr Leu His Tyr Phe Arg Asp Leu
35 40 45

Tyr Leu Pro Ala
50

<210> 2735
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W57L"

<400> 2735
Pro Arg Ile Ser Cys Pro Glu Gly Thr Asn Ala Tyr Arg Ser Tyr Cys
1 5 10 15

Tyr Tyr Phe Asn Glu Asp Pro Glu Thr Leu Leu Val Asp Ala Asp Leu
20 25 30

Tyr Cys Gln Asn Met Asn Ser Gly Asn Leu Val Ser Val Leu Thr Gln
35 40 45

Ala Glu Gly Ala
50

<210> 2736
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M67I"

<400> 2736
Ala Tyr Arg Ser Tyr Cys Tyr Tyr Phe Asn Glu Asp Pro Glu Thr Trp
1 5 10 15

Val Asp Ala Asp Leu Tyr Cys Gln Asn Ile Ile Asn Ser Gly Asn Leu
20 25 30

Val Ser Val Leu Thr Gln Ala Glu Gly Ala Phe Val Ala Ser Leu Ile
35 40 45

Lys Glu Ser Ser
50

<210> 2737
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S150L"

<400> 2737
Ser Asp Val Met Asn Tyr Phe Ala Trp Glu Arg Asn Pro Ser Thr Ile
1 5 10 15

Ser Ser Pro Gly His Cys Ala Ser Leu Leu Leu Arg Ser Thr Ala Phe
20 25 30

Leu Arg Trp Lys Asp Tyr Asn Cys Asn Val Arg Leu Pro Tyr Val Cys
35 40 45

Lys Phe Thr Asp
50

<210> 2738
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G110V"

<400> 2738
Gly Tyr Gln Arg Ser Gln Pro Ile Trp Ile Gly Leu His Asp Pro Gln
1 5 10 15

Lys Arg Gln Gln Trp Gln Trp Ile Asp Val Val Ala Met Tyr Leu Tyr
20 25 30

Arg Ser Trp Ser Gly Lys Ser Met Gly Gly Asn Lys His Cys Ala Glu
35 40 45

Met Ser Ser Asn
50

<210> 2739
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.15_16LL>L"

<400> 2739
Met Asp Gly Trp Arg Arg Met Pro Arg Trp Gly Leu Leu Leu Leu Leu
1 5 10 15

Trp Gly Ser Cys Thr Phe Gly Leu Pro Thr Asp Thr Thr Thr Phe Lys
20 25 30

Arg Ile Phe Leu Lys Arg Met Pro Ser Ile Arg Glu
35 40

<210> 2740
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K176N"

<400> 2740
Pro Ala Cys Ser Leu Pro Val Ala Ser Gln Pro Pro Gln His Leu Ser
1 5 10 15

Glu Ala Gly Arg Gly Pro Val Gly Ser Asn Asn Arg Asp His Leu Leu
20 25 30

Met Asn Val Lys Trp Tyr Tyr Arg Gln Ser Glu Val Pro Asp Ser Val
35 40 45

Tyr Gln His Leu

50

<210> 2741
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A30S"

<400> 2741
Arg Ile Val Thr Ala Asp Tyr Tyr Met Ala Ser Pro Leu Gln Gly Leu
1 5 10 15

Asp Thr Cys Gln Ser Pro Leu Thr Gln Ser Ser Pro Val Lys Lys Val
20 25 30

Pro Val Val Arg Val Phe Gly Ala Thr Pro Ala Gly Gln Lys Thr Cys
35 40 45

Leu His Leu His
50

<210> 2742
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I82N"

<400> 2742
Arg Glu Leu Tyr Gly Val Gly Val Glu Lys Leu Arg Ile Glu His Gln
1 5 10 15

Thr Ile Thr Thr Pro Ser Lys Lys Lys Asn Asn Glu Ile Ser Thr Ile
20 25 30

Ala Ser Asn Tyr His Leu Glu Val Asn Pro Ser Asp Ala Gly Asn Ser
35 40 45

Asp Arg Val Val
50

<210> 2743
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K296N"

<400> 2743
Leu Leu Glu Val Arg Gly Arg Leu Tyr Glu Leu Leu Thr His Cys Ile
1 5 10 15

Pro Pro Glu Ile Ile Met Lys Ala Cys Asn Asn Glu Glu Ser Arg Ser
20 25 30

Cys Asp Ile Phe
35

<210> 2744
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S63R"

<400> 2744
Ala Trp Thr Gly Met Gly Leu Arg Ala Ala Pro Ser Ser Ala Ala Ala
1 5 10 15

Ala Ala Ala Glu Val Glu Gln Arg Arg Arg Arg Pro Gly Leu Cys Pro
20 25 30

Pro Pro Leu Glu Leu Leu Leu Leu Leu Leu Phe Ser Leu Gly Leu Leu
35 40 45

His Ala Gly Asp
50

<210> 2745
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W366L"

<400> 2745
Leu Lys Asp Gln Val Gly Arg Asp Gln Phe Leu Arg Phe Leu Glu Ser
1 5 10 15

Glu Phe Ser Ser Glu Asn Leu Arg Phe Leu Leu Leu Ala Val Gln Asp
20 25 30

Leu Lys Lys Gln Pro Leu Gln Asp Val Ala Lys Arg Val Glu Glu Ile
35 40 45

Trp Gln Glu Phe
50

<210> 2746
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R44C"

<400> 2746
Pro Asn Met Leu Val Tyr Arg Lys Met Glu Asp Val Ile Ala Arg Met
1 5 10 15

Gln Asp Glu Lys Asn Gly Ile Pro Ile Cys Cys Thr Val Lys Ser Phe
20 25 30

Leu Ser Lys Ile Pro Ser Val Phe Ser Gly Ser Asp Ile Val Gln Trp
35 40 45

Leu Ile Lys Asn
50

<210> 2747
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A96S"

<400> 2747
Glu Arg Ala Glu Phe Glu Arg Leu Trp Val Ala Phe Ser Gly Cys Leu
1 5 10 15

Asp Leu Leu Glu Ala Asp Met Arg Arg Ser Ser Leu Glu Leu Gly Ala
20 25 30

Ala Phe Pro Leu His Ala Pro Arg Arg Pro Leu Val Arg Thr Gly Val
35 40 45

Ala Gly Ala Ser
50

<210> 2748
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V222I"

<400> 2748
His Thr Lys Met Thr Met Ala Lys Glu Glu Ala Cys His Gly Leu Met
1 5 10 15

Gln Glu Tyr Glu Thr Arg Leu Tyr Ser Ile Ile Cys Tyr Thr His Ile

20 25 30

Gly Gly Leu Pro Leu Asn Met Ser Ile Lys Lys Cys His His Phe Gln
35 40 45

Lys Arg Tyr Ser
50

<210> 2749
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G34fs"

<400> 2749
Ser Pro Ala Leu Pro Leu Ala Ser Ser Val Leu Met Leu Leu Met Ser
1 5 10 15

Thr Leu Trp Leu Val Gly Ala Gly Pro Arg Pro Gly Pro Gly Pro Gly
20 25 30

Ala Val Ala Gly Pro Leu Ala Gly Ala Pro Ala Ala Asp Pro Cys Pro
35 40 45

Gly Pro His Gly Pro Ala Arg Pro Ala Pro Glu Pro Ala Ala Pro Ala
50 55 60

His Cys Gly Leu Ala Ala Gly Val Pro Pro Gly His Ala Glu Ile Pro
65 70 75 80

Ala Cys Leu Ser Pro Ala Arg Pro Gly Phe Trp Ala Ala Gly Ser Ala
85 90 95

Ala Gly Arg Pro Trp Ala Val Gln Cys Ser Arg Gln Leu Trp Ile His
100 105 110

Ala Cys Pro Pro Gly His Ala Gly Trp Gly Gly Thr Pro Pro
115 120 125

<210> 2750
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y35N"

<400> 2750
Ala Ile Leu Gly Tyr Arg Ser Val Gly Lys Ser Ser Leu Thr Ile Gln
1 5 10 15

Phe Val Glu Gly Gln Phe Val Asp Ser Asn Asn Asp Pro Thr Ile Glu
20 25 30

Asn Thr Phe Thr Lys Leu Ile Thr Val Asn Gly Gln Glu Tyr His Leu
35 40 45

Gln Leu Val Asp
50

<210> 2751
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E40Q"

<400> 2751
Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
1 5 10 15

Pro Glu Val Tyr Val Pro Thr Val Phe Gln Gln Asn Tyr Val Ala Asp
20 25 30

Ile Glu Val Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala
35 40 45

Gly Gln Glu Asp
50

<210> 2752
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y42C"

<400> 2752
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu
1 5 10 15

Val Tyr Val Pro Thr Val Phe Glu Asn Cys Cys Val Ala Asp Ile Glu
20 25 30

Val Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln
35 40 45

Glu Asp Tyr Asp
50

<210> 2753
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T464M"

<400> 2753
Val Leu Glu Met Phe Asp Leu Arg Met Met Val Glu Asn Ile Met Asn
1 5 10 15

Lys Glu Ala Phe Met Asn Gln Glu Ile Met Met Lys Ala Phe His Val
20 25 30

Arg Lys Ala Asn Arg Ile Lys Glu Cys Leu Ser Lys Gly Thr Phe Ser
35 40 45

Asp Val Thr Phe
    50

<210> 2754
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V73M"

<400> 2754
Leu Lys Ala Val Arg Met Arg Thr Gly Ala Glu Asn Leu Leu Lys Val
1   5   10   15

Ala Thr Asn Ser Lys Val Arg Glu Gln Met Met Arg Leu Glu Leu Ser
            20   25   30

Phe Val Asn Ser Asp Leu Gln Met Leu Lys Glu Glu Leu Glu Gly Leu
        35   40   45

Asn Ile Ser Val
    50

<210> 2755
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S358R"

<400> 2755
Arg Ile Pro Gln Pro Pro Pro Ile Ala His Pro Arg Thr Ser Pro Gln
1   5   10   15

Pro Glu Ser Gly Ile Lys Arg Leu Phe Arg Arg Phe Phe Ser Arg Asp
            20   25   30

Lys Lys Arg Leu Ala Asn Thr Gln Arg Asn Val His Ile Gln Glu Ser

35 40 45

Phe Gly Gln Trp
50

<210> 2756
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R830H"

<400> 2756
Phe Pro Arg Gly Ser Ala Gly Pro Gln Arg Ser Arg Pro Val Thr Val
1 5 10 15

Pro Ser Ile Asp Asp Tyr Gly Arg Asp His His Leu Ser Pro Asp Phe
20 25 30

Tyr Glu Glu Ser Glu Thr Asp Pro Gly Ala Glu Glu Leu Pro Ala Arg
35 40 45

Ile Phe Val Ala
50

<210> 2757
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A396del"

<400> 2757
His Glu Leu Ile Lys Leu Asn Trp Leu Leu Ala Lys Ala Leu Trp Val
1 5 10 15

Leu Ala Arg Arg Cys Tyr Thr Leu Gln Glu Asn Lys Gln Leu Arg Arg
20 25 30

Ala Gly Cys Pro Tyr Gln Ala Asp Glu Lys Val Lys Arg Leu Lys Val
35 40 45

Lys Arg Ala Glu Leu
50

<210> 2758
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q1154R"

<400> 2758
Tyr Ala Asp Gly Leu Lys Val Cys Glu Val Ala Asp Ala Thr Ala Gly
1 5 10 15

Ser Thr Leu Leu Glu Phe Ser Gln Leu Arg Arg Val Pro Leu Thr Trp
20 25 30

Gln Lys Val Ser Val Arg Thr Met Ser Leu Cys Gly Glu Ser Leu Asp
35 40 45

Ser Val Pro Ala
50

<210> 2759
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.V401fs"

<400> 2759
Leu Gly Leu Lys Val Val Gly Gly Lys Met Thr Glu Ser Gly Arg Leu
1 5 10 15

Cys Ala Phe Ile Thr Lys Val Lys Lys Glu Val
20 25

<210> 2760
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R55L"

<400> 2760
Glu Arg Glu Glu Tyr Ser Gln Tyr Ala Thr Ser Asp Thr Ala Met Pro
1 5 10 15

Arg Ser Pro Ser Asp Tyr Ala Asp Arg Leu Leu Ser Gln His Glu Pro
20 25 30

Gln Phe Tyr Glu Asp Ser Asp His Leu Ser Tyr Arg Asp Ser Asn Arg
35 40 45

Arg Ser His Arg
50

<210> 2761
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R599Q"

<400> 2761
Lys Arg Arg Thr Lys Thr Val Lys Lys Thr Leu Glu Pro Lys Trp Asn
1 5 10 15

Gln Thr Phe Ile Tyr Ser Pro Val His Gln Gln Arg Glu Phe Arg Glu
20 25 30

Arg Met Leu Glu Ile Thr Leu Trp Asp Gln Ala Arg Val Arg Glu Glu
35 40 45

Glu Ser Glu Phe
50

<210> 2762
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L449V"

<400> 2762
Asp Thr Pro Arg Glu Ser Thr Glu Gln Gly Gln Asp Thr Glu Val Lys
1 5 10 15

Ala Ser Asp Pro His Ser Met Pro Glu Val Val Pro Arg Thr Ala Lys
20 25 30

Gln Pro Pro Val Pro Pro Pro Arg Lys Lys Arg Ile Ser Arg Gln Leu
35 40 45

Ala Ser Thr Leu
50

<210> 2763
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S708L"

<400> 2763
Leu Tyr Lys Cys Val Leu Lys Pro Leu Lys Glu Ala Ile Asn Ser Cys
1 5 10 15

Leu His Gln Ile His Ser Lys Asp Gly Leu Leu Leu Gln Gln Leu Lys

20 25 30

Glu Asn Gln Leu Val Ile Leu Ala Thr Thr Thr Asp Leu Gly Val
35 40 45

Thr Thr Ser Val
50

<210> 2764
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G171fs"

<400> 2764
Gln Ala Met His Arg Ala Gln Arg Val Arg Arg Pro Ile Pro Gly Ser
1 5 10 15

Asp Gln Thr Thr Thr Met Ser Gly Gly Lys Glu Ser Pro Gly Arg Glu
20 25 30

Lys Gly Met Glu Lys Met
35

<210> 2765
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P402L"

<400> 2765
Arg Arg Arg Gln Thr Ala Leu Arg Ala Gly Ala Gly Pro Pro Gly Ala
1 5 10 15

Gln Gly Pro Gly Pro Glu Gly Gln Ser Leu Leu Ala Pro Ala Leu Arg
20 25 30

Ser Arg Ile His Glu Arg Leu Ala His Leu His Ala Ala Cys Ala Pro
35 40 45

Arg Arg Lys Val
50

<210> 2766
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L107fs"

<400> 2766
Ser Lys Met Gln Leu Glu Glu Gln Val Leu Thr Ile Ser Ser Glu Ile
1 5 10 15

Pro Lys Arg Ile Arg Ser Ala Leu Lys Met Gln Lys Asn Gln Ser Asn
20 25 30

Phe Leu Ile Ser Phe Trp Ser Arg Lys Leu Ile Ser Ser Ala Pro Leu
35 40 45

Thr Ala Ile Cys
50

<210> 2767
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M90I"

<400> 2767
Asp Asp Glu Pro Ala Asn Leu Asp Ile Leu Asp Thr Ala Gly Gln Ala
1 5 10 15

Glu Phe Thr Ala Met Arg Asp Gln Tyr Ile Ile Arg Ala Gly Glu Gly
20 25 30

Phe Ile Ile Cys Tyr Ser Ile Thr Asp Arg Arg Ser Phe His Glu Val
35 40 45

Arg Glu Phe Lys
50

<210> 2768
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R85L"

<400> 2768
Gln Val Arg Ile Asp Asn Glu Pro Ala Tyr Leu Asp Ile Leu Asp Thr
1 5 10 15

Ala Gly Gln Ala Glu Phe Thr Ala Met Leu Leu Glu Gln Tyr Met Arg
20 25 30

Gly Gly Glu Gly Phe Ile Ile Cys Tyr Ser Val Thr Asp Arg Gln Ser
35 40 45

Phe Gln Glu Ala
50

<210> 2769
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A72V"

<400> 2769

Lys Ala Lys Asp Glu Leu Asn Glu Arg Glu Glu Thr Arg Glu Glu Ala
1 5 10 15

Val Arg Glu Leu Gln Glu Met Val Gln Val Val Gln Ala Ala Ser Gly
20 25 30

Glu Glu Leu Ala Val Ala Val Ala Glu Arg Val Gln Glu Lys Asp Ser
35 40 45

Gly Phe Phe Leu
50

<210> 2770
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D281N"

<400> 2770
Pro Phe Leu Lys Ser Lys Leu Leu Glu Arg Val Phe Val His Gly Asp
1 5 10 15

Asp Leu Ser Gly Phe Tyr Gln Glu Ile Asn Asn Glu Asn Ile Leu Pro
20 25 30

Ser Asp Phe Gly Gly Thr Leu Pro Lys Tyr Asp Gly Lys Ala Val Ala
35 40 45

Glu Gln Leu Phe
50

<210> 2771
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.S501L"

<400> 2771
Ser Pro Ser Ser Ser Ser Gly Gly Glu Ser Ser Glu Thr Ser Ser Asp
1 5 10 15

Leu Phe Glu Gly Ser Asn Glu Gly Ser Leu Leu Ser Ser Gly Ser Ser
20 25 30

Gly Ala Arg Arg Glu Gly Arg His Arg Ala Pro Val Thr Phe Asp Glu
35 40 45

Ser Gly Ser Leu
50

<210> 2772
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S138C"

<400> 2772
Gln Gln His Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu
1 5 10 15

Phe Lys Lys Leu Ile Arg Asn Arg Gln Cys Cys Glu Ala Ala Asp Ser
20 25 30

Ser Pro Ser Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys
35 40 45

Lys Arg Gln Leu
50

<210> 2773
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A127V"

<400> 2773
His Ser Phe Pro Asn Arg Ser Arg Phe Trp Lys His Glu Trp Glu Lys
1 5 10 15

His Gly Thr Cys Ala Ala Gln Val Asp Val Val Leu Asn Ser Gln Lys
20 25 30

Lys Tyr Phe Gly Arg Ser Leu Glu Leu Tyr Arg Glu Leu Asp Leu Asn
35 40 45

Ser Val Leu Leu
50

<210> 2774
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R771fs"

<400> 2774
His Glu Val Met Gln Arg Met Glu Val Gln Arg Arg Arg Met Met Gln
1 5 10 15

His Pro Thr Arg Ala His Glu Arg Pro His Pro Ile His Ile Gly Cys
20 25 30

Thr Gln Thr Met Val Met Gly Ile Ile Phe Met Cys Leu Arg Leu Cys
35 40 45

Pro His Ile Leu Asp Arg Leu Gln Arg Gly Leu Pro Gly Asn Trp Glu
50 55 60

Leu Lys Leu Glu
65

<210> 2775
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A172V"

<400> 2775
Tyr Arg Gly Ile His Ser Tyr Leu Arg Tyr Leu Lys Pro Lys Asp Thr
1 5 10 15

Ser Met Gly Asn Ser Ser Ser Gly Met Val Val Arg Lys Gly Pro Ile
20 25 30

Arg Ala Pro Gly His Leu Arg Ala Thr Val Arg Trp Asp Tyr Gln Pro
35 40 45

Asp Ile Cys Lys
50

<210> 2776
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S9G"

<400> 2776
Met Ala Trp Arg Arg Arg Glu Ala Gly Gly Val Gly Ala Arg Gly Val
1 5 10 15

Leu Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg
20 25 30

Gly Arg Ala
35

<210> 2777
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S208L"

<400> 2777
Leu Glu Arg Asn Ile Thr Val Thr Met Tyr Ile Thr Ile Gly Thr Arg
1 5 10 15

Asn Leu Gln Lys Tyr Val Ser Arg Thr Leu Leu Val Val Phe Val Ser
20 25 30

Ile Ser Phe Ile Val Leu Met Ile Ile Ser Leu Ala Trp Leu Val Phe
35 40 45

Tyr Tyr Ile Gln
50

<210> 2778
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R236Q"

<400> 2778
Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Leu Ala Trp
1 5 10 15

Leu Val Phe Tyr Tyr Ile Gln Arg Phe Gln Gln Tyr Ala Asn Ala Arg
20 25 30

Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser
35 40 45

Lys Leu Gln Ile
50

<210> 2779

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P95S"

<400> 2779
Pro Asp Asp Pro Glu Val Leu Ala Val Ile Ala Ile Pro His Thr Ser
1 5 10 15

Glu His Thr Pro Val Phe Ile Lys Leu Ser Ser Ser Asn Gly Cys Tyr
20 25 30

Met Leu Pro Leu Pro Ile Ser Lys Glu Arg Ala Leu Leu Pro Gly Asp
35 40 45

Met Gly Cys Arg
50

<210> 2780
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S351C"

<400> 2780
Lys Lys Tyr Asn Asn Lys Lys Glu Leu Ser Cys Tyr Asp Thr Tyr Pro
1 5 10 15

Pro Leu Glu Lys Lys Lys Val Asp Met Cys Cys Val Leu Thr Ser Glu
20 25 30

Ala Pro Pro Pro Pro Leu Gln Pro Glu Thr Asn Asp Val His Leu Glu
35 40 45

Ala Lys Asn Phe
50

<210> 2781
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A133T"

<400> 2781
Pro Leu Ala Ala Ser Ser Pro Ala Trp Arg Pro Pro Pro Gly Gln Ala
1 5 10 15

Arg Pro Pro Gly Ser Pro Gly Gln Ser Thr Thr Gln Leu Pro Leu Asp
20 25 30

Leu Leu Pro Ser Leu Pro Arg Glu Ser Gln Ile Phe Val Ile Ser Arg
35 40 45

His Gly Met Pro
50

<210> 2782
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G263C"

<400> 2782
His Arg Arg Leu Leu Ile Ser Ala Asp Arg Arg Ser Val Gln Leu Ala
1 5 10 15

Pro Pro Gly Thr Pro Ala Pro Pro Asp Cys Cys Pro Lys Arg Phe Asp
20 25 30

Gln Leu Pro Ala Val Leu Gly Ala Gln Gly Phe Gly Ala Gly Arg His
35 40 45

Cys Trp Glu Val
    50

<210> 2783
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.G659fs"

<400> 2783
Pro Ser Thr Ser Ser Leu Phe Asn Leu Gln Lys Ser Ser Leu Ser Ala
1   5   10   15

Arg His Pro Gln Arg Lys Arg Arg Gly Val Pro Pro Ser Pro Pro Leu
            20   25   30

Ala Leu Gly Pro Arg Met Gln Leu Cys Thr Gln Leu Ala Arg Phe Phe
        35   40   45

Pro Ile Thr Pro Pro Val Trp His Ile Leu Gly Pro Gln Arg His Thr
    50   55   60

Pro
65

<210> 2784
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.P116fs"

<400> 2784
Asn Ala Ser Asp Asp Asp Asn Leu Glu Pro Gly Phe Ile Ser Ile Val
1   5   10   15

Lys Leu Glu Ser Pro Arg Arg Ala Pro Pro Pro Leu Pro Val Thr Gly
20 25 30

<210> 2785
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S216L"

<400> 2785
Pro Pro Ala Trp Pro Asp Tyr Asp Val Trp Ile Leu Met Thr Val Val
1 5 10 15

Gly Thr Ile Phe Val Ile Ile Leu Ala Leu Leu Val Leu Arg Ile Arg
20 25 30

Cys Arg Pro Arg His Ser Arg Pro Asp Pro Leu Gln Gln Arg Thr Ala
35 40 45

Trp Ala Ile Ser
50

<210> 2786
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K392fs"

<400> 2786
Pro Glu Phe Leu Val Tyr Phe Pro Leu Leu Asn Glu Met Ala Lys Lys
1 5 10 15

Tyr Asn Met Lys Leu Val Tyr Lys Lys His Phe Trp Asn Ser Thr Lys
20 25 30

Lys Arg Leu Arg Thr Met Lys Ile Lys Cys Ser

35 40

<210> 2787
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E116fs"

<400> 2787
Leu Val Val Glu Phe Ala Lys Glu Gln Asp Arg Val His Ser Pro Cys
1 5 10 15

Pro Thr Ser Gly Ser Glu Lys Lys Lys Gly Leu Met Thr Leu Ser Lys
20 25 30

Met Ile Lys Lys Lys Lys Asn Leu Val Ile
35 40

<210> 2788
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D1018N"

<400> 2788
Ser Gln Ile Thr Gln Ala Thr Pro Tyr Ala Thr Thr Gln Ile Leu His
1 5 10 15

Ser Asn Ser Ile His Glu Leu Ala Val Asn Asn Leu Pro Asp Pro Gln
20 25 30

Trp Lys Ser Ser Ile Gln Gln Lys Thr Asp Leu Met Gly Phe Gly Tyr
35 40 45

Ser Leu Pro Asp
50

<210> 2789
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1080fs"

<400> 2789
Lys Asn Lys Asn Ser Ser Lys Pro Gln Lys Asn Asn Gly Ser Thr Trp
1 5 10 15

Ala Asn Val Pro Leu Pro Pro Pro Pro Ser Pro Ala Pro Ser Trp His
20 25 30

Gly Ala Gly Thr Leu Cys Ser Gly Thr Thr Arg Lys Trp Leu
35 40 45

<210> 2790
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K1293fs"

<400> 2790
Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser Ala Ala Leu Ser
1 5 10 15

Gln Ser Gln Arg Pro Arg Pro Thr Lys Asn Thr Arg Glu Gly Gly Trp
20 25 30

Thr Asn Asn Gln His Cys Leu Ile Glu Gly Lys Glu
35 40

<210> 2791
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T518S"

<400> 2791
His Arg Ile Asn Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys
1 5 10 15

Arg Arg Asn Val Glu Asn Glu Val Ser Ser Ser Leu Lys Asp Gln Leu
20 25 30

Glu Asp Leu Lys Lys Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys
35 40 45

Leu Ser Gln Leu
50

<210> 2792
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D672N"

<400> 2792
Lys Leu Leu Gly Asn Ser Leu Leu Pro Ile Arg Trp Met Ala Pro Glu
1 5 10 15

Ala Ile Met Tyr Gly Lys Phe Ser Ile Asn Asn Ser Asp Ile Trp Ser
20 25 30

Tyr Gly Val Val Leu Trp Glu Val Phe Ser Tyr Gly Leu Gln Pro Tyr
35 40 45

Cys Gly Tyr Ser
50

<210> 2793
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G94W"

<400> 2793
Asn Arg Asn Arg Cys Gln His Cys Arg Leu Gln Lys Cys Leu Ala Leu
1 5 10 15

Gly Met Ser Arg Asp Ala Val Lys Phe Trp Trp Arg Met Ser Lys Lys
20 25 30

Gln Arg Asp Ser Leu Tyr Ala Glu Val Gln Lys His Gln Gln Arg Leu
35 40 45

Gln Glu Gln Arg
50

<210> 2794
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R245I"

<400> 2794
Phe Pro Gly Gly Pro Ile Leu Gly Tyr Asn Leu Arg Leu Ile Ser Lys
1 5 10 15

Asn Gln Lys Leu Asp Ala Gly Thr Gln Ile Ile Thr Ser Phe Gln Phe
20 25 30

Tyr Ser Thr Leu Pro Asn Thr Ile Tyr Arg Phe Ser Ile Ala Ala Val
35 40 45

Asn Glu Val Gly

50

<210> 2795
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S1771L"

<400> 2795
Trp Leu Leu Lys Glu Asn His Leu Leu Arg Met Ser Ser Glu Asn Pro
1 5 10 15

Gly Met Cys Gly Asn Ala Asp Thr Thr Leu Leu Val Asp Thr Leu Leu
20 25 30

Asp Asn Asn Ser Ser Glu Val Pro Tyr Ser His Phe Gly Asn Leu Ala
35 40 45

Pro Gly Pro Thr
50

<210> 2796
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R31H"

<400> 2796
Ser Glu Gly Ala Ile Ala Ala Ile Met Gln Lys Gly Asp Thr Asn Ile
1 5 10 15

Lys Pro Ile Leu Gln Val Ile Asn Ile His His Pro Ile Thr Thr Gly
20 25 30

Asn Ser Pro Pro Arg Tyr Arg Leu Leu Met Ser Asp Gly Leu Asn Thr
35 40 45

Leu Ser Ser Phe
50

<210> 2797
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K187T"

<400> 2797
Arg Gln Lys Ile His Ile Ser Lys Lys Trp Gly Phe Thr Lys Phe Asn
1 5 10 15

Ala Asp Glu Phe Glu Asp Met Val Ala Thr Thr Lys Cys Leu Ile Pro
20 25 30

Asp Gly Cys Gly Val Lys Tyr Val Pro Ser His Gly Pro Leu Asp Lys
35 40 45

Trp Arg Val Leu
50

<210> 2798
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G107R"

<400> 2798
Gln Thr Met Arg Gly Met Pro Pro His Lys Thr Lys Pro Gly Gln Ala
1 5 10 15

Ala Leu Asp Cys Leu Lys Val Phe Asp Arg Arg Ile Pro Pro Pro Tyr
20 25 30

Asp Lys Lys Lys Arg Met Val Val Pro Ala Ala Leu Lys Val Val Arg
35 40 45

Leu Lys Pro Ala
50

<210> 2799
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R151C"

<400> 2799
Lys Val Lys Gly Asn Val Phe Lys Asn Lys Arg Ile Leu Met Glu His
1 5 10 15

Ile His Lys Leu Lys Ala Asp Lys Ala Cys Cys Lys Lys Leu Leu Ala
20 25 30

Asp Gln Ala Glu Ala Arg Arg Ser Lys Thr Lys Glu Ala Arg Lys Arg
35 40 45

Arg Glu Glu Arg
50

<210> 2800
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.K15fs"

<400> 2800
Met Ala Pro Val Lys Lys Leu Val Val Lys Gly Gly Lys Lys Arg Ser
1 5 10 15

Lys Phe

<210> 2801
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R58fs"

<400> 2801
Lys Arg Leu Val Ile Gln Asp Lys Asn Lys Tyr Asn Thr Pro Lys Tyr
1 5 10 15

Arg Met Ile Val Arg Val Thr Asn Arg Tyr His Leu Ser Asp Cys Leu
20 25 30

Cys Pro Tyr Arg Gly Gly Tyr Asp Ser Leu Arg Ser Val Cys Thr Arg
35 40 45

Thr Ala Lys Ile Trp Cys Glu Gly Trp Pro Asp Lys Leu Cys Cys Ser
50 55 60

Ile Leu Tyr Trp Pro Ala Ala Gly Pro Gln Ala Ser Gln
65 70 75

<210> 2802
<211> 52
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<223> /note="p.F193C"

<400> 2802
Leu Ala Ser Gly Leu Leu Leu Val Thr Gly Pro Leu Val Leu Asn Arg
1 5 10 15

Val Pro Leu Arg Arg Thr His Gln Lys Cys Cys Val Ile Ala Thr Ser

20 25 30

Thr Lys Ile Asp Ile Ser Asn Val Lys Ile Pro Lys His Leu Thr Asp
35 40 45

Ala Tyr Phe Lys
50

<210> 2803
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.R97S"

<400> 2803
Pro His Arg Leu Asn Leu Phe Tyr Leu Ala Asn Asp Val Ile Gln Asn
1 5 10 15

Cys Lys Arg Lys Asn Ala Ile Ile Phe Ser Ser Glu Ser Phe Ala Asp
20 25 30

Val Leu Pro Glu Ala Ala Ala Leu Val Lys Asp Pro Ser Val Ser Lys
35 40 45

Ser Val Glu Arg
50

<210> 2804
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.R200G"

<400> 2804
Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Arg Cys Gly Ser
1 5 10 15

Val Leu Val Arg Leu Ile Pro Ala Pro Gly Gly Gly Thr Gly Ile Val
20 25 30

Ser Ala Pro Val Pro Lys Lys Leu Leu Met Met Ala Gly Ile Asp Asp
35 40 45

Cys Tyr Thr Ser
50

<210> 2805
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2805
Thr His Leu Ser Gln Arg Glu Arg Phe Thr Glu His Glu Val Gln Ile
1 5 10 15

Tyr Val Gly Glu Ile Val Leu Ala Leu Lys Lys His Leu His Lys Leu
20 25 30

Gly Ile Ile Tyr Arg Asp Ile Lys Leu Glu Asn Ile Leu Leu Asp Ser
35 40 45

Asn Gly His Val
50

<210> 2806
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.S394Y"

<400> 2806
Ala Thr Ser Ile Ala Glu Glu Tyr Lys Ile Thr Pro Ile Thr Ser Ala
1 5 10 15

Asn Val Leu Pro Ile Val Gln Ile Asn Tyr Glu Asn Ala Ala Gln Phe
20 25 30

Gly Glu Val Tyr Glu Leu Lys Glu Asp Ile Gly Val Gly Ser Tyr Ser
35 40 45

Val Cys Lys Arg
50

<210> 2807
<211> 42
<212> PRT
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<220>
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<223> /note="p.K109fs"

<400> 2807
Lys Lys Ala Ser Leu Lys Val Arg Asp Arg Val Arg Thr Lys Met Glu
1 5 10 15

Arg Asp Ile Leu Val Glu Val Asn His His Leu Leu Ser Asn Cys Thr
20 25 30

Met Pro Phe Arg Leu Lys Gly Asn Cys Thr
35 40

<210> 2808
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q111E"

<400> 2808

Ala Val Leu Lys Phe Ala Ala Ala Thr Gly Ala Thr Pro Ile Ala Gly
1 5 10 15

Arg Phe Thr Pro Gly Thr Phe Thr Asn Glu Glu Ile Gln Ala Ala Phe
20 25 30

Trp Glu Pro Arg Leu Leu Val Val Thr Asp Pro Arg Ala Asp His Gln
35 40 45

Pro Leu Thr Glu
50

<210> 2809
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G364S"

<400> 2809
Gln Ser Ser His Tyr Gly Gln Met Asp Arg Lys Gly Gln Cys Tyr His
1 5 10 15

Tyr Asp Gln Thr Asn Arg Gln Gly Gln Ser Ser Ser His Tyr Ser Gln
20 25 30

Pro Asn Arg Gln Gly Gln Ser Ser His Tyr Gly Gln Pro Asp Thr Gln
35 40 45

Asp Gln Ser Ser
50

<210> 2810
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M538I"

<400> 2810
Gln Thr Asp Arg Gln Gly Gln Ser Phe His Tyr Gly Gln Pro Asp Arg
1 5 10 15

Gln Gly Gln Ser Ser His Tyr Ser Gln Ile Ile Asp Arg Gln Gly Gln
20 25 30

Ser Ser His Tyr Gly Gln Thr Asp Arg Gln Gly Gln Ser Ser His Tyr
35 40 45

Gly Gln Thr Asp
50

<210> 2811
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G296S"

<400> 2811
Cys Gly Gln Ser Glu Arg Leu Gly Gln Glu Leu Gly Cys Gly Gln Thr
1 5 10 15

Asp Arg Gln Gly Gln Ser Ser His Tyr Ser Ser Gln Thr Asp Arg Gln
20 25 30

Asp Gln Ser Tyr His Tyr Gly Gln Thr Asp Arg Gln Gly Gln Ser Ser
35 40 45

His Tyr Ser Gln
50

<210> 2812
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A278E"

<400> 2812
Leu Arg Arg Asp Ser Lys Glu Ala Asn Ala Arg Arg Gln Ala Gly Thr
1 5 10 15

Arg Arg Arg Glu Ser Leu Gly Lys Lys Glu Glu Lys Arg Phe Leu Gly
20 25 30

Arg Ile Val Ala Arg Asn Ser Arg Lys Met Ala Phe Arg Ala Lys Ser
35 40 45

Lys Ser Cys His
50

<210> 2813
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G783V"

<400> 2813
Cys Gly Glu Asp Leu Lys His Tyr Arg Ala Leu Arg Ile His Met Arg
1 5 10 15

Thr His Cys Gly Arg Gly Leu Gly Gly Val Val His Lys Gly Arg Lys
20 25 30

Pro Phe Glu Cys Lys Glu Cys Ser Ala Ala Phe Ala Ala Lys Arg Asn
35 40 45

Cys Ile His His
50

<210> 2814
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R9C"

<400> 2814
Met Ala Ala Pro Leu Leu His Thr Cys Cys Leu Pro Gly Asp Ala Ala
1 5 10 15

Ala Ser Ser Ser Ala Val Lys Lys Leu Gly Ala Ser Arg Thr Gly Ile
20 25 30

Ser Asn Met
35

<210> 2815
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.P11S"

<400> 2815
Met Ala Ala Pro Leu Leu His Thr Arg Leu Ser Ser Gly Asp Ala Ala
1 5 10 15

Ala Ser Ser Ser Ala Val Lys Lys Leu Gly Ala Ser Arg Thr Gly Ile
20 25 30

Ser Asn Met Arg Ala
35

<210> 2816
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

<221> source
<223> /note="p.L214F"

<400> 2816
Lys Glu Ala Gly Ser Ser Met Arg Lys Arg Ala Lys Leu Ile Ser Thr
1 5 10 15

Val Ser Lys Lys Asp Phe Ile Ser Val Phe Phe Arg Gly Met Asp Gly
20 25 30

Ser Thr Asn Glu Thr Ala Ser Ser Arg Lys Lys Pro Lys Ala Lys Gln
35 40 45

Thr Glu Val Lys
50

<210> 2817
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N45fs"

<400> 2817
Gln Arg Ile Thr Val His Lys Glu Leu Glu Leu Gln Phe Asp Leu Gly
1 5 10 15

Asn Leu Leu Ala Ser Asp Arg Asn Pro Arg Pro Gly Cys Gly Ala Pro
20 25 30

Asp Pro Arg Arg Arg Pro Ser Tyr Arg Pro Trp Arg Gly Thr Thr Arg
35 40 45

Asn Cys Ser Ser Thr Ser Cys Gly Ser Cys Pro Arg Ser Ala Trp Lys
50 55 60

Arg Arg
65

<210> 2818
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E572K"

<400> 2818
Ser Pro Phe Lys Arg Arg Arg Ser Met Asn Glu Ile Lys Asn Leu Gln
1 5 10 15

Tyr Leu Pro Arg Thr Ser Glu Pro Arg Lys Lys Val Leu Phe Glu Asp
20 25 30

Arg Thr Arg Ala His Ala Asp His Val Gly Gln Gly Phe Asp Trp Gln
35 40 45

Ser Thr Ala Ala
50

<210> 2819
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K386fs"

<400> 2819
His Glu Ile Thr Glu Lys Ser Thr Glu Glu Thr Glu Lys Leu Lys Asn
1 5 10 15

Asp Gln Gln Ala Lys Ile Pro Leu Lys Asn Glu Lys Leu Asn
20 25 30

<210> 2820
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R28C"

<400> 2820
Phe Arg Leu Phe Ser Phe Ala Leu Ile Ile Leu Asn Cys Met Asp Tyr
1 5 10 15

Ser His Cys Gln Gly Asn Arg Trp Arg Cys Cys Ser Lys Arg Ala Ser
20 25 30

Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys Asp
35 40 45

Asn Gly Cys Ser
50

<210> 2821
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S103W"

<400> 2821
Ala Ser Thr Gly Val Ala Gly Val Ser Ser Ala Met Asp His Thr Phe
1 5 10 15

Ser Thr Thr Ser Lys Asp Gly Glu Gly Trp Trp Cys Tyr Thr Ser Leu
20 25 30

Ile Ser Asp Ile Cys Tyr Pro Pro Gln Glu Asp Ser Thr Tyr Phe Thr
35 40 45

Gly Ile Leu Gln
50

<210> 2822
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P313fs"

<400> 2822
Lys Thr Val Pro Ile Leu Glu Leu Ser Pro Pro Leu Trp Thr Ala Ile
1 5 10 15

Gly Trp Val Gln Arg Gly Pro Thr Pro Leu Leu Leu Ser Ser Gly Phe
20 25 30

Tyr

<210> 2823
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D96fs"

<400> 2823
Leu Cys Ser Val Leu Pro Thr His Trp Arg Cys Asn Lys Thr Leu Pro
1 5 10 15

Ile Ala Phe Lys Val Val Ala Leu Gly Gly Cys Ser Arg Trp His Ser
20 25 30

Gly His Cys Asp Gly Trp Gln
35

<210> 2824
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

<221> source
<223> /note="p.R135G"

<400> 2824
Asp Glu Asn Tyr Ser Ala Glu Leu Arg Asn Ala Thr Ala Ala Met Lys
1 5 10 15

Asn Gln Val Ala Arg Phe Asn Asp Leu Gly Gly Phe Val Gly Arg Ser
20 25 30

Gly Arg Gly Lys Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro
35 40 45

Pro Gln Val Ala
50

<210> 2825
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R142fs"

<400> 2825
Leu Arg Asn Ala Thr Ala Ala Met Lys Asn Gln Val Ala Arg Phe Asn
1 5 10 15

Asp Leu Arg Phe Val Gly Arg Ser Gly Lys Arg Glu Lys Leu His Ser
20 25 30

Asp His His Cys Leu His Lys Pro Thr Ala Ser Arg His Leu Pro Gln
35 40 45

Ser His Gln Asn His Ser Gly Trp Ala Pro Arg Thr Ser Lys Thr Ser
50 55 60

Ala Glu Thr Arg
65

<210> 2826
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R337M"

<400> 2826
Ser Pro Ser Ile His Ser Thr Thr Pro Leu Ser Ser Thr Arg Gly Thr
1 5 10 15

Gly Leu Pro Ala Ile Thr Asp Val Pro Met Met Arg Ile Ser Asp Asp
20 25 30

Asp Thr Ala Thr Ser Asp Phe Cys Leu Trp Pro Ser Thr Leu Ser Lys
35 40 45

Lys Ser Gln Ala
50

<210> 2827
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.P466H"

<400> 2827
Ser Thr Pro Tyr Leu Tyr Tyr Gly Thr Ser Ser Gly Ser Tyr Gln Phe
1 5 10 15

Pro Met Val Pro Gly Gly Asp Arg Ser His His Ser Arg Met Leu Pro
20 25 30

Pro Cys Thr Thr Thr Ser Asn Gly Ser Thr Leu Leu Asn Pro Asn Leu
35 40 45

Pro Asn Gln Asn
50

<210> 2828
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q71E"

<400> 2828
Val Ala Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Glu Glu Ala Ala Ala Ala
20 25 30

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Val Pro Arg
35 40 45

Leu Arg Pro Pro
50

<210> 2829
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P486fs"

<400> 2829
Ser Ser Thr Gln Ala Ala Ala Ala Val Gly Pro Thr Val Leu Glu Gly
1 5 10 15

Gln Val Tyr Thr Asn Thr Ser Pro Pro Thr Ser Ala Leu Asp Val Ser
20 25 30

Ala Pro Ala Ala Met Ile Ala Ala Cys Ser Ala Ala Leu Leu Ser Ala
35 40 45

Trp Ala Arg Trp Asn Val Cys
50 55

<210> 2830
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E431K"

<400> 2830
Ser Val Gln Leu Leu Thr Pro Ala Asn Leu Leu Ala Lys Ile Asn Gly
1 5 10 15

Lys Asp Ser Ile Glu Lys Glu His Val Lys Lys Glu Ile Ser Glu Leu
20 25 30

Phe Tyr Asp Ala Lys Ser Ser Ala Lys Ile Leu Ala Asp Gln Gln Asp
35 40 45

Lys Tyr Met Lys
50

<210> 2831
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R117C"

<400> 2831
Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Thr Glu Ile Lys
1 5 10 15

Lys Thr Glu Val Leu Met Glu Asn Phe Cys Cys Arg Ala Ile Gly Leu
20 25 30

Arg Ile Lys Glu Thr Lys Glu Val Tyr Glu Gly Glu Val Thr Glu Leu
35 40 45

Thr Pro Cys Glu
    50

<210> 2832
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R254H"

<400> 2832
Val Glu Gly Pro Gln Ser Ala Cys Glu Glu Phe Trp Ser Arg Leu Arg
1   5   10   15

Lys Leu Asn Trp Lys Arg Ile Leu Ile His His His Arg Glu Asp Ile
            20   25   30

Pro Phe Asp Gly Thr Asn Asp Glu Thr Glu Arg Gln Arg Lys Phe Ser
        35   40   45

Ile Phe Glu Glu
    50

<210> 2833
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S223Y"

<400> 2833
His Arg Leu Glu Trp Leu Ile Ile Glu Asp Asn His Leu Ser Arg Ile
1   5   10   15

Ser Pro Pro Thr Phe Tyr Gly Leu Asn Tyr Tyr Leu Ile Leu Leu Val
            20   25   30

Leu Met Asn Asn Val Leu Thr Arg Leu Pro Asp Lys Pro Leu Cys Gln

35 40 45

His Met Pro Arg
50

<210> 2834
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S427Y"

<400> 2834
Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
1 5 10 15

Leu Leu Leu Arg Leu Pro Ala Leu Arg Tyr Tyr Ile Gly Leu Lys Cys
20 25 30

Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp
35 40 45

Thr Phe Leu Met
50

<210> 2835
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S427F"

<400> 2835
Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
1 5 10 15

Leu Leu Leu Arg Leu Pro Ala Leu Arg Phe Phe Ile Gly Leu Lys Cys
20 25 30

Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp
35 40 45

Thr Phe Leu Met
50

<210> 2836
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D668Y"

<400> 2836
Ile Arg Pro Asn Ile Phe Val Gly Arg Ala Glu Gly Thr Thr Gln Tyr
1 5 10 15

Ser Lys Trp Tyr Phe Glu Val Met Val Tyr Tyr Glu Val Thr Pro Phe
20 25 30

Leu Thr Ala Gln Ala Thr His Leu Arg Val Gly Trp Ala Leu Thr Glu
35 40 45

Gly Tyr Thr Pro
50

<210> 2837
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A2576T"

<400> 2837
Asn Arg Tyr Leu Cys Leu Ala Val Leu Pro Leu Ile Thr Lys Cys Ala
1 5 10 15

Pro Leu Phe Ala Gly Thr Glu His Arg Thr Thr Ile Met Val Asp Ser
20 25 30

Met Leu His Thr Val Tyr Arg Leu Ser Arg Gly Arg Ser Leu Thr Lys
35 40 45

Ala Gln Arg Asp
50

<210> 2838
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M4334I"

<400> 2838
Ile Cys Ser Leu Leu Leu Gly Gly Ser Leu Val Glu Gly Ala Lys Lys
1 5 10 15

Ile Lys Val Ala Glu Leu Leu Ala Asn Ile Ile Pro Asp Pro Thr Gln
20 25 30

Asp Glu Val Arg Gly Asp Gly Glu Glu Gly Glu Arg Lys Pro Leu Glu
35 40 45

Ala Ala Leu Pro
50

<210> 2839
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E711K"

<400> 2839

Val Thr Ala Glu Ala Thr His Leu Arg Val Gly Trp Ala Ser Thr Glu
1 5 10 15

Gly Tyr Ser Pro Tyr Pro Gly Gly Gly Lys Lys Glu Trp Gly Gly Asn
20 25 30

Gly Val Gly Asp Asp Leu Phe Ser Tyr Gly Phe Asp Gly Leu His Leu
35 40 45

Trp Ser Gly Cys
50

<210> 2840
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L2023F"

<400> 2840
Asp Phe His Glu Asp Leu Met Thr His Cys Gly Ile Glu Leu Asp Glu
1 5 10 15

Asp Gly Ser Leu Asp Gly Asn Ser Asp Phe Phe Thr Ile Arg Gly Arg
20 25 30

Leu Leu Ser Leu Val Glu Lys Val Thr Tyr Leu Lys Lys Lys Gln Ala
35 40 45

Glu Lys Pro Val
50

<210> 2841
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.K2413N"

<400> 2841
Ile Met Thr Phe Tyr Ser Ala Leu Ile Asp Leu Leu Gly Arg Cys Ala
1 5 10 15

Pro Glu Met His Leu Ile His Ala Gly Asn Asn Gly Glu Ala Ile Arg
20 25 30

Ile Arg Ser Ile Leu Arg Ser Leu Ile Pro Leu Gly Asp Leu Val Gly
35 40 45

Val Ile Ser Ile
50

<210> 2842
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P1670T"

<400> 2842
Asp Glu Ser Lys Arg His Gly Leu Pro Gly Val Gly Leu Arg Thr Cys
1 5 10 15

Leu Lys Pro Gly Phe Arg Phe Ser Thr Thr Thr Cys Phe Val Val Thr
20 25 30

Gly Glu Asp His Gln Lys Gln Ser Pro Glu Ile Pro Leu Glu Ser Leu
35 40 45

Arg Thr Lys Ala
50

<210> 2843
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R2705Q"

<400> 2843
Leu Ala Val Gly Trp Thr Val Glu Arg Thr Lys Glu Gly Glu Ala Leu
1 5 10 15

Val Gln Gln Arg Glu Asn Glu Lys Leu Gln Gln Ser Val Ser Gln Ala
20 25 30

Asn Gln Gly Asn Ser Tyr Ser Pro Ala Pro Leu Asp Leu Ser Asn Val
35 40 45

Val Leu Ser Arg
50

<210> 2844
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R2906Q"

<400> 2844
Phe His Val Asn Gly His Phe Ala Leu Asp Ser Ala Arg Arg Asn Leu
1 5 10 15

Trp Arg Asp Asp Asn Gly Val Gly Val Gln Gln Ser Asp Trp Asn Asn
20 25 30

Ser Leu Met Thr Ala Leu Ile Ala Pro Ala Tyr Val Glu Leu Leu Ile
35 40 45

Gln Leu Lys Lys
50

<210> 2845
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.W798fs"

<400> 2845
Arg Glu Gly Gln His Tyr Pro Glu Arg His Gly Gly Pro Glu Arg His
1 5 10 15

Gly Arg Asp Ser Arg Asp Gly Trp Gly Ala Met Ala Leu Thr Arg Gly
20 25 30

<210> 2846
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G799V"

<400> 2846
Glu Arg Glu Gly Gln His Tyr Pro Glu Arg His Gly Gly Pro Glu Arg
1 5 10 15

His Gly Arg Asp Ser Arg Asp Gly Trp Val Val Gly Tyr Gly Ser Asp
20 25 30

Lys Arg Met Ser Glu Gly Arg Gly Leu Pro Pro Pro Pro Arg Gly Arg
35 40 45

Arg Asp Trp Gly
50

<210> 2847
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.R229C"

<400> 2847
His Asn Val Cys Glu Gln Lys Met Glu Asn Val Gln Pro Ala Pro Asp
1 5 10 15

Asn Val Leu Leu Thr Leu Arg Pro Arg Cys Cys Ile Asn Met Thr Asp
20 25 30

Thr Gly Ile Ser Pro Met Ser Thr Arg Asp Pro Tyr Ala Thr Ile Thr
35 40 45

Tyr Asn Val Pro
50

<210> 2848
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.H298Q"

<400> 2848
Ser Thr Gly Leu Ile Asn Val Ala Gly Ala Gly Thr Pro Ala Ile Ser
1 5 10 15

Thr Asn Gly Leu Tyr Ser Thr Val Pro Gln Gln Asn Val Cys Glu Glu
20 25 30

Lys Met Glu Asn Asp Gln Pro Gln Pro Asn Asn Val Leu Ser Thr Val
35 40 45

Gln Pro Val Ile
50

<210> 2849
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L593V"

<400> 2849
Pro Gly Leu Asn His Val Glu Ser Gly Val Ser Ala Thr Ala Glu Ser
1 5 10 15

Pro Gln Ser Leu Leu Gly Gly Pro Pro Val Val Thr Lys Ala Glu Pro
20 25 30

Val Ser Leu Pro Cys Thr Asn Ala Arg Ala Gly Asp Ala Pro Val Gly
35 40 45

Ala Gln Ala Ser
50

<210> 2850
<211> 38
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V995fs"

<400> 2850
Asn Gln Tyr Thr Ser Met Leu Asn Gly Gly Leu Ala Val Lys Thr Asn
1 5 10 15

Glu Ile Ser Val Ile Gln Ser Gly Gly Phe Leu Pro Ser Arg Phe Pro
20 25 30

Trp Gly Pro Pro Pro Leu
35

<210> 2851
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R187L"

<400> 2851
Pro Pro Thr Pro Gln Asp Ile Ser Tyr Leu Ala Lys Gly Lys Val Ala
1 5 10 15

Asn Thr Asn Val Thr Leu Gln Ala Leu Leu Leu Gly Thr Lys Val Ala
20 25 30

Val Asn Gln Arg Ser Ala Asp Ala Leu Pro Ala Pro Val Pro Gly Ala
35 40 45

Asn Ser Ile Pro
50

<210> 2852
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q206H"

<400> 2852
Asp Met Thr Lys Tyr Leu Glu Gly Ser Leu Tyr Pro Ser Thr Gln Gln
1 5 10 15

Tyr Asn Asp Val Val Asn Ala Leu Leu His His Ala His Pro Phe Leu
20 25 30

Asp Glu Asp Gly Cys Gly Phe Phe Leu Trp Lys Arg Ala Leu Lys Asp
35 40 45

Arg Phe Lys Tyr
50

<210> 2853
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R477W"

<400> 2853
Ala Pro Ala Pro Thr Asp Gly Ser Glu Pro Ala Pro Ala Pro Val Ala
1 5 10 15

Asp Gly Asp Ile Pro Ser Gln Phe Thr Trp Trp Val Met Gly Lys Val
20 25 30

Cys Thr Gln Leu Leu Val Ser Arg Pro Asp Glu Glu Asn Ile Thr Ser
35 40 45

Tyr Leu Gln Leu
50

<210> 2854
<211> 52
<212> PRT
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polypeptide"

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<223> /note="p.P1076fs"

<400> 2854
Ser Arg Asn Leu Val Lys Asn Ala Lys Lys Thr Ile Gly Arg Gln His
1 5 10 15

Val Thr Arg Lys Lys Tyr Asn Pro Pro Ala Gly Ser Thr Gly Ala Ser
20 25 30

Arg Pro Leu Arg Thr Arg Arg Thr Arg Ser Gln Cys Arg Arg Ser Trp
35 40 45

Ser Pro Ala Arg
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<210> 2855
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.N1139fs"

<400> 2855
Glu Val His Gln Gln Asn Ala Leu Phe Gln Tyr Phe Ala Asp Thr Leu
1 5 10 15

Thr Ala Val Val Gln Asn Ala Lys Lys Lys Trp Lys Ile
20 25

<210> 2856
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G133W"

<400> 2856
Gly Gly Ala Pro Cys Pro Pro Leu Glu Glu Arg Ala Gly Cys Leu Glu
1 5 10 15

Tyr Ser Thr Pro Gln Gly Gln Asp Cys Trp Trp His Thr Tyr Val Pro
20 25 30

Ala Phe Ile Thr Thr Ser Ala Phe Asn Lys Glu Arg Thr Arg Gln Ala
35 40 45

Thr Ser Pro His
50

<210> 2857
<211> 43
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P208fs"

<400> 2857
Pro Pro Pro Ala Pro Ser Ser Ala Ser Ser Ser Pro Ser Pro Ser Pro
1 5 10 15

Ser Ser Ser Ser Pro Ser Pro Pro Pro Thr Pro Thr Ala Pro Cys Thr
20 25 30

Pro Ser Pro Thr Cys Pro Pro Ile Arg Tyr Leu
35 40

<210> 2858
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E926fs"

<400> 2858
Ser Ser Pro Gly Glu Lys Ser Arg Ser Gln Ser Arg Glu Arg Glu Ser
1 5 10 15

Asp Arg Asp Gly Gln Arg Arg Glu Arg Lys Glu Asn Gln Lys Val Val
20 25 30

<210> 2859
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G740C"

<400> 2859
Leu Val Gln Pro Ser Leu Ser Met Thr Pro Glu Thr Val Lys Asp Val
1 5 10 15

Gly Phe Gly Ser Leu Val Ile Pro Gly Cys Cys Ser Val Ala Ser Asn
20 25 30

Leu Ala Thr Ser Ala Leu Pro Ala Gly Asn Val Phe Asn Ala Pro Thr
35 40 45

Lys Gln Ala Glu
50

<210> 2860
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R366Q"

<400> 2860
Ala Glu Lys Thr Gln Phe Thr Val Ser Thr Leu Asp Asp Val Lys Asn
1 5 10 15

Ser Gly Ser Ile Arg Asp Asn Tyr Val Gln Gln Thr Ser Glu Ile Ser
20 25 30

Ala Val His Ile Asp Thr Glu Cys Val Ser Val Met Leu Gln Ala Gly
35 40 45

Thr Pro Pro Leu
50

<210> 2861
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R614Q"

<400> 2861
Ser Val Ser Phe Ala Glu Gly Thr Lys Phe Ala Pro Gln Ser Arg Arg
1 5 10 15

Ser Ser Gly Glu Leu Ser Ser Pro Leu Gln Gln Lys Pro Lys Arg Leu
20 25 30

Ser Arg Gly Ala Gln Ser Gly Pro Glu Gly Arg Glu Ala Glu Glu Ser
35 40 45

Thr Gly Pro Glu
50

<210> 2862
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R545W"

<400> 2862
Thr Asp Trp Asp Ser Ser Ile Asn Leu Thr Phe His Lys Ser Lys Ile
1 5 10 15

Ala Val Asp Glu Leu Phe Thr Ser Leu Trp Trp Asp Ile Ala Gly Ala
20 25 30

Arg Ser Leu Leu Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His
35 40 45

Thr His Gln Ala
50

<210> 2863
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.K109fs"

<400> 2863
Met Lys Leu Gln Leu Glu Asn Val Ile Lys Glu Asn Glu Arg Leu His
1 5 10 15

Ser Glu Leu Lys Asp Ala Val Glu Lys Asn Trp Arg Pro Phe Pro Trp
20 25 30

Ala Gln Arg
35

<210> 2864
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R194Q"

<400> 2864
Gly Lys Gln His Leu Arg Ser Leu Pro Val Val Asn Ser Ile Gly Tyr
1 5 10 15

Val Leu Arg Phe Leu Ala Lys Leu Cys Gln Gln Ser Leu Leu Cys Asp
20 25 30

Asp Leu Phe Ser His Gln Pro Phe Pro Arg Gly Cys Ser Ala Ser Glu
35 40 45

Lys Val Gln Glu
50

<210> 2865
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L261F"

<400> 2865
Tyr Leu Val Asn Pro Val Gly Met Asn Arg Tyr Ser Val Asp Thr Ser
1 5 10 15

Ala Ser Thr Phe Asn His Arg Gly Ser Phe Phe His Pro Ser Ser Ser
20 25 30

Leu Tyr Cys Lys Arg Gln Asn Ser Gly Asp Ser His Leu Gly Gly Gly
35 40 45

Pro Ala Ala Thr
50

<210> 2866
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1142H"

<400> 2866
Glu Gly Cys Ile Arg His Cys Pro Cys Cys Lys Leu Asp Thr Thr Lys
1 5 10 15

Ser Pro Trp Asp Val Gly Trp Gln Val His His Lys Thr Cys Tyr Arg
20 25 30

Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu
35 40 45

Leu Ser Ser Gly
50

<210> 2867
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T1570M"

<400> 2867
Ile Val Val Val Leu Ser Ile Ala Ser Leu Ile Phe Ser Ala Ile Leu
1 5 10 15

Lys Ser Leu Gln Ser Tyr Phe Ser Pro Met Met Leu Phe Arg Val Ile
20 25 30

Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys
35 40 45

Gly Ile Arg Thr
50

<210> 2868
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R36K"

<400> 2868
Pro Asp Ser Phe Arg Phe Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu
1 5 10 15

Gln Arg Ile Ala Glu Glu Lys Ala Lys Lys Lys Pro Lys Gln Glu Arg
20 25 30

Lys Asp Glu Asp Asp Glu Asn Gly Pro Lys Pro Asn Ser Asp Leu Glu
35 40 45

Ala Gly Lys Ser
50

<210> 2869
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.T155K"

<400> 2869
Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val Phe
1 5 10 15

Met Thr Met Ser Asn Pro Pro Asp Trp Lys Lys Lys Asn Val Glu Tyr
20 25 30

Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala
35 40 45

Arg Gly Phe Cys
50

<210> 2870
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R1358H"

<400> 2870
Met Thr Val Gly Ser Tyr Leu Val Pro Pro Ser Leu Val Gln Leu Ile
1 5 10 15

Leu Leu Ser Arg Ile Ile His Met Leu His His Leu Gly Lys Gly Pro
20 25 30

Lys Val Phe His Asn Leu Met Leu Pro Leu Met Leu Ser Leu Pro Ala
35 40 45

Leu Leu Asn Ile
50

<210> 2871
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R564H"

<400> 2871
Met Ser Cys Ser Val Val Cys Val Ile Glu Ile Ile Glu Val Phe Phe
1 5 10 15

Ile Asp Phe Phe Ser Ile Ile Ala Arg His His Gln Trp Gln Lys Ala
20 25 30

Lys Glu Trp Trp Ala Trp Lys Gln Ala Pro Pro Cys Pro Glu Ala Pro
35 40 45

Arg Ser Pro Gln
50

<210> 2872
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G332V"

<400> 2872
Ser Leu Gly Lys Leu Thr Lys Leu Thr Asn Leu Asn Val Asp Arg Asn
1 5 10 15

His Leu Glu Ala Leu Pro Pro Glu Ile Val Val Gly Cys Val Ala Leu
20 25 30

Ser Val Leu Ser Leu Arg Asp Asn Arg Leu Ala Val Leu Pro Pro Glu
35 40 45

Leu Ala His Thr
50

<210> 2873

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S133A"

<400> 2873
Val Ser Glu Gly Tyr Ala Ala Asp Ala Phe Phe Ile Thr Asp Gly Arg
1 5 10 15

Ser Arg Arg Lys Ala Ser Asn Ala Gly Ala Ala Ala Ala Ala Pro Ser
20 25 30

Thr Ala Ser Ala Ala Ala Pro Asp Gly Asp Ala Gly Gly Gly Gly Gly
35 40 45

Ala Gly Gly Arg
50

<210> 2874
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V342M"

<400> 2874
Asp Gly Lys Thr Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly
1 5 10 15

Gly Cys Asp His Phe Cys Lys Asn Ile Met Met Gly Ser Phe Asp Cys
20 25 30

Gly Cys Lys Lys Gly Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln
35 40 45

Asp Val Asp Glu
50

<210> 2875
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K275fs"

<400> 2875
Tyr Ala Thr Gly Lys Lys Ser Ser Lys Asn Lys Lys Lys Leu Glu Lys
1 5 10 15

Ala Met Lys Val Leu Lys Lys Gln Lys Arg Arg Lys Asn Gln Arg Cys
20 25 30

Leu Thr Phe Gln Pro Phe Thr
35

<210> 2876
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H66Y"

<400> 2876
Asp Tyr Lys Val Arg Ile Asp Glu Tyr Asp His Ser Lys Pro Ile Gln
1 5 10 15

Gly Gln Gln Lys Lys Pro Phe Glu Glu Tyr Tyr Trp Arg Lys His Thr
20 25 30

Leu Ser Tyr Val Asp Val Ser Thr Gly Lys Val Thr Val Glu Tyr Arg
35 40 45

Pro Ile Ile Asp
50

<210> 2877
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S37fs"

<400> 2877
Val Gly Arg Pro Pro Val Pro Leu His Met Val Ser Thr Ala Ser Gly
1 5 10 15

Gln Thr Arg Cys Trp Thr Trp Leu Ser Leu Val Arg His Val Pro
20 25 30

<210> 2878
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R31C"

<400> 2878
Leu Cys Pro Ala Cys Thr Pro Val Gly Arg Pro Pro Val Pro Leu His
1 5 10 15

Met Val Ser Thr Ala Ser Gly Gln Thr Cys Cys Cys Trp Thr Trp Leu
20 25 30

Ser Gly Gln Ala Cys Ala Leu Ser Ile Ala Glu Ser Cys Arg Pro Gly
35 40 45

Asp Lys Val Pro
50

<210> 2879
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A66T"

<400> 2879
Ala Ala Cys Ala Ser Val His Gly Ala Asn Arg Leu Gly Ala Asn Ser
1 5 10 15

Leu Leu Asp Leu Val Val Phe Gly Gln Thr Thr Cys Ala Leu Ser Ile
20 25 30

Glu Glu Ser Cys Arg Pro Gly Asp Lys Val Pro Pro Ile Lys Pro Asn
35 40 45

Ala Gly Glu Glu
50

<210> 2880
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K508fs"

<400> 2880
Arg Pro Val Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg
1 5 10 15

Cys Glu Val Ser Gly Ala Pro Lys Pro Arg His His Leu Glu Lys Arg
20 25 30

Lys Pro His Ser Gly Gln Trp Leu Cys Pro Asp Ser
35 40

<210> 2881
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T1181M"

<400> 2881
Pro Ser Pro Tyr Ser Pro Ser Ser Arg Val Ile Gln Thr Leu Gln Ala
1 5 10 15

Pro Pro Asp Val Ala Pro Thr Ser Val Met Met Val Arg Thr Ala Ser
20 25 30

Glu Thr Ser Leu Arg Leu Arg Trp Val Pro Leu Pro Asp Ser Gln Tyr
35 40 45

Asn Gly Asn Pro
50

<210> 2882
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Y2146C"

<400> 2882
Ala Asp Ala Ser Glu Ser Glu Ala Thr Asp Ser Asp Tyr Glu Asp Ala
1 5 10 15

Leu Pro Lys His Ser Phe Val Asn His Cys Cys Met Ser Asp Pro Thr
20 25 30

Tyr Tyr Asn Ser Trp Lys Arg Arg Ala Gln Gly Arg Ala Pro Ala Pro
35 40 45

His Arg Tyr Glu
50

<210> 2883
<211> 28

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.A50fs"

<400> 2883
Tyr Gly His Tyr Gly Asp Pro Ser His Thr Ala Ser Pro Thr Gly Met
1 5 10 15

Met Lys Pro Ala Gly Pro Leu Gly Ala His Arg His
20 25

<210> 2884
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P905S"

<400> 2884
Gly Val Arg Pro Ala Ser Ser Gln Pro Gln Leu Leu Gly Gly Gln Arg
1 5 10 15

Val Gln Val Pro Asn Pro Val Gly Phe Ser Ser Gly Thr Trp Pro Leu
20 25 30

Pro Gly Ser Pro Leu Pro Met Ala Cys Pro Gly Ile Met Arg Pro Gly
35 40 45

Ser Thr Ser Leu
50

<210> 2885
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G126V"

<400> 2885
Glu Val Gly Asp Thr Pro Lys Asp Arg Ala Leu Phe Asn Gly Ala Gln
1 5 10 15

Lys Leu Phe Gly Met Ile Ile Thr Ile Val Val Gln Ala Ile Val Tyr
20 25 30

Val Met Thr Gly Met Tyr Gly Asp Pro Ala Glu Met Gly Ala Gly Ile
35 40 45

Cys Leu Leu Ile
50

<210> 2886
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D608E"

<400> 2886
Gly Met Asp Glu Leu Ile Ser Thr Pro Ser Val Glu Asp Lys Ser Glu
1 5 10 15

Glu Pro Pro Gly Thr Glu Leu Gln Arg Glu Glu Thr Glu Ala Ser His
20 25 30

Leu Ala Pro Asn His Thr Thr Phe Pro Lys Ile His Ser Arg Arg Phe
35 40 45

Arg Asp Tyr Cys
50

<210> 2887
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R429W"

<400> 2887
Arg Ala Phe Gln Tyr Asp Thr Asn Cys Ser Phe Arg Cys Ala Glu Gly
1 5 10 15

Phe Met Leu Arg Gly Ala Asp Ile Val Trp Trp Cys Asp Asn Leu Gly
20 25 30

Gln Trp Thr Ala Pro Ala Pro Val Cys Gln Ala Leu Gln Cys Gln Asp
35 40 45

Leu Pro Val Pro
50

<210> 2888
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A297T"

<400> 2888
Asn Met Thr Cys Leu His Ser Ala Lys Ala Phe Gln His Gln Ser Ser
1 5 10 15

Cys Ser Phe Ser Cys Glu Glu Gly Phe Thr Thr Leu Val Gly Pro Glu
20 25 30

Val Val Gln Cys Thr Ala Ser Gly Val Trp Thr Ala Pro Ala Pro Val
35 40 45

Cys Lys Ala Val
50

<210> 2889

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D81N"

<400> 2889
Ser Tyr His Thr Phe Leu Leu Asp Glu Glu Arg Ser Arg Leu Tyr Val
1 5 10 15

Gly Ala Lys Asp His Ile Phe Ser Phe Asn Asn Leu Val Asn Ile Lys
20 25 30

Asp Phe Gln Lys Ile Val Trp Pro Val Ser Tyr Thr Arg Arg Asp Glu
35 40 45

Cys Lys Trp Ala
50

<210> 2890
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R252Q"

<400> 2890
Glu Asp Asp Arg Val Tyr Phe Phe Phe Thr Glu Val Ser Val Glu Tyr
1 5 10 15

Glu Phe Val Phe Arg Val Leu Ile Pro Gln Gln Ile Ala Arg Val Cys
20 25 30

Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr Ser
35 40 45

Phe Leu Lys Ala
50

<210> 2891
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R292C"

<400> 2891
Gln His Gln Thr Lys Asn Leu Ser Gln Asp Gln Glu His Gly Arg Lys
1 5 10 15

Ala His Lys Ile Ser Tyr Pro Ser Ser Cys Cys Thr Glu Glu Arg Gln
20 25 30

Leu His His Gly Glu Lys Ser Val Gln Lys Asp Val Ser Lys Gly Ser
35 40 45

Ile Ser Ile Gln
50

<210> 2892
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S673Y"

<400> 2892
Glu Leu Glu Leu Ser Tyr Pro Leu Ser Trp Val Gln Ala Phe Pro Leu
1 5 10 15

Phe Gln Asn Leu Ser Ser Lys Glu Ser Tyr Tyr Phe Ile His Tyr Tyr
20 25 30

Cys Val Ser Thr Cys Ser Phe Pro Ala Gly Val Ala Val Ala Glu Glu
35 40 45

Met Lys Leu Lys
50

<210> 2893
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<400> 2893
Gly Glu Gly His Gln Ala Trp Ile Ile Gly Ile Val Glu Lys Gly Asn
1 5 10 15

Arg Thr Ala Arg Ile Ile Asp Lys Pro Gln Gln Ile Ile Glu Val Ala
20 25 30

Pro Gln Val Ala Thr Gln Asn Val Asn Pro Thr Pro Gly Ala Thr Ser
35 40 45

<210> 2894
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.E13K"

<400> 2894
Met Ser Thr Arg Glu Ser Phe Asn Pro Glu Ser Tyr Lys Lys Leu Asp
1 5 10 15

Lys Ser Phe Arg Leu Thr Arg Phe Thr Glu Leu Lys Gly Thr Gly Cys
20 25 30

Lys Val Pro Gln Asp Val Leu
35

<210> 2895
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.R211G"

<400> 2895
His Gly Lys Ile Asn Asn Leu Ile Glu Asn Ile Asp Pro Gly Thr Val
1 5 10 15

Met Leu Leu Ala Asn Tyr Ile Phe Phe Gly Gly Ala Arg Trp Lys His
20 25 30

Glu Phe Asp Pro Asn Val Thr Lys Glu Glu Asp Phe Phe Leu Glu Lys
35 40 45

Asn Ser Ser Val
50

<210> 2896
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.D253Y"

<400> 2896
Phe Phe Leu Glu Lys Asn Ser Ser Val Lys Val Pro Met Met Phe Arg
1 5 10 15

Ser Gly Ile Tyr Gln Val Gly Tyr Asp Tyr Tyr Lys Leu Ser Cys Thr
20 25 30

Ile Leu Glu Ile Pro Tyr Gln Lys Asn Ile Thr Ala Ile Phe Ile Leu
35 40 45

Pro Asp Glu Gly

50

<210> 2897
<211> 52
<212> PRT
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<220>
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<220>
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<400> 2897
Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys Glu Gln Leu Ser
1 5 10 15

Leu Leu Asp Arg Phe Thr Glu Asp Ala Asn Asn Arg Leu Tyr Gly Ser
20 25 30

Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala Lys Lys Leu
35 40 45

Ile Asn Asp Tyr
50

<210> 2898
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R98C"

<400> 2898
His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser Leu Lys Ile
1 5 10 15

Ala Pro Ala Asn Ala Asp Phe Ala Phe Cys Cys Phe Tyr Tyr Leu Ile
20 25 30

Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu Ser Ile
35 40 45

Ser Ala Ala Tyr
    50

<210> 2899
<211> 48
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.M414I"

<400> 2899
Thr Thr Lys Phe Ile Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr
1   5   10   15

Val Ser Phe Asn Arg Thr Phe Leu Met Ile Ile Ile Thr Asn Lys Ala
            20   25   30

Thr Asp Gly Ile Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser
        35   40   45

<210> 2900
<211> 63
<212> PRT
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<220>
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<220>
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<400> 2900
Pro Ile Cys Gln Glu Tyr Leu Asp Gly Val Ile Gln Phe Tyr His Thr
1   5   10   15

Thr Ile Glu Ser Val Asp Phe Gln Lys Thr Leu Lys Asn Pro Asp Lys
            20   25   30

Arg Leu Thr Ser Gly Leu Asn Val Asn Pro Lys Val Lys Ser Arg Asn
        35   40   45

Ser Ser Ala Arg Thr Leu Leu Met Leu Arg Leu Cys Trp Tyr Trp
50 55 60

<210> 2901
<211> 52
<212> PRT
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<220>
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<223> /note="p.S209C"

<400> 2901
Gly Gln Trp Glu Asn Lys Phe Lys Lys Glu Asn Thr Lys Glu Glu Lys
1 5 10 15

Phe Trp Pro Asn Lys Asn Thr Tyr Lys Cys Cys Val Gln Met Met Arg
20 25 30

Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu Glu Asp Val Gln Ala Lys
35 40 45

Val Leu Glu Ile
50

<210> 2902
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R45L"

<400> 2902
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser
1 5 10 15

Pro Val Asp Ile Cys Thr Ala Lys Pro Leu Leu Asp Ile Pro Met Asn
20 25 30

Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
35 40 45

Gly Ser Glu Gln
50

<210> 2903
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.L81fs"

<400> 2903
Gly Met Met Glu Leu Gly Ala Gln Gly Ser Thr Gln Lys Glu Ile Arg
1 5 10 15

His Ser Met Gly Tyr Asp Ser Leu Lys Met Val Lys Asn Phe Leu Ser
20 25 30

<210> 2904
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I306M"

<400> 2904
Val Met Gln Val Val Asn Trp Leu Glu Gly Pro Gly Ser Glu Gln Leu
1 5 10 15

Arg Ala Gln Trp Gly Ile Gly Asp Ser Met Met Arg Ala Ser Gln Ala
20 25 30

Leu Gln Gln Lys His Glu Glu Ile Glu Ser Gln His Ser Glu Trp Phe
35 40 45

Ala Val Tyr Val

50

<210> 2905
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R715fs"

<400> 2905
Tyr Gly Tyr Glu Ala Gly Thr Val Pro Glu Lys Glu Ile Phe Cys Gln
1 5 10 15

Cys Gly Val Asn Lys Cys Arg Lys Lys Tyr Tyr Lys Tyr Val Thr Asn
20 25 30

Ala Cys Leu
35

<210> 2906
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S207L"

<400> 2906
Val Pro Leu Trp Leu Asp Arg Lys Glu Ser Ala Val Pro Thr Thr Pro
1 5 10 15

Ala Pro Leu Gln Ile Ser Pro Phe Thr Leu Leu Gln Pro Tyr Val Ala
20 25 30

His Thr Leu Pro Gln Arg Pro Glu Pro Gly Glu Pro Gly Pro Asp Met
35 40 45

Ala Gln Glu Ala
50

<210> 2907
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R74P"

<400> 2907
Glu Ala Leu Ala Glu Leu Leu His Gly Ala Leu Leu Arg Arg Gly Pro
1 5 10 15

Glu Met Gly Tyr Leu Pro Gly Ser Asp Pro Pro Asp Pro Thr Leu Ala
20 25 30

Thr Pro Pro Ala Gly Gln Thr Leu Ala Val Pro Ser Leu Pro Arg Ala
35 40 45

Thr Glu Pro Gly
50

<210> 2908
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<400> 2908
Ile Glu Thr Pro Glu Asp Gln Asn Asp Leu Arg Lys Met Gln Leu Arg
1 5 10 15

Glu Leu Ala Arg Leu Asn Gly Thr Leu Trp Trp Glu Asp Asp Asn Arg
20 25 30

Ile Leu Arg Pro Trp Gln Ser Ser Glu Thr Arg Ser Ile Thr Asn Thr
35 40 45

Thr Val Cys Thr
    50

<210> 2909
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<400> 2909
Ser Asn Leu Ala Lys Ala Ala Gly Leu Ala Thr Met Ile Ser Thr Met
1   5   10   15

Arg Pro Asp Ile Asp Asn Met Asp Glu Cys Cys Val Arg Asn Thr Thr
            20   25   30

Ala Arg Ala Phe Ala Val Val Ala Ser Ala Leu Gly Ile Pro Ser Leu
        35   40   45

Leu Pro Phe Leu
    50

<210> 2910
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<400> 2910
Ala Lys Ala Ala Gly Leu Ala Thr Met Ile Ser Thr Met Arg Pro Asp
1   5   10   15

Ile Asp Asn Met Asp Glu Tyr Val Arg Tyr Tyr Thr Thr Ala Arg Ala
            20   25   30

Phe Ala Val Val Ala Ser Ala Leu Gly Ile Pro Ser Leu Leu Pro Phe
35 40 45

Leu Lys Ala Val
50

<210> 2911
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2911
Ile Pro Ser Leu Leu Pro Phe Leu Lys Ala Val Cys Lys Ser Lys Lys
1 5 10 15

Ser Trp Gln Ala Arg His Thr Gly Ile Glu Glu Ile Val Gln Gln Ile
20 25 30

Ala Ile Leu Met Gly Cys Ala Ile Leu Pro His Leu Arg Ser Leu Val
35 40 45

Glu Ile Ile Glu
50

<210> 2912
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K700E"

<400> 2912
Met Gly Cys Ala Ile Leu Pro His Leu Arg Ser Leu Val Glu Ile Ile
1 5 10 15

Glu His Gly Leu Val Asp Glu Gln Gln Glu Glu Val Arg Thr Ile Ser

20 25 30

Ala Leu Ala Ile Ala Ala Leu Ala Glu Ala Ala Thr Pro Tyr Gly Ile
35 40 45

Glu Ser Phe Asp
50

<210> 2913
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E902K"

<400> 2913
Gly Asn Leu Gly Ala Ala Asp Ile Asp His Lys Leu Glu Glu Gln Leu
1 5 10 15

Ile Asp Gly Ile Leu Tyr Ala Phe Gln Lys Lys Gln Thr Thr Glu Asp
20 25 30

Ser Val Met Leu Asn Gly Phe Gly Thr Val Val Asn Ala Leu Gly Lys
35 40 45

Arg Val Lys Pro
50

<210> 2914
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R957Q"

<400> 2914
Ile Cys Gly Thr Val Leu Trp Arg Leu Asn Asn Lys Ser Ala Lys Val
1 5 10 15

Arg Gln Gln Ala Ala Asp Leu Ile Ser Gln Gln Thr Ala Val Val Met
20 25 30

Lys Thr Cys Gln Glu Glu Lys Leu Met Gly His Leu Gly Val Val Leu
35 40 45

Tyr Glu Tyr Leu
50

<210> 2915
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 2915
Thr His His Leu Gln Cys Val Arg Lys Arg Leu Leu His Arg Gln Ser
1 5 10 15

Thr Gln Leu Leu Ala Gln Arg Leu Ser Gln Gln Thr Cys Phe Arg Gln
20 25 30

Trp Arg Gln Gln Leu Ala Ala Arg Arg Gln Glu Gln Arg Ala Thr Val
35 40 45

Arg Ala Leu Trp
50

<210> 2916
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R611Q"

<400> 2916
Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met Gly
1 5 10 15

Tyr Met Asp Pro Arg Glu Arg Asp Met Gln Gln Met Gly Gly Gly Gly
20 25 30

Ala Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro
35 40 45

Pro Leu Gly Gly
50

<210> 2917
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R232Q"

<400> 2917
Gln Arg Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu
1 5 10 15

Ile Phe Lys Ser Ser Ser Pro Ile Pro Gln Gln Thr Gln Val Pro Leu
20 25 30

Ile Thr Asn Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp
35 40 45

Val Leu Ile Met
50

<210> 2918
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<221> source
<223> /note="p.S617Y"

<400> 2918
Pro Leu Glu Lys Asn Arg Val Lys Leu Asp Asp Asp Ser Asp Asp Asp
1 5 10 15

Glu Glu Ser Lys Glu Gly Gln Glu Ser Tyr Tyr Ser Ser Ala Ala Asn
20 25 30

Thr Asn Pro Ala Val Ala Pro Pro Cys Val Val Val Glu Glu Lys Lys
35 40 45

Pro Gln Leu Thr
50

<210> 2919
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A220V"

<400> 2919
Glu Ser Pro Thr Arg Ser Leu Ser Met Asp Ala Pro Arg Gly Val His
1 5 10 15

Ile Gln Ala His Ala Gly Lys Ile Glu Val Val Leu Ser Gln Met Asp
20 25 30

Ile Leu Phe His Ser Ser Asp Gly Met Leu Val Leu Asp Ala Glu Thr
35 40 45

Val Cys Leu Pro
50

<210> 2920
<211> 52
<212> PRT
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<220>
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<223> /note="p.I41M"

<400> 2920
Arg Glu Gln Tyr Ile Leu Ala Thr Gln Gln Asn Asn Leu Pro Arg Thr
1 5 10 15

Glu Asn Ala Gln Leu Tyr Pro Val Gly Met Met Tyr Gly Trp Arg Lys
20 25 30

Arg Cys Leu Tyr Phe Phe Val Leu Leu Leu Val Thr Met Ile Val
35 40 45

Asn Leu Ala Met
50

<210> 2921
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R502L"

<400> 2921
Gly Val Gly Asp Val Ser Arg Pro Phe Ser Pro Pro Ile His Ser Ser
1 5 10 15

Ser Pro Pro Pro Ile Ala Pro Leu Ala Leu Leu Ala Glu Ser Thr Ser
20 25 30

Ser Ile Ser Ser Thr Asn Ser Leu Ser Ala Ala Thr Thr Pro Thr Val
35 40 45

Glu Asn Glu Gln
50

<210> 2922
<211> 53
<212> PRT
<213> Artificial Sequence

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K367del"

<400> 2922
Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His Val Phe Phe Ser Leu
1 5 10 15

Ile Asn Trp Asp Asp Leu Ile Asn Lys Ile Thr Pro Pro Phe Asn Pro
20 25 30

Asn Val Ser Gly Pro Asn Asp Leu Arg His Phe Asp Pro Glu Phe Thr
35 40 45

Glu Glu Pro Val Pro
50

<210> 2923
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<223> /note="p.L61fs"

<400> 2923
Ser Glu Trp Phe Val Phe Arg Arg Tyr Ala Glu Phe Asp Lys Leu Tyr
1 5 10 15

Asn Thr Leu Lys Lys Gln Phe Pro Ala Trp Pro
20 25

<210> 2924
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E407fs"

<400> 2924
Lys Lys Ser Asn Lys Lys Thr Asn Glu His Gly Met Lys Thr Phe Arg
1 5 10 15

Lys Val Lys Asp Ser Ser Ser Glu Lys Arg Glu Lys Asp Gln Arg Asp
20 25 30

Ser Leu Lys Ile Val Gln Met Ser Ile Leu Gly Lys Arg Leu Lys Thr
35 40 45

Gly Gln Lys Asp Leu Met Ser Trp Met Ala Lys Gly Val Gln Lys Ile
50 55 60

Pro Val Leu Phe Ser Ile Met Asn Ser Trp Leu Arg
65 70 75

<210> 2925
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E818K"

<400> 2925
Val Leu Asp Ala Gln Arg Asn Thr Pro Thr Val Leu Arg Pro Arg Asp
1 5 10 15

Gly Ser Val Asp Asp Arg Gln Ser Ser Lys Lys Ala Thr Thr Ser Gln
20 25 30

Asp Glu Ala Pro Arg Glu Glu Leu Ala Val Gln Asp Ser Leu Glu Ser
35 40 45

Asp Leu Leu Ala
50

<210> 2926
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.F1117L"

<400> 2926
Ile Ala Leu Ala Leu Val Glu Val Tyr Arg Asp Ile Ile Leu Glu Asn
1 5 10 15

Asn Met Asp Phe Thr Asp Ile Ile Lys Leu Leu Phe Asn Glu Met Ala
20 25 30

Glu Arg His Asn Thr Lys Gln Val Leu Lys Leu Ala Arg Asp Leu Val
35 40 45

Tyr Lys Val Gln
50

<210> 2927
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P563fs"

<400> 2927
Ile Ser Gln Val Ser Asp Asn Lys Ala Ser Leu Pro Pro Lys Pro Gly
1 5 10 15

Thr Met Ala Ala Gly Gly Gly Gly Pro Ser Pro Ser Val Leu Ser Gly
20 25 30

Ala Leu Pro Pro Val Ile Leu Phe Gly Asn Ser Trp Thr Gln Ser Gln
35 40 45

Leu Pro Val Ser Val Arg His Gly Arg Lys Thr Lys Asp Gly Ala Cys
50 55 60

Gly Gln Gln Pro Gly Gly Arg Gly Gly Ala Lys Asp Thr Gly Pro Arg

65 70 75 80

Ala Glu Glu His His Arg Asp His Glu Gly Pro Ala Glu Thr Arg Asp
85 90 95

<210> 2928
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L574fs"

<400> 2928
Leu Pro Pro Lys Pro Gly Thr Met Ala Ala Gly Gly Gly Gly Pro Ala
1 5 10 15

Pro Leu Ser Ser Ala Ala Pro Ser Pro Cys His Pro Leu Trp Glu Gln
20 25 30

Leu Asp Thr Glu Pro Thr Pro Arg Leu Cys Ser Ala Arg Lys Glu Asn
35 40 45

Gln Arg Trp Ser Leu Arg Pro Ala Ala Arg Arg Pro Trp Arg Ser
50 55 60

<210> 2929
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S759L"

<400> 2929
Ser Ser Asp Leu Ile Thr Leu Pro Ala Thr Thr Pro Pro Cys Pro Thr
1 5 10 15

Lys Lys Glu Trp Glu Gly Pro Ala Thr Leu Leu Tyr Met Thr Cys Ser
20 25 30

Ala Tyr Gln Lys Val Gln Asp Ser Glu Ile Ser Phe Pro Ala Gly Val
35 40 45

Glu Val Gln Val
50

<210> 2930
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R318C"

<400> 2930
Arg Lys Val Pro Gly Gln Phe Ser Ile Thr Thr Ala Leu Asn Thr Leu
1 5 10 15

Asn Arg Met Val His Ser Pro Ser Gly Cys Cys His Met Val Glu Ile
20 25 30

Ser Thr Pro Val Leu Ile Ser Ser Ser Asn Pro Ser Val Ile Thr Gln
35 40 45

Pro Met Glu Lys
50

<210> 2931
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R89C"

<400> 2931
Arg Cys Val Asn Gly Pro Leu Gln Glu Ala Ala Arg Arg Arg Leu Trp
1 5 10 15

Ala Leu Glu Asn Glu Asp Gln Glu Val Cys Cys Met Leu Phe Lys Asp
20 25 30

Leu Ser Ala Arg Leu Val Ser Ile Gln Ser Gln Arg Ala Gln Phe Leu
35 40 45

Ile Thr Phe Lys
50

<210> 2932
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A460T"

<400> 2932
Arg Asn Ser Gln Thr Ser Lys His Asp Tyr Ser Leu Ser Leu Arg Ser
1 5 10 15

Asn Gln Gly Phe Met His Met Lys Leu Thr Thr Lys Thr Lys Glu Lys
20 25 30

Tyr Val Leu Gly Gln Asn Ser Pro Pro Phe Asp Ser Val Pro Glu Val
35 40 45

Ile His Tyr Tyr
50

<210> 2933
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<400> 2933

Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
1 5 10 15

Glu Glu Glu Ala Glu Glu Glu Glu Glu Glu Leu Pro Pro Gln Tyr Phe
20 25 30

Ser Ser Glu Thr Ser Gly Ser Cys Ala Leu Asn Pro Glu Glu Val Leu
35 40 45

Glu Gln Pro Gln Pro Leu
50

<210> 2934
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V1217F"

<400> 2934
Leu Asp Phe Tyr Met Phe Leu Gly Pro Thr Pro Glu Val Ala Thr Lys
1 5 10 15

Gln Tyr His Glu Val Ile Gly His Pro Phe Phe Met Pro Ala Tyr Trp
20 25 30

Ala Leu Gly Phe Gln Leu Cys Arg Tyr Gly Tyr Ala Asn Thr Ser Glu
35 40 45

Val Arg Glu Leu
50

<210> 2935
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I1681K"

<400> 2935
Trp Phe Asp Tyr His Thr Gly Lys Asp Ile Gly Val Arg Gly Gln Phe
1 5 10 15

Gln Thr Phe Asn Ala Ser Tyr Asp Thr Lys Lys Asn Leu His Val Arg
20 25 30

Gly Gly His Ile Leu Pro Cys Gln Glu Pro Ala Gln Asn Thr Phe Tyr
35 40 45

Ser Arg Gln Lys
50

<210> 2936
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P318fs"

<400> 2936
Gln Ala Ala Trp Ser Asp Ala Gly Val Tyr Thr Cys Gln Ala Glu Asn
1 5 10 15

Gly Val Gly Ser Leu Val Ser Pro Pro Ser Ala Ser Thr Ser Ser Trp
20 25 30

Leu Arg Ser Arg
35

<210> 2937
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> source
<223> /note="p.T250M"

<400> 2937
Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro Arg Asp
1 5 10 15

Leu Val Ile Ser Ile Ser Arg Asp Asn Met Met Pro Ala Leu Glu Pro
20 25 30

Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys Gly Gln Phe
35 40 45

Leu Arg Leu Leu
50

<210> 2938
<211> 52
<212> PRT
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<400> 2938
Asn Arg Leu Gly Ser Gln Gln Gln Ala Leu Asp Leu Ser Val Gln Tyr
1 5 10 15

Pro Pro Glu Asn Leu Arg Val Met Val Phe Phe Gln Ala Asn Arg Thr
20 25 30

Val Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly
35 40 45

Gln Ser Leu Arg
50

<210> 2939
<211> 32
<212> PRT
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<223> /note="p.Q678fs"

<400> 2939
Glu Val Leu Glu Gln Gln Arg Leu Leu Gln Leu Gln His His Pro Ala
1 5 10 15

Ala Ala Pro Gly Cys Ser Gln Ala Pro Ser Arg Pro Leu Pro Arg Leu
20 25 30

<210> 2940
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.V213M"

<400> 2940
Tyr Leu Lys Ile Arg Gln Tyr Ser Leu Asp Met Ser Pro Phe Asp Gly
1 5 10 15

Cys Tyr Gln Asn Val Gly Leu Val Ala Met Met Gly His Ser Leu Pro
20 25 30

Pro Ser Ala Val Thr Glu Ile Lys Leu His Ser Asn Met Phe Met Phe
35 40 45

Arg Ala Ser Leu
50

<210> 2941
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.R1063Q"

<400> 2941

Ser Glu Thr Tyr Arg Met Pro Val Met Glu Tyr Lys Met Asn Glu Gly
1 5 10 15

Val Ser Tyr Glu Phe Lys Phe Pro Phe Gln Gln Asn Asn Asn Lys Trp
20 25 30

Gln Arg Asn Ala Ser Lys Gly Pro His Ser Pro Gln Val Pro Ser Gln
35 40 45

Val Gln Ser Pro
50

<210> 2942
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S1227Y"

<400> 2942
Pro Ser Trp Gln Arg Ser Glu Asp Ser Ile Ala Asp Gln Met Ala Tyr
1 5 10 15

Ser Tyr Arg Gly Pro Gln Asp Phe Asn Tyr Tyr Phe Val Leu Glu Gln
20 25 30

His Glu Tyr Thr Glu Pro Thr Cys His Leu Pro Ala Val Ser Lys Val
35 40 45

Leu Pro Ala Phe
50

<210> 2943
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G777A"

<400> 2943
Arg Val His Asn Pro Cys Thr Asp Asn Val Cys Tyr Ser Met Ala Val
1 5 10 15

Thr Arg Ser Lys Asp Ala Pro Pro Phe Ala Ala Pro Pro Ile Pro Ser
20 25 30

Gly Thr Thr Phe Arg Lys Ser Asp Val Phe Arg Asp Phe Leu Leu Ala
35 40 45

Lys Val Ile Asn
50

<210> 2944
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D131del"

<400> 2944
Ile Arg Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr Cys
1 5 10 15

Val Lys Phe Arg Lys Gly Ser Pro Asp Val Glu Phe Lys Ser Gly Ala
20 25 30

Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser Ala Pro Val Val Ser
35 40 45

Gly Pro Ala Ala Arg
50

<210> 2945
<211> 52
<212> PRT
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<220>
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<223> /note="p.V233I"

<400> 2945
Ser Ile His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His
1 5 10 15

Ser Gln Val Ile Cys Glu Val Ala His Ile Ile Thr Leu Gln Gly Asp
20 25 30

Pro Leu Arg Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro
35 40 45

Thr Leu Glu Val
50

<210> 2946
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E191K"

<400> 2946
Thr Gln Val Ser Asn Trp Phe Lys Asn Arg Arg Gln Arg Asp Arg Ala
1 5 10 15

Ala Glu Ala Lys Glu Arg Glu Asn Thr Lys Lys Asn Asn Asn Ser Ser
20 25 30

Ser Asn Lys Gln Asn Gln Leu Ser Pro Leu Glu Gly Gly Lys Pro Leu
35 40 45

Met Ser Ser Ser
50

<210> 2947
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I27L"

<400> 2947
Val Phe Arg Ser Pro Leu Asp Leu Tyr Ser Ser His Phe Leu Leu Pro
1 5 10 15

Asn Phe Ala Asp Ser His His Arg Ser Leu Leu Leu Leu Ala Ser Ser
20 25 30

Gly Gly Gly Asn Gly Ala Gly Gly Gly Gly Gly Ala Gly Gly Gly Ser
35 40 45

Gly Gly Gly Asn
50

<210> 2948
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.A62G"

<400> 2948
Ala Phe Ser Ala Arg Trp Ala Gln Glu Ala Tyr Lys Lys Glu Ser Ala
1 5 10 15

Lys Glu Ala Gly Ala Ala Ala Val Pro Gly Gly Pro Val Pro Ala Ala
20 25 30

Thr Glu Pro Pro Pro Val Leu His Leu Pro Ala Ile Gln Pro Pro Pro
35 40 45

Pro Val Leu Pro
50

<210> 2949
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<400> 2949
Glu Glu Met Val Gln Gln Leu Gln Ile Val Arg Asp Thr Leu Cys Asn
1 5 10 15

Glu Leu Asp Gln Glu Arg Lys Ala Arg Cys Cys Ala Ile Gln Gln Lys
20 25 30

Leu Lys Glu Ala His Asp Ala Leu His His Phe Ser Cys Lys Met Leu
35 40 45

Thr Pro Arg His
50

<210> 2950
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.S277fs"

<400> 2950
Leu Ile Met Val Val Ile Leu Gln Leu Arg Arg Arg Gly Lys Thr Asn
1 5 10 15

His Tyr Gln Thr Thr Val Glu Lys Lys Ala Leu Arg Ser Met Pro Lys
20 25 30

Ser Arg Asn Gln Val Leu Phe Arg Arg Asn Leu Thr Pro Ser Gln Leu
35 40 45

Arg Thr Leu Ala Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln
50 55 60

Ser Leu Ser Arg Lys Gln Ile Pro Ser Gln Ser Met Leu Val

65 70 75

<210> 2951
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F281L"

<400> 2951
Tyr Lys Tyr Ser Arg Val Ala Asp Tyr Ile Val Lys Val Ser Leu Trp
1 5 10 15

Ser Leu Leu Val Thr Leu Val Val Leu Leu Leu Ile Met Thr Gly Thr
20 25 30

Met Leu Gly Pro Glu Leu Leu Ala Ser Ile Pro Ala Ala Val Tyr Val
35 40 45

Ile Ala Ile Phe
50

<210> 2952
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G109fs"

<400> 2952
Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln Ala Ile Ala
1 5 10 15

Val Leu Ile Met Gly Cys Cys Pro Gly Ala Pro Ser Leu Thr Phe Ser
20 25 30

Pro Ser Gly Leu Met Glu Ile Trp Ile Ser Ala Ser Val
35 40 45

<210> 2953
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S261L"

<400> 2953
Leu Ile Leu Phe Ile Ile Phe Ser Ile Gln Leu Ser Phe Met Leu Leu
1 5 10 15

Thr Phe Ile Phe Ser Thr Arg Asn Asn Leu Leu Gly Phe Thr Pro Ala
20 25 30

Asp Thr Val Ala Ile Ile Phe Cys Ser Thr His Lys Ser Leu Thr Leu
35 40 45

Gly Ile Pro Met
50

<210> 2954
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S292L"

<400> 2954
Ala Asn Ala Val Ala Val Ala Met Tyr Val Val Gly Phe Ala Glu Thr
1 5 10 15

Val Val Asp Leu Leu Lys Glu Ser Asp Leu Leu Met Met Val Asp Pro
20 25 30

Thr Asn Asp Ile Arg Ile Ile Gly Ser Ile Thr Val Val Ile Leu Leu
35 40 45

Gly Ile Ser Val
    50

<210> 2955
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.R828Q"

<400> 2955
Ala Leu Leu His Leu Val His Asp Phe Thr Lys Asn Val Gly Leu Met
1   5   10   15

Ile Cys Gly His Val His Met Gly Pro Gln Gln Arg Gln Ala Met Lys
            20   25   30

Glu Met Ser Ile Asp Gln Ala Lys Tyr Gln Arg Trp Leu Ile Lys Asn
        35   40   45

Lys Met Lys Ala
    50

<210> 2956
<211> 35
<212> PRT
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<220>
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<223> /note="p.H686fs"

<400> 2956
Trp Gly Asp Gly Ile Arg Gly Leu Ser Leu Asn Ala Ala Arg Tyr Ala
1   5   10   15

Leu Leu Arg Val Glu His Gly Pro Pro Thr Pro Arg Thr Gly Gly Pro
            20   25   30

Arg Cys Trp
35

<210> 2957
<211> 54
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L493fs"

<400> 2957
Ile Val Leu Leu Leu Gly Gly Gly Tyr Ala Leu Ala Lys Gly Ser Glu
1 5 10 15

Arg Ser Gly Leu Ser Glu Trp Leu Gly Lys Gln Ala Asp Pro Thr Ala
20 25 30

Glu Cys Ala Ser Ser Ser His Cys His His Pro Leu Pro Pro Gly Gly
35 40 45

His Leu His Arg Val His
50

<210> 2958
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q273P"

<400> 2958
Val Asn Phe Ala Ser Trp Phe Ala Phe Ala Phe Pro Asn Met Leu Val
1 5 10 15

Met Leu Leu Phe Ala Trp Leu Trp Leu Pro Pro Phe Val Tyr Met Arg
20 25 30

Phe Asn Phe Lys Lys Ser Trp Gly Cys Gly Leu Glu Ser Lys Lys Asn

35 40 45

Glu Lys Ala Ala
50

<210> 2959
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R495Q"

<400> 2959
Tyr Asp Phe Ser Phe Tyr Ile Cys Gly Leu Leu Tyr Met Ile Gly Ile
1 5 10 15

Leu Phe Leu Leu Ile Gln Pro Cys Ile Gln Gln Ile Ile Glu Gln Ser
20 25 30

Arg Arg Lys Tyr Met Asp Gly Ala His Val
35 40

<210> 2960
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G98fs"

<400> 2960
Leu Thr Phe Ser Ala Pro Leu Ala Thr Val Leu Ser Asn Arg Phe Gly
1 5 10 15

His Arg Leu Val Val Met Leu Gly Gly Ala Thr Cys Gln His Arg Asp
20 25 30

Gly Gly Arg Leu Leu Leu Thr Arg Gly Phe Ser Tyr Val Arg Arg His
35 40 45

Arg His His Leu Trp Ser Gly Ile Leu Leu
50 55

<210> 2961
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.CVLLGG470del"

<400> 2961
Leu Gly Pro Pro Ile Val Gly Trp Phe Tyr Asp Trp Thr Gln Thr Tyr
1 5 10 15

Asp Ile Ala Phe Tyr Phe Ser Gly Phe Phe Ile Leu Leu Leu Ala Ala
20 25 30

Leu Pro Ser Trp Asp Thr Cys Asn Lys Gln Leu Pro Lys Pro Ala Pro
35 40 45

Thr Thr Phe Leu Tyr Lys Val Ala Ser Asn Val
50 55

<210> 2962
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V324I"

<400> 2962
His Leu Ile Asn Gln Gly Tyr Arg Ala Ile Thr Val Arg Lys Leu Met
1 5 10 15

Gln Gly Met Gly Leu Gly Leu Ser Ser Ile Ile Phe Ala Leu Cys Leu
20 25 30

Gly His Thr Ser Ser Phe Cys Glu Ser Val Val Phe Ala Ser Ala Ser
35 40 45

Ile Gly Leu Gln
50

<210> 2963
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F348fs"

<400> 2963
Leu Ile Ile His Gly Gly Ile Phe Leu Pro Leu Ile Tyr Phe Val Val
1 5 10 15

Thr Arg Lys Asn Pro Phe Ser Phe Phe Cys Trp His Phe Pro Ser Leu
20 25 30

Asp His Cys Pro Gly His Arg Phe Gln Cys Trp Asn Phe Ala Cys His
35 40 45

Leu Ser Leu Pro Gly Arg Lys Ser Gly Asp
50 55

<210> 2964
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P328fs"

<400> 2964
Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys Leu Gly
1 5 10 15

Asp Leu Glu Glu Ala Pro Glu Arg Glu Ala Ser Gln Arg Gly Leu Glu
20 25 30

Arg Gly Asn Gln His Arg
35

<210> 2965
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S201L"

<400> 2965
Asn Gly Gly Met Ser Leu Val Ala Phe Val Leu Leu Asn Glu Cys Val
1 5 10 15

Gly Thr Ala Tyr Trp Ala Leu Ala Gly Leu Leu Ile Gly Gly Leu Phe
20 25 30

Phe Ala Val Gly Ile Ala Gln Tyr Ala Leu Leu Gly Tyr Phe Ile Arg
35 40 45

Ser Trp Arg Thr
50

<210> 2966
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R407Q"

<400> 2966
Leu Gln Thr Leu Phe Gly Ala Val Ile Leu Leu Ala Asn Cys Val Ala
1 5 10 15

Pro Trp Ala Leu Lys Tyr Met Asn Arg Gln Gln Ala Ser Gln Met Leu

20 25 30

Leu Met Phe Leu Leu Ala Ile Cys Leu Leu Ala Ile Ile Phe Val Pro
35 40 45

Gln Glu Met Gln
50

<210> 2967
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A134V"

<400> 2967
Ser Glu Asn Ser Thr Asp His Ala Gln Gly Asp Tyr Pro Lys Asp Ile
1 5 10 15

Phe Ser Leu Glu Glu Arg Arg Lys Gly Val Val Ile Ile Leu His Val
20 25 30

Ile Gly Met Ile Tyr Met Phe Ile Ala Leu Ala Ile Val Cys Asp Glu
35 40 45

Phe Phe Val Pro
50

<210> 2968
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R35S"

<400> 2968
Ala Arg Arg Ala Leu Leu Leu Gly Ile Leu Trp Ala Thr Ala His Leu
1 5 10 15

Pro Leu Ser Gly Thr Ser Leu Pro Gln Ser Ser Leu Pro Arg Ala Thr
20 25 30

Gly Asn Ser Thr Gln Cys Val Ile Ser Pro Ser Ser Glu Phe Pro Glu
35 40 45

Gly Phe Phe Thr
50

<210> 2969
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F28fs"

<400> 2969
Leu Ser Tyr Glu Ser Leu Val His Ala Val Ala Gly Ala Val Gly Ser
1 5 10 15

Val Thr Ala Met Thr Val Phe Phe Pro Trp Ile Gln Leu Asp Phe Asp
20 25 30

Phe Arg Leu Met Arg Lys Glu Asn Pro Lys Leu His Thr Trp Cys Ser
35 40 45

Trp Arg Ser Leu Lys Lys Lys Asp Ser Trp His His Ile Glu Gly Gly
50 55 60

Phe Gln
65

<210> 2970
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q83E"

<400> 2970
Leu Arg Pro Lys Tyr Asn Gly Ile Leu His Cys Leu Thr Thr Ile Trp
1 5 10 15

Lys Leu Asp Gly Leu Arg Gly Leu Tyr Glu Glu Gly Val Thr Pro Asn
20 25 30

Ile Trp Gly Ala Gly Leu Ser Trp Gly Leu Tyr Phe Phe Phe Tyr Asn
35 40 45

Ala Ile Lys Ser
50

<210> 2971
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R96Q"

<400> 2971
Glu Gly Gly Asn Lys Leu Trp Tyr Lys Lys Pro Gly Asn Phe Gln Gly
1 5 10 15

Thr Leu Asp Ala Phe Phe Lys Ile Ile Gln Gln Asn Glu Gly Ile Lys
20 25 30

Ser Leu Trp Ser Gly Leu Pro Pro Thr Leu Val Met Ala Val Pro Ala
35 40 45

Thr Val Ile Tyr
50

<210> 2972
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.G106C"

<400> 2972
Leu Leu Val Leu Thr Ala Thr Ser His Gln Glu Arg Arg Ala Gln Pro
1 5 10 15

Pro Ser Tyr Met His Ile Phe Leu Ala Cys Cys Cys Thr Gly Gly Phe
20 25 30

Leu Gln Ala Tyr Cys Leu Ala Pro Phe Asp Leu Ile Lys Val Arg Leu
35 40 45

Gln Asn Gln Thr
50

<210> 2973
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.A67T"

<400> 2973
Thr Leu Ser Cys Ile Arg Val Val Tyr Arg Arg Glu Ser Met Phe Gly
1 5 10 15

Phe Phe Lys Gly Met Ser Phe Pro Leu Thr Thr Ser Ile Ala Val Tyr
20 25 30

Asn Ser Val Val Phe Gly Val Phe Ser Asn Thr Gln Arg Phe Leu Ser
35 40 45

Gln His Arg Cys
50

<210> 2974
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R101S"

<400> 2974
Val Phe Gly Val Phe Ser Asn Thr Gln Arg Phe Leu Ser Gln His Arg
1 5 10 15

Cys Gly Glu Pro Glu Ala Ser Pro Pro Ser Ser Thr Leu Ser Asp Leu
20 25 30

Leu Leu Ala Ser Met Val Ala Gly Val Val Ser Val Gly Leu Gly Gly
35 40 45

Pro Val Asp Leu
50

<210> 2975
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I79F"

<400> 2975
Ile Ile Asp Cys Val Val Arg Ile Pro Lys Glu Gln Gly Val Leu Ser
1 5 10 15

Phe Trp Arg Gly Asn Leu Ala Asn Val Phe Phe Arg Tyr Phe Pro Thr
20 25 30

Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys Gln Ile Phe Leu
35 40 45

Gly Gly Val Asp
50

<210> 2976
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A118T"

<400> 2976
Asp Lys Tyr Lys Gln Ile Phe Leu Gly Gly Val Asp Lys Arg Thr Gln
1 5 10 15

Phe Trp Leu Tyr Phe Ala Gly Asn Leu Thr Thr Ser Gly Gly Ala Ala
20 25 30

Gly Ala Thr Ser Leu Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr
35 40 45

Arg Leu Ala Ala
50

<210> 2977
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V88I"

<400> 2977
Trp Leu Pro Ala Tyr Arg Leu Lys Glu Trp Leu Leu Ser Asp Ile Val
1 5 10 15

Ser Gly Ile Ser Thr Gly Ile Val Ala Ile Ile Leu Gln Gly Leu Ala
20 25 30

Phe Ala Leu Leu Val Asp Ile Pro Pro Val Tyr Gly Leu Tyr Ala Ser
35 40 45

Phe Phe Pro Ala
50

<210> 2978
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I629fs"

<400> 2978
Leu Ala His Cys Thr Ala Ser Leu Ile Lys Ala Met Thr Tyr Tyr Gly
1 5 10 15

Asn Leu Asp Ser Glu Lys Pro Ile Phe Leu Asn Arg Tyr Leu Leu Gln
20 25 30

<210> 2979
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P643fs"

<400> 2979
Val Asn Val Tyr Gly Val Thr Val Pro Gly His Glu Gly Arg Ala Gly
1 5 10 15

Met Ala Ala Leu Val Leu Arg Pro Pro Thr Leu Trp Thr Leu Cys Ser
20 25 30

Ser Thr Pro Thr Cys Leu Arg Thr Cys His Leu Met Pro Gly Pro Asp
35 40 45

Ser Ser Gly Ser Arg Ser Leu Trp Pro Pro Gln Arg Pro Ser Asn Ser
50 55 60

Arg Lys Phe Gly Trp Gln Met Arg Ala Ser Thr Pro Ala Pro Cys Leu
65 70 75 80

Thr His Cys Thr Phe Trp Thr Arg Leu
85

<210> 2980
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A230D"

<400> 2980
Leu Ile Met Ile Leu Leu Leu Ser Phe Met Pro Asn Ser Pro Arg Phe
1 5 10 15

Leu Leu Ser Arg Gly Arg Asp Glu Glu Asp Asp Leu Arg Ala Leu Ala
20 25 30

Trp Leu Arg Gly Thr Asp Val Asp Val His Trp Glu Phe Glu Gln Ile
35 40 45

Gln Asp Asn Val
50

<210> 2981
<211> 52
<212> PRT
<213> Artificial Sequence

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<400> 2981
Tyr Asn Leu Ser Val Val Asn Thr Pro His Lys Val Phe Lys Ser Phe
1 5 10 15

Tyr Asn Glu Thr Tyr Phe Glu Arg His Thr Thr Thr Phe Met Asp Gly
20 25 30

Lys Leu Met Leu Leu Leu Trp Ser Cys Thr Val Ser Met Phe Pro Leu

35 40 45

Gly Gly Leu Leu
50

<210> 2982
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.H268Q"

<400> 2982
Leu Arg Gly His Thr Asp Met Glu Ala Glu Leu Glu Asp Met Arg Ala
1 5 10 15

Glu Ala Arg Ala Glu Arg Ala Glu Gly Gln Gln Leu Ser Val Leu His
20 25 30

Leu Cys Ala Leu Arg Ser Leu Arg Trp Gln Leu Leu Ser Ile Ile Val
35 40 45

Leu Met Ala Gly
50

<210> 2983
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R194H"

<400> 2983
Leu Arg Ser Asp Val Glu Ala Lys Ser Leu Glu Val Trp Gly Ser Pro
1 5 10 15

Glu Ala Leu Ala Arg Glu Lys Lys Leu His His Lys Glu Ala Glu Ile
20 25 30

Glu Tyr Arg Glu Arg Leu Phe Arg Asn Gln Lys Ile Leu Arg Glu Tyr
35 40 45

Arg Asp Phe Leu
50

<210> 2984
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V494I"

<400> 2984
Cys Phe Leu Leu Pro Ser Leu Phe His Leu Arg Leu Leu Trp Arg Lys
1 5 10 15

Leu Leu Trp His Gln Val Phe Phe Asp Ile Ile Ala Ile Phe Val Ile
20 25 30

Gly Gly Ile Cys Ser Val Ser Gly Phe Val His Ser Leu Glu Gly Leu
35 40 45

Ile Glu Ala Tyr
50

<210> 2985
<211> 34
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S542L"

<400> 2985
Cys Val Phe Ile Gly Phe Gly Trp Trp Phe Phe Leu Gly Pro Lys Phe
1 5 10 15

Lys Lys Leu Gln Asp Glu Gly Ser Ser Leu Leu Trp Lys Cys Lys Arg
20 25 30

Asn Asn

<210> 2986
<211> 43
<212> PRT
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<220>
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<220>
<221> source
<223> /note="p.*417S"

<400> 2986
Val Trp Arg Leu Val Arg Gly Thr Arg Tyr Met Lys Lys Asp Tyr Leu
1 5 10 15

Ile Glu Asn Glu Glu Leu Pro Ser Pro Ser Ser Glu Gly Gly Ala Cys
20 25 30

Thr Tyr Leu Cys Ala Tyr Thr Tyr Phe Ile Cys
35 40

<210> 2987
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A280T"

<400> 2987
Cys Asn Lys Ala Phe Val Phe Leu Leu Ser Trp Ile Val Leu Arg Asp
1 5 10 15

Arg Phe Met Gly Val Arg Ile Val Ala Thr Thr Ile Leu Ala Ile Ala
20 25 30

Gly Ile Val Met Met Thr Tyr Ala Asp Gly Phe His Ser His Ser Val
35 40 45

Ile Gly Ile Ala
50

<210> 2988
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K62fs"

<400> 2988
Ile Asn Glu Gly Tyr Gly Asn Phe Met Glu Glu Asn Pro Lys Lys Gly
1 5 10 15

Leu Leu Ser Glu Met Lys Lys Lys Gly Glu Leu Ser Leu Glu Pro Trp
20 25 30

Ile Pro Tyr Leu His Gln Gln Lys Thr Gln
35 40

<210> 2989
<211> 32
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V528I"

<400> 2989
Ala Cys Ala Leu Leu Phe Leu Ile Arg Leu Ile His Lys Glu Leu Ser
1 5 10 15

Cys Pro Gly Ser Ala Thr Gly Asp Gln Ile Ile Pro Phe Lys Glu Gln
20 25 30

<210> 2990

<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G100R"

<400> 2990
Met Ser Val Phe Asn Leu Ser Asn Ala Ile Met Gly Ser Gly Ile Leu
1 5 10 15

Gly Leu Ala Phe Ala Leu Ala Asn Thr Arg Arg Ile Leu Leu Phe Leu
20 25 30

Val Leu Leu Thr Ser Val Thr Leu Leu Ser Ile Tyr Ser Ile Asn Leu
35 40 45

Leu Leu Ile Cys
50

<210> 2991
<211> 54
<212> PRT
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<220>
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<223> /note="p.1071_1072II>I"

<400> 2991
Ser Asp Leu Arg Arg Arg Arg Arg Asp Leu Gly Pro His Ala Glu Gly
1 5 10 15

Gln Leu Ala Pro Arg Asp Gly Val Ile Ile Gly Leu Asn Pro Leu Pro
20 25 30

Asp Val Gln Val Asn Asp Leu Arg Gly Ala Leu Asp Ala Gln Leu Arg
35 40 45

Gln Ala Ala Gly Gly Ala
50

<210> 2992
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C628S"

<400> 2992
Ile Leu Met Asn Phe Ile Ser Ser Leu Thr Ala Phe Met Gly Leu Tyr
1 5 10 15

Ile Gly Leu Ser Val Ser Ala Asp Pro Ser Ser Val Gln Asp Trp Ile
20 25 30

Phe Thr Val Thr Ala Gly Met Phe Leu Tyr Leu Ser Leu Val Glu Met
35 40 45

Leu Pro Glu Met
50

<210> 2993
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R53L"

<400> 2993
Ala Phe Pro Gln Thr Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly
1 5 10 15

Ile Asn Val Asp Leu Ala Ile Ser Thr Leu Leu Gln Tyr His Leu Gln
20 25 30

Gln Leu Phe Tyr Arg Tyr Gly Glu Asn Asn Ser Leu Ser Val Glu Gly
35 40 45

Phe Arg Lys Leu
    50

<210> 2994
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.R382C"

<400> 2994
Leu His Glu Val Pro His Glu Val Gly Asp Phe Ala Ile Leu Val Gln
1   5   10   15

Ser Gly Cys Ser Lys Lys Gln Ala Met Cys Cys Leu Gln Leu Leu Thr
            20   25   30

Ala Val Gly Ala Leu Ala Gly Thr Ala Cys Ala Leu Leu Thr Glu Gly
        35   40   45

Gly Ala Val Gly
    50

<210> 2995
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.L456fs"

<400> 2995
Ser Val Leu Pro Glu Leu Leu Arg Glu Ala Ser Pro Leu Gln Ser Leu
1   5   10   15

Leu Glu Val Leu Gly Leu Leu Gly Gly Ser Tyr His Asp Gly Ala Asp
            20   25   30

Cys Pro Pro
35

<210> 2996
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P133L"

<400> 2996
Leu Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu
1 5 10 15

Ala Ser Arg Asp Val Glu Ala Leu Ser Leu Leu Leu Ile Phe Leu Ala
20 25 30

Leu Ser Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu
35 40 45

Thr Leu Pro Asn
50

<210> 2997
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R216H"

<400> 2997
Leu Leu Tyr Glu Lys Gly Ile Ser Leu Arg Ala Ser Phe Ile Phe Ile
1 5 10 15

Ser Val Cys Ser Thr Trp His Val Ala His His Thr Phe Leu Leu Met
20 25 30

Pro Arg Gly His Ile Pro Tyr Pro Leu Pro Pro Asn Tyr Ser Tyr Gly

35 40 45

Leu Cys Pro Gly
50

<210> 2998
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V70F"

<400> 2998
Lys Pro Ala Asp Thr Pro Ser Glu Glu Glu Asp Phe Gly Asp Pro Arg
1 5 10 15

Thr Tyr Asp Pro Asp Phe Lys Gly Pro Phe Phe Ala Asn Arg Ser Cys
20 25 30

Thr Asp Val Leu Cys Cys Met Ile Phe Leu Leu Cys Ile Ile Gly Tyr
35 40 45

Ile Val Leu Gly
50

<210> 2999
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R185H"

<400> 2999
Cys Pro Glu Lys Phe Leu Thr Tyr Val Glu Met Gln Leu Leu Tyr Thr
1 5 10 15

Lys Asp Lys Ser Tyr Trp Glu Asp Tyr His His Gln Phe Cys Lys Thr
20 25 30

Thr Ala Lys Pro Val Lys Ser Leu Thr Gln Leu Leu Leu Asp Asp Asp
35 40 45

Cys Pro Thr Ala
50

<210> 3000
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L1061fs"

<400> 3000
Ser Gln Lys Ala Arg Arg Leu Leu Lys Gly Ser Gly Phe His Leu Asp
1 5 10 15

Leu Leu Leu Ile Gly Ser Leu Gly Gly Ser Val Gly Cys Leu Gly Cys
20 25 30

Pro Gly Ser Arg Leu Pro Arg Ser Ala Pro Ser Pro Met Ser Met Arg
35 40 45

<210> 3001
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I533V"

<400> 3001
Trp Phe Pro Ser Asp Phe Tyr Asp Gly Phe His Ile Gln Ser Ile Ser
1 5 10 15

Ala Ile Leu Phe Ile Tyr Leu Gly Cys Val Val Thr Asn Ala Ile Thr
20 25 30

Phe Gly Gly Leu Leu Gly Asp Ala Thr Asp Asn Tyr Gln Gly Val Met
35 40 45

Glu Ser Phe Leu
50

<210> 3002
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N229K"

<400> 3002
Leu Asn Asp Ser Met Arg Val Lys Val Arg Glu Ala Leu Leu Lys Lys
1 5 10 15

His His His Gln Asn Glu Lys Lys Arg Lys Lys Asn Leu Ile Pro Ile
20 25 30

Val Arg Ser Phe Ala Glu Val Gly Lys Lys Gln Ser Asp Pro His Leu
35 40 45

Met Asp Lys His
50

<210> 3003
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G370del"

<400> 3003
Leu Ser Leu Leu Gly Met Leu Phe Gly Ala Tyr Leu Met Ala Leu Ala
1 5 10 15

Ile Leu Ser Pro Cys Pro Pro Leu Val Thr Thr Ala Gly Val Val Leu
20 25 30

Val Val Leu Ser Trp Val Leu Cys Leu Cys Val Phe Ser Tyr Val Lys
35 40 45

Val Ala Ala Ser Ser
50

<210> 3004
<211> 67
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G399fs"

<400> 3004
Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr Val Lys Val Ala
1 5 10 15

Ala Ser Ser Leu Leu His Gly Gly Gly Pro Ala Gly Ile Ala Gly Ser
20 25 30

Arg Arg Gly His Pro Gly Gly Leu Ser Ala Arg Arg Cys Cys Tyr Val
35 40 45

Pro Pro Asp Gln His Leu Ser Arg Val Pro Gln Gln Lys Gly Leu Cys
50 55 60

Arg Pro Leu
65

<210> 3005
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.G53W"

<400> 3005
Asp Ile Ser Ile Ile Val Ile Tyr Phe Val Val Val Met Ala Val Gly
1 5 10 15

Leu Trp Ala Met Phe Ser Thr Asn Arg Trp Trp Thr Val Gly Gly Phe
20 25 30

Phe Leu Ala Gly Arg Ser Met Val Trp Trp Pro Ile Gly Ala Ser Leu
35 40 45

Phe Ala Ser Asn
50

<210> 3006
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G336C"

<400> 3006
Lys Thr Thr Glu Glu Ala Asp Met Ile Leu Pro Ile Val Leu Gln Tyr
1 5 10 15

Leu Cys Pro Val Tyr Ile Ser Phe Phe Cys Cys Leu Gly Ala Val Ser
20 25 30

Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile Leu Ser Ala Ser Ser
35 40 45

Met Phe Ala Arg
50

<210> 3007
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G442V"

<400> 3007
Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Val Lys Gly Thr Asn Thr
1 5 10 15

Tyr Gly Ala Val Ala Gly Tyr Val Ser Val Val Leu Phe Leu Arg Ile
20 25 30

Thr Gly Gly Glu Pro Tyr Leu Tyr Leu Gln Pro Leu Ile Phe Tyr Pro
35 40 45

Gly Tyr Tyr Pro
50

<210> 3008
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K88N"

<400> 3008
Trp Ser Phe Phe Thr Pro Leu Val Cys Met Gly Ile Phe Ile Phe Asn
1 5 10 15

Val Val Tyr Tyr Lys Pro Leu Val Tyr Asn Asn Asn Thr Asn Val Tyr
20 25 30

Pro Trp Trp Gly Glu Ala Met Gly Trp Ala Phe Val Leu Ser Ser Met
35 40 45

Leu Cys Met Pro
50

<210> 3009
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.W299L"

<400> 3009
Thr Leu Pro Gly Ala Ser Glu Gly Ile Lys Phe Tyr Leu Tyr Pro Asp
1 5 10 15

Leu Ser Arg Leu Ser Asp Pro Gln Val Leu Leu Val Asp Ala Gly Thr
20 25 30

Gln Ile Phe Phe Ser Tyr Ala Ile Cys Leu Gly Cys Leu Thr Ala Leu
35 40 45

Gly Ser Tyr Asn
50

<210> 3010
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A85fs"

<400> 3010
Phe Pro Tyr Leu Thr Tyr Ser Asn Gly Gly Gly Ala Phe Leu Ile Pro
1 5 10 15

Tyr Ala Ile Met Leu Ala Leu Ala Gly Phe Thr Phe Val Leu Ser Gly
20 25 30

Val Phe Thr Gly Thr Ile Cys
35

<210> 3011
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R94K"

<400> 3011
Leu Leu Pro Gln Leu Met Ala Gln His Ser Leu Ala Met Ala Gln Asn
1 5 10 15

Gly Ala Val Pro Ser Glu Ala Thr Lys Lys Lys Asp Gln Asn Leu Lys
20 25 30

Arg Gly Asn Trp Gly Asn Gln Ile Glu Phe Val Leu Thr Ser Val Gly
35 40 45

Tyr Ala Val Gly
50

<210> 3012
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R243W"

<400> 3012
Ala Tyr Cys Asn Asn Pro Trp Asn Thr His Asp Cys Ala Gly Val Leu
1 5 10 15

Asp Ala Ser Asn Leu Thr Asn Gly Ser Trp Trp Pro Ala Ala Leu Pro
20 25 30

Ser Asn Leu Ser His Leu Leu Asn His Ser Leu Gln Arg Thr Ser Pro
35 40 45

Ser Glu Glu Tyr
50

<210> 3013
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P157fs"

<400> 3013
Thr Ser Leu Ala Val Ile Ser Met Thr Phe Ser Asn Tyr Val Leu Gln
1 5 10 15

Pro Val Phe Pro Asn Cys Ile Pro Pro Pro Gln Pro Pro Gly Cys Cys
20 25 30

Pro Trp Pro Ala
35

<210> 3014
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R322W"

<400> 3014
Thr Leu Ala Gly Ala Ala Thr Cys Phe Tyr Ala Phe Val Gly Phe Asp
1 5 10 15

Cys Ile Ala Thr Thr Gly Glu Glu Val Trp Trp Asn Pro Gln Lys Ala
20 25 30

Ile Pro Ile Gly Ile Val Thr Ser Leu Leu Val Cys Phe Met Ala Tyr
35 40 45

Phe Gly Val Ser
50

<210> 3015
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R431H"

<400> 3015
Val Ser Lys Ile Phe Phe Glu Gln Gly Thr Tyr Gln Cys Leu Glu Asn
1 5 10 15

Cys Gly Thr Val Ala Leu Thr Ile Ile His His Arg Gly Gly Asp Leu
20 25 30

Thr Asn Thr Val Phe Val Asp Phe Arg Thr Glu Asp Gly Thr Ala Asn
35 40 45

Ala Gly Ser Asp
50

<210> 3016
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G433C"

<400> 3016
Lys Ile Phe Phe Glu Gln Gly Thr Tyr Gln Cys Leu Glu Asn Cys Gly
1 5 10 15

Thr Val Ala Leu Thr Ile Ile Arg Arg Cys Cys Gly Asp Leu Thr Asn
20 25 30

Thr Val Phe Val Asp Phe Arg Thr Glu Asp Gly Thr Ala Asn Ala Gly
35 40 45

Ser Asp Tyr Glu
50

<210> 3017
<211> 58
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T746fs"

<400> 3017
Ser Pro Gln Ser Tyr Lys Met Glu Trp Lys Asn Glu Val Asp Val Asp
1 5 10 15

Ser Gly Arg Asp Met Pro Ser Thr Pro Gln His Pro Thr Ala Glu Lys
20 25 30

Arg Ala Pro Arg Arg Gln Ala Tyr Tyr Ser Ser Pro Phe Ser Leu Lys
35 40 45

Thr Ser Leu Ala Gln Arg Gly Lys Thr Val
50 55

<210> 3018
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R631H"

<400> 3018
Arg Thr Leu Ser Tyr Asn Lys Tyr Asn Leu Lys Pro Gln Thr Ser Glu
1 5 10 15

Lys Gln Ala Lys Glu Ile Leu Ile Arg His His Gln Asn Thr Leu Arg
20 25 30

Glu Ser Met Arg Lys Gly His Ser Leu Pro Trp Gly Lys Pro Ala Gly
35 40 45

Thr Lys Asn Ile
50

<210> 3019
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L447F"

<400> 3019
Thr Lys Val Pro Ala Lys Asp Tyr Phe Val Ala Thr Thr Ile Val Val
1 5 10 15

Val Phe Phe Thr Val Ile Val Gln Gly Phe Phe Thr Ile Lys Pro Leu
20 25 30

Val Lys Trp Leu Lys Val Lys Arg Ser Glu His His Lys Pro Thr Leu
35 40 45

Asn Gln Glu Leu
50

<210> 3020
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V446fs"

<400> 3020
Phe Ala Gly Phe Ser Phe Lys Glu Lys Ile Phe Ile Ala Leu Ala Trp
1 5 10 15

Met Pro Lys Ala Thr Val Gln Ala Val Arg Ser Ser Gly Ser Arg Asn
20 25 30

Ser Lys Ser Leu Arg Thr Pro Leu Gly Thr Ile Cys Glu Gly Cys Asp
35 40 45

Asp Ser Ser Ile Phe Ser His Leu Asp His Ser Ser Lys Trp Ser Ser

50 55 60

Thr Tyr Gly His Ser Gly Ala
65 70

<210> 3021
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M479I"

<400> 3021
Ile Phe His Pro Val Cys Gly Asp Asn Gly Ile Glu Tyr Leu Ser Pro
1 5 10 15

Cys His Ala Gly Cys Ser Asn Ile Asn Ile Ile Ser Ser Ala Thr Ser
20 25 30

Lys Gln Leu Ile Tyr Leu Asn Cys Ser Cys Val Thr Gly Gly Ser Ala
35 40 45

Ser Ala Lys Thr
50

<210> 3022
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R1460L"

<400> 3022
Ser Gly Thr Lys Gly Ala His Cys Val Cys Asp Pro Gly Phe Ser Gly
1 5 10 15

Glu Leu Cys Glu Gln Glu Ser Glu Cys Leu Leu Gly Asp Pro Val Arg
20 25 30

Asp Phe His Gln Val Gln Arg Gly Tyr Ala Ile Cys Gln Thr Thr Arg
35 40 45

Pro Leu Ser Trp
50

<210> 3023
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K45fs"

<400> 3023
Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn Glu Ile Glu
1 5 10 15

Gly Asp Leu His Val Asp Cys Glu Lys Arg Ala Ser Gln Val Cys Ser
20 25 30

Val Ser Leu Pro Arg Leu Pro Ser Phe Thr Ile Tyr Phe Cys Met Ala
35 40 45

Ile Pro Ser Leu Asp Phe Ser Leu Met Ser Ser Leu Thr Phe Ile Met
50 55 60

Arg Leu Val Cys Thr Trp Lys Thr Met Ala Cys Met Lys Ser Phe Arg
65 70 75 80

Gly Leu Phe Trp Gly Cys Ser Trp
85

<210> 3024
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R52H"

<400> 3024
Lys Ile Cys Ser Cys Asn Glu Ile Glu Gly Asp Leu His Val Asp Cys
1 5 10 15

Glu Lys Lys Gly Phe Thr Ser Leu Gln His His Phe Thr Ala Pro Thr
20 25 30

Ser Gln Phe Tyr His Leu Phe Leu His Gly Asn Ser Leu Thr Arg Leu
35 40 45

Phe Pro Asn Glu
50

<210> 3025
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R214L"

<400> 3025
Pro Thr Asn Leu Phe Lys Ala Val Ser Leu Thr His Leu Asp Leu Arg
1 5 10 15

Gly Asn Arg Leu Lys Val Leu Phe Tyr Leu Leu Gly Met Leu Asp His
20 25 30

Ile Gly Arg Ser Leu Met Glu Leu Gln Leu Glu Glu Asn Pro Trp Asn
35 40 45

Cys Thr Cys Glu
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<210> 3026
<211> 52
<212> PRT
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<400> 3026
Arg Glu Ile Arg Lys Thr Glu Leu Cys Pro Leu Leu Ser Asp Ser Glu
1 5 10 15

Val Glu Ala Ser Leu Gly Ile Pro His Leu Leu Ser Ser Ser Lys Glu
20 25 30

Asn Ala Trp Pro Thr Lys Pro Ser Ser Met Leu Ser Ser Val His Phe
35 40 45

Thr Ala Ser Ser
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<210> 3027
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3027
Asn Arg Ile Ser Met Ile Gln Asp Arg Ala Phe Gly Asp Leu Thr Asn
1 5 10 15

Leu Arg Arg Leu Tyr Leu Asn Gly Asn Met Met Ile Glu Arg Leu Ser
20 25 30

Pro Glu Leu Phe Tyr Gly Leu Gln Ser Leu Gln Tyr Leu Phe Leu Gln
35 40 45

Tyr Asn Leu Ile
50

<210> 3028
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R68L"

<400> 3028
Tyr Tyr Gly Glu Ile Cys Asp Asn Ala Cys Pro Cys Glu Glu Lys Asp
1 5 10 15

Gly Ile Leu Thr Val Ser Cys Glu Asn Leu Leu Gly Ile Ile Ser Leu
20 25 30

Ser Glu Ile Ser Pro Pro Arg Phe Pro Ile Tyr His Leu Leu Leu Ser
35 40 45

Gly Asn Leu Leu
50

<210> 3029
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.N741K"

<400> 3029
His Leu Gln Arg Ser Leu Leu Glu Gln Glu Asn His Ser Pro Leu Thr
1 5 10 15

Gly Ser Asn Met Lys Tyr Lys Thr Thr Lys Lys Gln Ser Thr Glu Phe
20 25 30

Leu Ser Phe Gln Asp Ala Ser Ser Leu Tyr Arg Asn Ile Leu Glu Lys
35 40 45

Glu Arg Glu Leu
50

<210> 3030
<211> 52

<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3030
Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe
1 5 10 15

Cys Leu Gly Leu Leu Ser Asn Val Asn Gln Gln Asn Ala Thr Val Glu
20 25 30

Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly
35 40 45

Gly Glu Val Phe
50

<210> 3031
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3031
Gly Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp
1 5 10 15

Gly Tyr Val Asp Pro Ser Gly Gly Asp His His Phe Cys Leu Gly Gln
20 25 30

Leu Ser Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His
35 40 45

Ile Gly Lys Gly
50

<210> 3032
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3032
Gln Pro Leu Val Ser Ser Pro Ser Leu Gln Ala Ala Val Asp Lys Asn
1 5 10 15

Lys Leu Glu Lys Glu Lys Glu Lys Lys Arg Lys Arg Lys Arg Glu Lys
20 25 30

Arg Ser Gln Lys Ser Arg Gln Asn His Leu Gln Leu Lys Ser Cys Arg
35 40 45

Arg Lys Ile Ser Asn Trp Ser Leu Lys Lys Val Pro Ala Leu Lys Lys
50 55 60

Leu Arg Ser Pro Leu Trp Ile Phe
65 70

<210> 3033
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R381Q"

<400> 3033
Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln Glu Arg Glu
1 5 10 15

Tyr Arg Leu Gln Ala Arg Ile Ala His Gln Gln Ile Gln Glu Leu Glu
20 25 30

Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala Thr Ile
35 40 45

Glu Leu Lys Ala
50

<210> 3034
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3034
Asn His His Cys Lys Leu Thr Gln Val Leu Asn Thr His Tyr Val Ala
1 5 10 15

Pro Arg Arg Leu Leu Leu Thr Gly Thr Leu Leu Leu Gln Asn Lys Leu
20 25 30

Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Thr Ile Phe Lys
35 40 45

Ser Cys Ser Thr
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<210> 3035
<211> 42
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3035
Lys Gln Asn Leu Leu Ser Val Gly Asp Tyr Arg His Arg Arg Thr Glu
1 5 10 15

Gln Glu Glu Asp Glu Glu Leu Leu Thr Ala Pro Lys Gln Pro Met Phe

20 25 30

Ala Leu Asp Leu Lys Thr Leu His Arg Met
35 40

<210> 3036
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E970Q"

<400> 3036
Glu Leu Gly Ser Leu Pro Gln Glu Ala Phe Glu Lys Tyr Gln Thr Leu
1 5 10 15

Ser Leu Lys Gln Leu Phe Arg Lys Leu Gln Gln Gln Cys Asn Thr Glu
20 25 30

Leu Lys Lys Tyr Ser His Val Asn Lys Lys Ala Leu Asp Gln Phe Val
35 40 45

Asn Phe Ser Glu
50

<210> 3037
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3037
Val Arg Pro Phe Cys Met Ala Tyr Ile Ser Ala Asp Gln His Lys Ile
1 5 10 15

Met Gln Gln Phe Gln Glu Leu Ser Ala Lys Lys Phe Ser Arg Ala Ser
20 25 30

Glu Cys Leu Lys Thr Gly Asn Arg Lys Ala Phe Ala Gly Glu Leu Glu
35 40 45

Lys Lys Leu Lys
50

<210> 3038
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P2696H"

<400> 3038
Leu Ile Cys Asn Thr Thr Val Glu Arg Cys Gln Glu Leu Tyr Arg Lys
1 5 10 15

Tyr Glu Met Gln Tyr Ala Pro Gln Pro His His Pro Thr Val Cys Gln
20 25 30

Phe Ile Thr Ala Thr Glu Met Thr Leu Gln Arg Tyr Ala Ala Asp Ile
35 40 45

Asn Ser Arg Leu
50

<210> 3039
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.E846fs"

<400> 3039
Thr Gln Asp Pro Ile Lys Leu Phe Glu Pro Ser Leu Gln Pro Pro Val
1 5 10 15

Met Gln Gln Gln Pro Leu Glu Lys Lys Asn Glu Ala Phe Ser His Gly
20 25 30

Ala Ile

<210> 3040
<211> 31
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D211fs"

<400> 3040
Gln Asn Met Lys His Val Ile Ser Val Asp Lys Ser Lys Pro Asp Lys
1 5 10 15

Ala Leu Ser Leu Ile Lys Asp Asp Phe Leu Thr Ile Leu Arg Thr
20 25 30

<210> 3041
<211> 35
<212> PRT
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<220>
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<220>
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<223> /note="p.T292fs"

<400> 3041
Ile Pro Ala Gly Gly Ser Leu Gly Pro Ala Ala Glu Gly Asp Gly Ala
1 5 10 15

Gly Ser Lys Ala Pro Glu Glu Thr Pro Gln Pro Pro Arg Arg Pro Ser
20 25 30

Thr Ala Asn
35

<210> 3042
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q38E"

<400> 3042
Gly Pro Ala Val Pro Thr Val Gln Arg Gly Ile Ile Lys Met Val Leu
1 5 10 15

Ser Gly Cys Ala Ile Ile Val Arg Gly Glu Glu Pro Arg Gly Gly Pro
20 25 30

Pro Pro Glu Arg Gln Ile Asn Leu Ser Asn Ile Arg Ala Gly Asn Leu
35 40 45

Ala Arg Arg Ala
50

<210> 3043
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.H721fs"

<400> 3043
Val Gln Asp Val Glu Thr Gly Thr Gln Leu Glu Lys Leu Met Glu Asn
1 5 10 15

Met Arg Asn Asp Ile Ala Ser His Pro Leu
20 25

<210> 3044
<211> 26
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.F64fs"

<400> 3044
Gly Arg Ile Asp Ile Lys Gln Leu Ile Ala Lys Lys Ile Lys Leu Thr
1 5 10 15

Ala Glu Ala Glu Glu Leu Lys Pro Phe Leu
20 25

<210> 3045
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R714H"

<400> 3045
Gly Phe Leu Met Gly Ala Ser Cys Gly Gly Gly Asn Met Lys Val Asp
1 5 10 15

Asp Ser Ala Tyr Glu Ser Leu Gly Leu His His Pro Arg His Ala Tyr
20 25 30

Ser Ile Leu Asp Val Arg Asp Val Gln Gly Thr Arg Leu Leu Arg Leu
35 40 45

Arg Asn Pro Trp
50

<210> 3046
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S908L"

<400> 3046
Ala Gln Met Leu Ala Ser Gly Thr Met Asp Ala Gln Met Leu Ala Ser
1 5 10 15

Ser Thr Gln Asp Ser Ala Met Leu Gly Leu Leu Lys Ser Pro Asp Pro
20 25 30

Tyr Arg Leu Ala Gln Asp Pro Tyr Arg Leu Ala Gln Asp Pro Tyr Arg
35 40 45

Leu Gly His Asp
50

<210> 3047
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.VLESSAVT1359del"

<400> 3047
Leu Ala Glu Ser Ile Leu Glu Pro Pro Ala Met Ala Ala Pro Glu Ser
1 5 10 15

Ser Ala Met Ala Val Leu Glu Ser Ser Thr Val Thr Val Leu Glu Ser
20 25 30

Ser Thr Val Thr Val Leu Glu Pro Ser Val Val Thr Val Pro Glu Pro
35 40 45

Pro Val Val Ala Glu Pro Asp Tyr Val Thr Ile Pro Val Pro Val Val
50 55 60

Ser Ala Leu Glu Pro Ser Val Pro Val Leu
65 70

<210> 3048
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F570L"

<400> 3048
Val Leu Thr Asn Glu Lys Met Ser Arg Asp Ile Ser Pro Glu Glu Ile
1 5 10 15

Asp Leu Lys Asn Glu Pro Trp Tyr Lys Leu Leu Phe Ser Glu Leu Glu
20 25 30

Phe Gly Lys Pro Pro Pro Lys Lys Ile Trp Asp Tyr Thr Pro Gly Asp
35 40 45

Cys Ser Ile Leu
50

<210> 3049
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V1156M"

<400> 3049
Ala Glu Arg Gly Ala Gly Glu Arg Gly Pro Gly Gly Pro Lys Ile Ser
1 5 10 15

Lys Lys Ser Cys Leu Lys Pro Ser Asp Met Met Val Arg Cys Leu Ser
20 25 30

Thr Glu Gln Arg Leu Ser Asp Leu Asn Thr Pro Glu Glu Ser Arg Pro
35 40 45

Gly Lys Pro Leu
50

<210> 3050
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P866S"

<400> 3050
Val Phe Glu Ala Leu Asp Ser Ala Leu Lys Asp Ile Cys Asp Gln Ile
1 5 10 15

Lys Ala Glu Lys Lys Arg Gly Ser Leu Ser Ser Asp Asn Ser Ile Leu
20 25 30

His Arg Leu Ile Ser Glu Leu Leu Pro Asp Val Pro Glu Arg Asn Ser
35 40 45

Ser Leu Arg Ala
50

<210> 3051
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E1158fs"

<400> 3051
Asp Arg Ile His Ser Leu Ser Ser Asn Lys Pro Gln Arg Pro Val Phe
1 5 10 15

Thr His Glu Asn Ile Gln Gly Gly Gly Asn Arg Phe Arg Leu Cys Ile
20 25 30

Thr Ile Leu Pro Gly Met Lys Met Ser Trp Ser Ser Glu Lys Val Met
35 40 45

Ser Leu Met Ser Trp Lys Ser Val Met Thr Ala Gly Leu Trp Gly Pro

50 55 60

Gln Glu Glu Pro Asn Ser Leu Val Leu Ser Pro Glu Thr Thr Ser Arg
65 70 75 80

Gly Cys Glu Leu Arg Ser Leu Leu Leu
85

<210> 3052
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R320W"

<400> 3052
Phe Trp Ser Val Ser Gly Val Asp Ala Asp Pro Asp Leu Val His Val
1 5 10 15

Glu Ala Gln Asp Leu Gly Gly Asp Phe Trp Trp Tyr Val Thr Cys Ala
20 25 30

Ile His Asn Cys Ser Glu Lys Met Leu Thr Ala Pro Phe Ala Gly Pro
35 40 45

Ile Asp His Gly
50

<210> 3053
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R205L"

<400> 3053
Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp Phe Cys Asn
1 5 10 15

Thr Leu Gln Gly Phe Ser Ile Pro Phe Leu Leu Ala Ala Asp Leu Leu
20 25 30

Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg Ser His
35 40 45

Pro Asn Lys Gln
50

<210> 3054
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N233Y"

<400> 3054
Phe Met Ala Glu Ile Arg Gln Tyr Ile Arg Glu Leu Asn Leu Ile Ile
1 5 10 15

Lys Val Phe Arg Glu Pro Phe Val Ser Tyr Tyr Ser Lys Leu Phe Ser
20 25 30

Ala Asn Asp Val Glu Asn Ile Phe Ser Arg Ile Val Asp Ile His Glu
35 40 45

Leu Ser Val Lys
50

<210> 3055
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R124P"

<400> 3055
Ala Ala Gln Pro Ser Lys Pro Thr Ser Thr Val Leu Pro Arg Ser Ala
1 5 10 15

Ser Ala Pro Gly Ala Pro Pro Leu Val Pro Pro Val Pro Arg Pro Val
20 25 30

Glu Pro Pro Gly Asp Leu Gly Leu Pro Thr Glu Pro Gln Asp Thr Pro
35 40 45

Gly Gly Pro Ala
50

<210> 3056
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S403I"

<400> 3056
Pro Tyr Gln Gly His Asp Ser Gly Val Asn Leu Pro Asp Ser His Gly
1 5 10 15

Ala Ile Ser Ser Val Val Ser Asp Ala Ile Ile Ser Ala Val Tyr Tyr
20 25 30

Cys Asn Tyr Pro Asp Val
35

<210> 3057
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R719W"

<400> 3057

His Leu Glu Lys Tyr Pro Asn Tyr Lys Tyr Lys Pro Arg Pro Lys Arg
1 5 10 15

Thr Cys Ile Val Asp Gly Lys Lys Leu Trp Trp Ile Gly Glu Tyr Lys
20 25 30

Gln Leu Met Arg Ser Arg Arg Gln Glu Met Arg Gln Phe Phe Thr Val
35 40 45

Gly Gln Gln Pro
50

<210> 3058
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L309fs"

<400> 3058
Arg Arg Ile Pro His Leu Pro Gly His Pro Tyr Ser Pro Glu Tyr Ala
1 5 10 15

Pro Ser Pro Leu His Cys Ser His Pro Trp Ala Pro Trp Pro Leu Ala
20 25 30

Ser Pro Pro Ala Ser Pro
35

<210> 3059
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E75K"

<400> 3059
Glu Asn Thr Phe Pro Lys Gly Glu Pro Asp Leu Lys Lys Glu Ser Glu

1 5 10 15

Glu Asp Lys Phe Pro Val Cys Ile Arg Lys Lys Ala Val Ser Gln Val
20 25 30

Leu Lys Gly Tyr Asp Trp Thr Leu Val Pro Met Pro Val Arg Val Asn
35 40 45

Gly Ser Ser Lys
50

<210> 3060
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E11del"

<400> 3060
Met Ser Asp Gln Lys Lys Glu Glu Glu Glu Ala Ala Ala Ala Ala Ala
1 5 10 15

Met Ala Thr Glu Gly Gly Lys Thr Ser Glu Pro Glu Asn Asn Asn Lys
20 25 30

Lys Pro Lys Thr Ser Gly
35

<210> 3061
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E7K"

<400> 3061
Met Ser Asp Gln Lys Lys Lys Lys Glu Glu Glu Glu Ala Ala Ala Ala
1 5 10 15

Ala Ala Met Ala Thr Glu Gly Gly Lys Thr Ser Glu Pro Glu Asn Asn
20 25 30

Asn

<210> 3062
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V439L"

<400> 3062
Gly Asp Thr Thr Val Lys Leu Trp Asp Leu Cys Lys Gly Asp Cys Ile
1 5 10 15

Leu Thr Phe Glu Gly His Ser Arg Ala Leu Leu Trp Ser Cys Thr Trp
20 25 30

His Ser Cys Gly Asn Phe Val Ala Ser Ser Ser Leu Asp Lys Thr Ser
35 40 45

Lys Ile Trp Asp
50

<210> 3063
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P488S"

<400> 3063
Trp Asp Val Asn Ser Glu Arg Cys Arg Cys Thr Leu Tyr Gly His Thr
1 5 10 15

Asp Ser Val Asn Ser Ile Glu Phe Phe Ser Ser Phe Ser Asn Thr Leu
20 25 30

Leu Thr Ser Ser Ala Asp Lys Thr Leu Ser Ile Trp Asp Ala Arg Thr
35 40 45

Gly Ile Cys Glu
50

<210> 3064
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.Q1264fs"

<400> 3064
Gly Gln Glu Ser Thr Gly Gln Tyr Val Ile Asp Glu Glu Pro Thr Trp
1 5 10 15

Asp Ile Met Val Arg Gln Ser Tyr Pro Arg Gly
20 25

<210> 3065
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R346Q"

<400> 3065
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
1 5 10 15

Val Ile Trp Gly Thr Leu Ser Ile Met Gln Gln Ser Met Lys Ser Cys
20 25 30

Leu Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile
35 40 45

Asn Val Thr Leu
50

<210> 3066
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R72K"

<400> 3066
Gln Val Arg Ala Tyr Ile Arg His Leu Asn Arg Ile Val Thr Ile Ile
1 5 10 15

Gln Lys Trp Trp Arg Ser Phe Leu Gly Lys Lys Lys Gln Tyr Gln Leu
20 25 30

Thr Val Gln Val Ala Tyr Tyr Thr Met Met Met Asn Leu Tyr Asn Ala
35 40 45

Met Ala Val Arg
50

<210> 3067
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S150L"

<400> 3067
Asn Asp Phe Lys Pro Gln Cys Lys Arg Thr Asn Leu Val Ala Asn Asp
1 5 10 15

Gly Lys Asn Ser Cys Pro Val Ser Ser Leu Val Ala Gln Gln Gln Lys

20 25 30

Gln Leu Arg Ile Pro Glu Pro Pro Asn Leu Ser Arg Asn Lys Glu Thr
35 40 45

Glu Leu Leu Arg
50

<210> 3068
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C685fs"

<400> 3068
Lys Val Cys Thr Lys Thr Met Pro Ile Gly Pro Asp Val Ser Leu Glu
1 5 10 15

Asn Leu Ala Ala Glu Thr Cys Phe Phe Leu Glu Leu Ile Leu Glu Thr
20 25 30

Ser Ala Gln Lys Leu Leu Cys Trp Leu Cys Lys Lys Met Asp
35 40 45

<210> 3069
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C189F"

<400> 3069
Ala Val Leu Lys Lys Val Lys Asn Ile Phe Gln Glu Glu Glu Ser Ile
1 5 10 15

Arg Gln Asn Arg Glu Glu Ser Glu Asn Phe Phe Arg Lys Ala Phe Ser
20 25 30

Glu Pro Val Leu Ser Glu Pro Met Phe Ala Glu Gly Glu Ile Lys Ala
35 40 45

Lys Pro Tyr Arg
50

<210> 3070
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A944V"

<400> 3070
Glu Ala Glu Gly Gly Leu Cys Arg Leu Arg Ile Leu Ala Ala Glu Arg
1 5 10 15

Gly Asp Ala Gly Phe Tyr Thr Cys Lys Val Val Val Asn Glu Tyr Gly
20 25 30

Ala Arg Gln Cys Glu Ala Arg Leu Glu Val Arg Ala His Pro Glu Ser
35 40 45

Arg Ser Leu Ala
50

<210> 3071
<211> 27
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<400> 3071
Ala Val Leu Ala Pro Leu Gln Asp Val Asp Val Gly Ala Gly Glu Met
1 5 10 15

Ala Leu Phe Glu Cys Leu Val Ala Gly Ala His
20 25

<210> 3072
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E803fs"

<400> 3072
Arg Leu Glu Arg Tyr Thr Lys Asn Glu Lys Thr Asp Lys Glu Arg Thr
1 5 10 15

Phe Asp Pro Glu Arg Val Glu Arg Glu Thr Leu Asn Thr Glu Gly Lys
20 25 30

Ser Gly Lys Gly Gln Asn
35

<210> 3073
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F121L"

<400> 3073
Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly Phe Thr Pro Glu Ile Gly
1 5 10 15

Lys Lys Lys His Thr Glu Ser Thr Pro Leu Leu Trp Ser Ile Lys Pro
20 25 30

Asn Asn Val Ser Ile Val Leu His Ala Glu Glu Pro Tyr Ile Glu Asn
35 40 45

Glu Glu Pro Glu
50

<210> 3074
<211> 26
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.F232fs"

<400> 3074
Gln Pro Pro Pro Leu Glu Thr Leu Gly Leu Asp Ala Asp Glu Leu Ile
1 5 10 15

Leu Ile Pro Asn Gly Val Gln Ile Phe Leu
20 25

<210> 3075
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M150V"

<400> 3075
Ala Asn Thr Ile Ile Gly Lys Ala Val Glu His Met Phe Glu Gly Glu
1 5 10 15

His Gly Ser Lys Asp Glu Trp Arg Gly Val Val Val Leu Ala Gln Ala
20 25 30

Pro Ile Met Lys Ala Trp Phe Tyr Ile Thr Tyr Glu Lys Asp Pro Val
35 40 45

Leu Tyr Met Tyr
50

<210> 3076

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y171C"

<400> 3076
Pro Val Met Asp Thr Trp Phe Tyr Ile Thr Tyr Glu Lys Asp Pro Val
1 5 10 15

Leu Tyr Met Tyr Thr Leu Leu Asp Asp Cys Cys Lys Asp Gly Asp Leu
20 25 30

Arg Ile Ile Pro Asp Ser Asn Tyr Tyr Phe Pro Thr Ala Glu Gln Glu
35 40 45

Pro Gly Glu Val
50

<210> 3077
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A316V"

<400> 3077
Leu Arg Glu Glu Glu Cys Ile Leu Ala Cys Arg Gly Val Gln Gly Gly
1 5 10 15

Pro Leu Arg Gly Ser Ser Gly Ala Gln Val Val Thr Phe Pro Gln Gly
20 25 30

Pro Ser Met Glu Arg Arg His Pro Val Cys Ser Gly Thr Cys Gln Pro
35 40 45

Thr Gln Phe Arg
50

<210> 3078
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E50K"

<400> 3078
Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile Asn Asn
1 5 10 15

Phe Ser Phe Cys Arg Glu Glu Met Gly Lys Lys Val Ile Lys Ser Ser
20 25 30

Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg Val
35 40 45

Asn Pro Lys Gly
50

<210> 3079
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.F102V"

<400> 3079
Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser
1 5 10 15

Cys Pro Lys Ser Glu Val Arg Ala Lys Val Val Lys Phe Ser Ile Leu
20 25 30

Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr
35 40 45

Arg Phe Val Gln
    50

<210> 3080
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="p.F102C"

<400> 3080
Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser
1   5   10   15

Cys Pro Lys Ser Glu Val Arg Ala Lys Cys Cys Lys Phe Ser Ile Leu
            20   25   30

Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr
        35   40   45

Arg Phe Val Gln
    50

<210> 3081
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.W131G"

<400> 3081
Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg
1   5   10   15

Ala Tyr Arg Phe Val Gln Gly Lys Asp Gly Gly Gly Phe Lys Lys Phe
            20   25   30

Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu Pro Asp
        35   40   45

Asp Lys Leu Thr
    50

<210> 3082
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.F133I"

<400> 3082
Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr
1   5   10   15

Arg Phe Val Gln Gly Lys Asp Trp Gly Ile Ile Lys Lys Phe Ile Arg
            20   25   30

Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys
        35   40   45

Leu Thr Leu Phe
    50

<210> 3083
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.F133V"

<400> 3083
Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr
1   5   10   15

Arg Phe Val Gln Gly Lys Asp Trp Gly Val Val Lys Lys Phe Ile Arg

20 25 30

Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys
35 40 45

Leu Thr Leu Phe
50

<210> 3084
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F133C"

<400> 3084
Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr
1 5 10 15

Arg Phe Val Gln Gly Lys Asp Trp Gly Cys Cys Lys Lys Phe Ile Arg
20 25 30

Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys
35 40 45

Leu Thr Leu Phe
50

<210> 3085
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F133L"

<400> 3085
Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr
1 5 10 15

Arg Phe Val Gln Gly Lys Asp Trp Gly Leu Leu Lys Lys Phe Ile Arg
20 25 30

Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys
35 40 45

Leu Thr Leu Phe
50

<210> 3086
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K1732T"

<400> 3086
Glu Lys Leu Lys Glu Ala Tyr Ala Leu Phe Gln Phe Phe Gln Asp Leu
1 5 10 15

Asp Asp Glu Glu Ser Trp Ile Glu Glu Thr Thr Leu Ile Arg Val Ser
20 25 30

Ser Gln Asp Tyr Gly Arg Asp Leu Gln Gly Val Gln Asn Leu Leu Lys
35 40 45

Lys His Lys Arg
50

<210> 3087
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A2011V"

<400> 3087
Pro Glu Ile Thr Asp Leu Lys Asp Lys Leu Ile Ser Ala Gln His Asn
1 5 10 15

Gln Ser Lys Ala Ile Glu Glu Arg Tyr Val Val Ala Leu Leu Lys Arg
20 25 30

Trp Glu Gln Leu Leu Glu Ala Ser Ala Val His Arg Gln Lys Leu Leu
35 40 45

Glu Lys Gln Leu
50

<210> 3088
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D2243Y"

<400> 3088
Asp Leu Gly Asp Asn Leu Glu Asp Ala Leu Ile Leu Asp Ile Lys Tyr
1 5 10 15

Ser Thr Ile Gly Leu Ala Gln Gln Trp Tyr Tyr Gln Leu Tyr Gln Leu
20 25 30

Gly Leu Arg Met Gln His Asn Leu Glu Gln Gln Ile Gln Ala Lys Asp
35 40 45

Ile Lys Gly Val
50

<210> 3089
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.G2367C"

<400> 3089
Phe Leu Ile Asp Lys Glu Ser Glu Asn Ile Lys Ser Ser Asp Glu Ile
1 5 10 15

Glu Asn Ala Phe Gln Ala Leu Ala Glu Cys Cys Lys Ser Tyr Ile Thr
20 25 30

Lys Glu Asp Met Lys Gln Ala Leu Thr Pro Glu Gln Val Ser Phe Cys
35 40 45

Ala Thr His Met
50

<210> 3090
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R86C"

<400> 3090
Lys Trp Val Asn Ser His Leu Ala Arg Val Ser Cys Arg Ile Thr Asp
1 5 10 15

Leu Tyr Lys Asp Leu Arg Asp Gly Arg Cys Leu Leu Ile Lys Leu Leu
20 25 30

Glu Val Leu Ser Gly Glu Met Leu Pro Lys Pro Thr Lys Gly Lys Met
35 40 45

Arg Ile His Cys
50

<210> 3091
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T1864I"

<400> 3091
Ala Phe Glu Arg Glu Leu His Leu Leu Gly Val Gln Val Gln Gln Phe
1 5 10 15

Gln Asp Val Ala Thr Arg Leu Gln Thr Ile Val Tyr Ala Gly Glu Lys
            20 25 30

Ala Glu Ala Ile Gln Asn Lys Glu Gln Glu Val Ser Ala Ala Trp Gln
        35 40 45

Ala Leu Leu Asp
    50

<210> 3092
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.A1993V"

<400> 3092
Ala Asp Lys Pro Arg Asp Val Ser Ser Val Glu Val Leu Met Asn Tyr
1 5 10 15

His Gln Gly Leu Lys Thr Glu Leu Glu Val Val Arg Val Pro Glu Leu
            20 25 30

Thr Thr Cys Gln Glu Leu Gly Arg Ser Leu Leu Leu Asn Lys Ser Ala
        35 40 45

Met Ala Asp Glu
    50

<210> 3093
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R97K"

<400> 3093
Ile Gly Thr Leu Phe Gly Tyr Leu Arg Asp Phe Leu Arg Asn Trp Gly
1 5 10 15

Ile Glu Lys Cys Asn Ala Ala Val Glu Lys Lys Lys Glu Gln Lys Asp
20 25 30

Phe Val Pro Leu Tyr Gln Asp Phe Glu Asn Phe Tyr Thr Arg Asn Leu
35 40 45

Tyr Met Arg Ile
50

<210> 3094
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P485fs"

<400> 3094
Gly Ser Ser Arg Gly Pro Gly Arg Pro Val Ser Ser Pro His Glu Leu
1 5 10 15

Arg Arg Pro Val Ser Gly Leu Gly Pro Arg Gly Gly Leu Ser Val Ala
20 25 30

Leu Gly Asp Pro
35

<210> 3095
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Q1875fs"

<400> 3095
Arg Ser Gly Pro Pro Ser Pro Pro Ser Thr Ala Thr Ser Phe Gly Gly
1 5 10 15

Pro Arg Pro Arg Arg Gln Pro Pro Pro Thr Thr Ser Phe Pro Phe Leu
20 25 30

Ser Gly Leu Pro Gly Gly Lys Ala Glu Ala Ala Ala Val
35 40 45

<210> 3096
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P1876fs"

<400> 3096
Arg Ser Gly Pro Pro Ser Pro Pro Ser Thr Ala Thr Ser Phe Gly Gly
1 5 10 15

Pro Arg Pro Arg Arg Gln Pro Pro Pro Thr Thr Ser Phe Pro Phe Leu
20 25 30

Ser Gly Leu Pro Gly Gly Lys Ala Glu Ala Ala Ala Val
35 40 45

<210> 3097
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>

<221> source
<223> /note="p.P865fs"

<400> 3097
Leu Ser Gln Ser Pro Lys Lys Val Thr Ala Glu Thr Asp Phe Asn Lys
1 5 10 15

Ser Val Asp Phe Glu Met Pro Pro Pro Ala Pro Arg
20 25

<210> 3098
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H763fs"

<400> 3098
Leu Ser Arg Ala Gln Ser Leu Cys Gly Pro Glu His Ser Ala Val Pro
1 5 10 15

Asp Ser Leu Arg Trp Leu Cys His Pro Trp Ala Arg Ser Phe Ser Trp
20 25 30

Ser Gly Ala Gly Leu
35

<210> 3099
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T61M"

<400> 3099
Glu Gln Gln Thr Glu Met Arg Val Gln Leu Leu Gln Asp Leu Gln Asp
1 5 10 15

Phe Phe Arg Lys Lys Ala Glu Ile Glu Met Met Glu Tyr Ser Arg Asn

20 25 30

Leu Glu Lys Leu Ala Glu Arg Phe Met Ala Lys Thr Arg Ser Thr Lys
35 40 45

Asp His Gln Gln
50

<210> 3100
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G14S"

<400> 3100
Met Ala Ser Ala Asp Ser Arg Arg Val Ala Asp Gly Gly Ser Ser Ala
1 5 10 15

Gly Gly Thr Phe Gln Pro Tyr Leu Asp Thr Leu Arg Gln Glu Leu Gln
20 25 30

Gln Thr Asp Pro Thr Leu Leu Ser
35 40

<210> 3101
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A2257S"

<400> 3101
Ile Pro Ala Ala Ser Ala Ala Ala Met Asn Leu Ala Ser Ala Arg Thr
1 5 10 15

Pro Ala Ile Pro Thr Ala Val Asn Leu Ser Ser Asp Ser Arg Thr Pro
20 25 30

Ala Ala Ala Ala Ala Met Asn Leu Ala Ser Pro Arg Thr Ala Val Ala
35 40 45

Pro Ser Ala Val
50

<210> 3102
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G17fs"

<400> 3102
Met Ser Asn Thr Thr Val Val Pro Ser Thr Ala Gly Pro Gly Pro Ser
1 5 10 15

Gly Gly Ala Arg Trp Arg Arg Trp Trp Trp Arg Arg Arg Arg Arg His
20 25 30

Arg Gly Asn Pro Gly Asp
35

<210> 3103
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S4198fs"

<400> 3103
Pro Arg Gly Gln Gln Ser Arg Phe Arg Ser Ser Thr Ser Gly Ser Trp
1 5 10 15

Ala Pro Glu Cys Arg Glu Glu Gln Ser Arg Ala Ser Pro Ala Leu Ser
20 25 30

Pro Arg Ala His Pro Cys Ala Cys Arg Ala Leu Ala Pro Ala Pro Trp
35 40 45

Gly Thr Ala Gly Cys Arg Gly Ser Ala Ser Gly Ala Pro Ala Pro Arg
50 55 60

Arg Val
65

<210> 3104
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H778Q"

<400> 3104
Lys Thr Leu Lys Ser Leu Met Ala Ala Asn Ser Gln Glu Leu Lys Cys
1 5 10 15

Pro Thr Pro Gly Cys Asp Gly Ser Gly Gln Gln Val Thr Gly Asn Tyr
20 25 30

Ala Ser His Arg Ser Leu Ser Gly Cys Pro Arg Ala Arg Lys Gly Gly
35 40 45

Val Lys Met Thr
50

<210> 3105
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S354N"

<400> 3105

Glu Leu Asn Tyr Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro
1 5 10 15

Val Pro Gln Gln Gln Leu Leu Leu Ala Asn Asn Leu Pro Ala Gly Ser
20 25 30

Leu Arg Cys Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn
35 40 45

Asn Ser His Met
50

<210> 3106
<211> 61
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1120fs"

<400> 3106
Ala Ser Val Asp Val Ala Asp Leu Leu Ala Thr Asn Gly Val Leu His
1 5 10 15

Ile Leu Ser Gln Val Leu Leu Pro Pro Pro Arg Gly Cys Ala Arg Trp
20 25 30

Ala Gly Val Ala Ala Ala Ala Gly Leu Gly Ala Cys Leu Gln Pro Leu
35 40 45

Pro Gly Ile Ala Ala Ala Pro Trp Val Gly Ala Pro Asp
50 55 60

<210> 3107
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.G117W"

<400> 3107
Phe Lys Asp His Phe Phe Lys Lys Pro Lys Phe Cys Asp Val Cys Ala
1 5 10 15

Arg Met Ile Val Leu Asn Asn Lys Phe Trp Trp Leu Arg Cys Lys Asn
20 25 30

Cys Lys Thr Asn Ile His Glu His Cys Gln Ser Tyr Val Glu Met Gln
35 40 45

Arg Cys Phe Gly
50

<210> 3108
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y143H"

<400> 3108
Thr Asp Glu Leu Lys Asn Asp Leu Leu Lys Lys Tyr Asn Val Glu Tyr
1 5 10 15

Gln Glu Tyr Leu Gln Ser Lys Asn Lys His His Lys Ala Glu Ile Leu
20 25 30

Lys Lys Leu Glu His Gln Arg Leu Ile Glu Ala Glu Arg Lys Arg Ile
35 40 45

Ala Gln Met Arg
50

<210> 3109
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G662A"

<400> 3109
Arg Arg Asn Lys Thr Pro Asp Tyr Arg Gly Gln His Val Phe Gly Val
1 5 10 15

Pro Pro Leu Ile His Val Gln Arg Thr Ala Ala Gln Pro Leu Pro Gln
20 25 30

Ser Ile Gln Gln Ala Met Arg Tyr Leu Arg Ser Gln Cys Leu Asp Gln
35 40 45

Val Gly Ile Phe
50

<210> 3110
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P489fs"

<400> 3110
Ala Trp Ala Ser Val Leu Trp Phe Asn Leu Leu Ser Pro Asn Leu Gln
1 5 10 15

Asn Gln Gln Phe Phe Ser Asn Pro Pro Asn Gly Pro Leu Glu Leu Ala
20 25 30

Gly Pro Cys Ser Gln Leu Ala Val Leu Leu Leu Cys Trp Pro Arg Pro
35 40 45

Gln Leu Arg Pro Ala Glu His Ala Glu Lys Gln Ala Val Arg Ala Glu
50 55 60

Leu
65

<210> 3111
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D661V"

<400> 3111
Ser Val Glu Pro Tyr Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala
1 5 10 15

Glu Ile Ile Met Gly Tyr Lys Ile Met Val Val Ala Thr Asn Ile Leu
20 25 30

Val Ser Pro Leu Val Tyr Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala
35 40 45

Phe Gly Lys Tyr
50

<210> 3112
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P367fs"

<400> 3112
Lys Thr Gln Thr Lys Phe Ala Ala Thr Val Arg Leu Leu Val Gly Gly
1 5 10 15

Lys Leu Asn Val His Met Asn Pro Pro Pro Gly Glu Gly His His His
20 25 30

Gln

<210> 3113
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P354fs"

<400> 3113
Gln Val Leu Lys Thr Gln Thr Lys Phe Gln Ala Gly Val Arg Phe Leu
1 5 10 15

Leu Gly Leu Arg Phe Leu Gly Ala Pro Ser Gln Ala Ser Ala Gly Gln
20 25 30

Gly Arg His Gly Asp Arg Glu Ala Gly Ala Gly Ala Glu Cys Ala Ser
35 40 45

Gly Ser Trp Gly Trp Ser Arg Lys His Trp Arg Asn His Gln Gln His
50 55 60

Cys Ala Leu Gly Glu Gln His Ser Trp Glu Leu Leu Leu Cys Pro Val
65 70 75 80

Gln Glu Pro Ala Ser Gln Glu Asp Gln Ala Val
85 90

<210> 3114
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D468H"

<400> 3114
Leu Gly Pro Gly Lys Leu Pro Ile Gln Leu Gln Ala Leu Ser Leu Pro
1 5 10 15

Leu Val Val Ile Val His Gly Asn Gln His His Asn Asn Ala Lys Ala
20 25 30

Thr Ile Leu Trp Asp Asn Ala Phe Ser Glu Met Asp Arg Val Pro Phe

35 40 45

Val Val Ala Glu
50

<210> 3115
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G279fs"

<400> 3115
Glu Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser
1 5 10 15

Tyr Ala Ile Pro Gly Asp Cys Gly Pro Arg Ser Leu Thr Cys
20 25 30

<210> 3116
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A155E"

<400> 3116
Pro Leu His Cys Leu His Gly Leu Arg Gly Ile Tyr Ser Gln Leu Glu
1 5 10 15

Thr Leu Ile Cys Ser Arg Ser Leu Gln Glu Glu Leu Glu Glu Leu Leu
20 25 30

Ser Ala Cys Gly Gly Asp Phe Cys Ser Ala Leu Pro Trp Leu Ala Leu
35 40 45

Leu Ser Ala Asn
50

<210> 3117
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D89N"

<400> 3117
Arg Gly Ala Arg Pro Gly Gly Gly Asp Ala Gly Gly Thr Pro Gly Glu
1 5 10 15

Thr Val Arg His Cys Ser Ala Pro Glu Asn Asn Pro Ile Phe Arg Phe
20 25 30

Ser Ser Leu His Ser Tyr Pro Phe Pro Gly Thr Ile Lys Ser Arg Asp
35 40 45

Met Ser Trp Lys
50

<210> 3118
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R18fs"

<400> 3118
Met Gln Lys Trp Phe Ser Ala Phe Asp Asp Ala Ile Ile Gln Arg Gln
1 5 10 15

Trp Arg Gly Lys Pro Leu Pro Gly Arg Gly Arg Cys Glu Leu His Glu
20 25 30

Gly Gly

<210> 3119
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D86Y"

<400> 3119
Val Val Phe Arg Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro
1 5 10 15

Gly Leu Ile Leu Val Leu Pro Cys Ile Tyr Tyr Val Phe Val Lys Val
20 25 30

Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr
35 40 45

Arg Asp Ser Val
50

<210> 3120
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N451S"

<400> 3120
Lys Val Thr Lys Glu Gly Lys Phe Val Glu Ser Ala Val Ile Thr Gln
1 5 10 15

Ile Tyr Cys Leu Cys Phe Val Asn Gly Ser Ser Leu Glu Cys Phe Leu
20 25 30

Thr Leu Asn Asp Leu Glu Leu Pro Lys Arg Asp Glu Ser Tyr Tyr Glu
35 40 45

Lys Asp Ser Glu
    50

<210> 3121
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.Q68R"

<400> 3121
Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu Asp Tyr Ser
1   5   10   15

Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Arg Arg Gly Gly Glu Glu Leu
            20   25   30

Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro Pro Gly
        35   40   45

Leu Tyr His Ala
    50

<210> 3122
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.R333fs"

<400> 3122
Glu Glu Leu Thr Met Ser Pro Ser Arg Ser Val Ala Asn Ser Gly Leu
1   5   10   15

Ser Asp Ser Leu Thr Thr Ser Thr Pro Gly Pro Pro Thr Val Thr Arg
            20   25   30

Pro Pro Thr Pro Thr Thr Glu Pro Ser Pro Pro Thr Ser Thr Thr Leu

35 40 45

Trp Ser Ser Ala Phe Ser Ala Thr Arg Met Pro Gly Pro Val Pro Ala
50 55 60

Pro Ser
65

<210> 3123
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K218N"

<400> 3123
Leu Asp Val Arg Ser Gln Arg Val Arg Ser Leu Leu Gly Leu Ser Asn
1 5 10 15

Ser Glu Pro Asn Gly Ser Val Glu Thr Asn Asn Asn Leu Glu Gln Ile
20 25 30

Leu Asn Gly Gly Glu Ser Pro Lys Gln Lys Gly Gln Glu Ile Lys Arg
35 40 45

Ser Ser Gly Asp
50

<210> 3124
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D583Y"

<400> 3124
Thr Ser Asn Ala Tyr Ser Ser Pro Ser Val Val Leu Ala Ser Tyr Asn
1 5 10 15

His Asp Gly Thr Arg Asn Ile Leu Asp Tyr Tyr Phe Arg Glu Ala Tyr
20 25 30

Phe Trp Leu Arg Gln Asn Thr Asp Glu His Ala Arg Val Met Ser Trp
35 40 45

Trp Asp Tyr Gly
50

<210> 3125
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R107L"

<400> 3125
Lys Lys Thr Ala Asn Lys Ile Arg Ala Lys Leu Lys Ala Ile Glu Gln
1 5 10 15

Ser Phe Asp Gln Asp Glu Ser Gly Asn Leu Leu Thr Ser Val Asp Leu
20 25 30

Arg Ile Arg Arg Thr Gln His Ser Val Leu Ser Arg Lys Phe Val Glu
35 40 45

Ala Met Ala Glu
50

<210> 3126
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K252fs"

<400> 3126
Met Ile Asn Asn Ile Glu Arg Asn Val Met Asn Ala Thr Asp Tyr Val
1 5 10 15

Glu His Ala Lys Glu Glu Thr Lys Lys Leu Ser Asn Ile Arg Ala Arg
20 25 30

Gln Glu Gly Lys Ser Gly
35

<210> 3127
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D92N"

<400> 3127
Gln Phe Glu Gly Ser Thr Ser Phe Val Arg Arg Ser Gln Trp Met Leu
1 5 10 15

Glu Gln Leu Arg Gln Val Asn Gly Ile Asn Asn Pro Asn Gly Asp Ser
20 25 30

Ala Glu Phe Asp Leu Leu Phe Glu Asn Ala Phe Asp Gln Trp Val Ala
35 40 45

Ser Thr Ala Ser
50

<210> 3128
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R85Q"

<400> 3128

Trp Thr Gln Glu Ile Val Glu Leu Ile Gln Asn Glu Gly Asp Val Glu
1 5 10 15

Lys Ser Lys Arg Ala Pro Thr His Gln Gln Gln Phe Pro Phe Leu Glu
20 25 30

Met Lys Ile Pro Ser Leu Gly Ser Gly Leu Glu Gln Ala His Ala Met
35 40 45

Pro Ser Pro Arg
50

<210> 3129
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R77Q"

<400> 3129
Trp Val Ser Glu Ile Val Tyr Met Ile Tyr Lys Glu Gly Asp Val Glu
1 5 10 15

Lys Cys Lys Glu Asp Val Ile Phe Asn Gln Gln Ile Pro Phe Leu Glu
20 25 30

Cys Arg Lys Glu Asn Leu Met Asn Gly Val Lys Gln Leu Asp Glu Met
35 40 45

Asn Ser Pro Arg
50

<210> 3130
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.G110E"

<400> 3130
Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu Lys
1 5 10 15

Lys Tyr Arg Thr Glu Ala Glu Met Phe Glu Glu Trp Ser Phe Val Phe
20 25 30

Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
35 40 45

Lys Ser Val Leu
50

<210> 3131
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P339Q"

<400> 3131
Thr Phe Glu Leu Gln His Ala Val Ser Glu Tyr Leu Leu Cys Val Lys
1 5 10 15

Leu Asn Ile Phe Ser Asn Trp Gly His Gln Gln Lys Tyr Thr Cys Leu
20 25 30

Tyr Arg Phe Arg Val His Gly Thr Pro Gly Lys His Ile
35 40 45

<210> 3132
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L124I"

<400> 3132
Leu Arg Met Pro Lys Glu Gln Leu Glu Leu Leu Lys Lys Glu Ser Gln
1 5 10 15

Asn Leu Glu Asn Asn Phe Arg Gln Ile Ile Ile Phe Leu Ile Glu Gln
20 25 30

Ile Asp Val Leu Lys Ala Leu Leu Arg Asp Met Lys Asp Gly Met Asp
35 40 45

Asn Asn His Asn
50

<210> 3133
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E128K"

<400> 3133
Lys Glu Gln Leu Glu Leu Leu Lys Lys Glu Ser Gln Asn Leu Glu Asn
1 5 10 15

Asn Phe Arg Gln Ile Leu Phe Leu Ile Lys Lys Gln Ile Asp Val Leu
20 25 30

Lys Ala Leu Leu Arg Asp Met Lys Asp Gly Met Asp Asn Asn His Asn
35 40 45

Trp Asn Thr His
50

<210> 3134
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A957T"

<400> 3134
Ser Ser Asp Glu Asp Ile Leu Cys Leu Lys Phe His Pro Leu Gln Glu
1 5 10 15

His Val Val Lys Glu Glu Leu Leu Asn Thr Thr Leu Tyr Cys Glu Phe
20 25 30

Ile Asn Arg Val Asn Glu Val Gly Val Asp Val Asn Arg Ala Ile Ala
35 40 45

His Pro Tyr Ser
50

<210> 3135
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R343C"

<400> 3135
Ser Arg Arg Ile Asn Pro Lys Ile Ser Tyr Val Ile Ser Ile Lys Gly
1 5 10 15

Gln Arg Leu Asp Pro Met Glu Ser Val Cys Cys Glu Glu Thr Val Asn
20 25 30

Leu Thr Thr Asp Ser Arg Thr Pro Glu Val Cys Leu Ala Leu Tyr Pro
35 40 45

Gly Thr Asn Tyr
50

<210> 3136
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.T513M"

<400> 3136
Tyr Glu Leu Thr Ser Ser Thr Leu Glu Ile Leu Thr Val Asn Thr Val
1 5 10 15

Lys Gln Thr Pro Asn His Ile Pro Ser Met Met Ile Met Ala Thr Thr
20 25 30

Gln Pro Pro Val Glu Thr Thr Val Pro Glu Ile Gln Asp Ser Phe Pro
35 40 45

Tyr Leu Leu Ser
50

<210> 3137
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E138fs"

<400> 3137
Met Ala Asp Gly Ala Pro Leu Ala Gly Val Arg Gly Gly Leu Ser Asp
1 5 10 15

Gly Glu Gly Pro Pro Gly Gly Arg Gly Arg His Asn Asp Gly Lys Asn
20 25 30

Glu Lys Asn Trp Pro Asn Ser Met Lys Pro Ser Tyr Gly Ser Val Ala
35 40 45

Thr Ala Ala Ser Ser Gly His Cys Ile Leu Cys Leu Val Trp Arg
50 55 60

<210> 3138
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P60Q"

<400> 3138
Asp Arg Ala Gln Asp Glu Tyr Thr Gln Arg Ser Tyr Ser Arg Phe Gln
1 5 10 15

Asp Glu Glu Asp Asp Asp Asp Tyr Tyr Gln Gln Ala Gly Glu Thr Tyr
20 25 30

Asn Gly Glu Ala Asn Asp Asp Glu Gly Ser Ser Glu Ala Thr Glu Gly
35 40 45

His Asp Glu Asp
50

<210> 3139
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M93T"

<400> 3139
Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser Gly Val His
1 5 10 15

Gly Asp Ser Pro Tyr Gly Ser Gly Thr Thr Thr Asp Thr His Ser Leu
20 25 30

Glu Ser Lys Ala Glu Arg Ile Ala Arg Tyr Lys Ala Glu Arg Arg Arg
35 40 45

Gln Leu Ala Glu
50

<210> 3140
<211> 68

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G1862fs"

<400> 3140
Glu Glu Arg Gly Ala Gln Val Gln Val Leu Gln Gly Lys Glu Pro Pro
1 5 10 15

Cys Phe Leu Gln Cys Phe Gln Gly Gly Trp Trp Cys Thr Arg Gly Gly
20 25 30

Gly Lys Arg Lys Lys Lys Met Cys Lys Val Ser Gly Gly Cys Thr Ala
35 40 45

Cys Val Glu Arg Cys Pro Trp Lys Gly Ile Cys Trp Lys Trp Pro Val
50 55 60

Thr Val Ala Ala
65

<210> 3141
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K474N"

<400> 3141
Lys Pro Ser Lys Tyr Ile Lys Asn Ser Asp Lys Gly Asn Arg Asn Asn
1 5 10 15

Ser Gln Leu Glu Lys Thr Thr Pro Ser Asn Asn Arg Lys Met Ser Glu
20 25 30

Ala Ser Met Ile Val Ser Gly Ala Asp Arg Tyr Thr Met Arg Ser Pro
35 40 45

Val Leu Phe Ser
    50

<210> 3142
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A336G"

<400> 3142
His Pro Ala Ser Leu Glu Phe Gln Ala Gln Ile Thr Thr Leu Leu Val
1   5   10   15

Asp Leu Gly Thr Pro Gln Ala Glu Ile Gly Gly Arg Asn Met Pro Ser
            20   25   30

Ser Lys Asp Thr Arg Lys Arg Pro Arg Asp Asp Ser Asp Ser Thr Leu
        35   40   45

Lys Lys Met Lys
    50

<210> 3143
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.A34del"

<400> 3143
Leu Ser Asp Ser Ser Phe Ile Ala Asn Leu Pro Asn Gly Tyr Met Thr
1   5   10   15

Asp Leu Gln Arg Pro Glu Pro Gln Gln Pro Thr Pro Pro Pro Pro Gly
            20   25   30

Pro Gly Ala Ala Ser Ala Ala Ala Pro Pro Thr Ala Ser Pro Gly Pro
35 40 45

Glu Arg Thr Pro Pro
50

<210> 3144
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D135Y"

<400> 3144
Cys Cys Glu Thr Thr Phe Ile Glu Asp Arg Ser Pro Thr Lys Asp Ser
1 5 10 15

Leu Glu Tyr Pro Asp Gly Lys Phe Ile Tyr Tyr Leu Ser Ala Asp Asp
20 25 30

Ile Lys Ile His Thr Leu Ser Tyr Asp Val Glu Glu Glu Glu Glu Phe
35 40 45

Gln Glu Leu Glu
50

<210> 3145
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K3103N"

<400> 3145
Glu Ser Arg Arg Leu Asn Ala Gln Ile Leu Ser Gln Arg Ile Glu Lys
1 5 10 15

Ala Lys Cys Leu Cys Asp Glu Ile Ile Asn Asn Lys Leu Asn Glu Asn

20 25 30

Lys Thr Phe Asp Asp Ser Phe Lys Glu Lys Glu Ile Leu Gln Ile Lys
35 40 45

Leu Asn Ala Glu
50

<210> 3146
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R169Q"

<400> 3146
Gln Ala Ala Ile Ala Phe Thr Phe Phe Ser Ile Leu Val Trp Ile Phe
1 5 10 15

Gln Ala Tyr Leu Ala Phe Gln Asp Leu Gln Gln Asn Asp Ala Pro Val
20 25 30

Pro Tyr Lys Arg Phe Leu Asp Glu Gly Gly Met Val Leu Thr Thr Leu
35 40 45

Pro Leu Pro Ser
50

<210> 3147
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I681F"

<400> 3147
Lys Thr Ile Ser Arg Asp Asn Lys Tyr Val Leu Leu Ala Ser Glu Gln
1 5 10 15

Leu Val Gly Val Cys Leu Phe Val Phe Phe Phe Arg Pro Gln His Ala
20 25 30

Pro Phe Ile Arg Asp Val Ala Val Asp Thr Val Lys Thr Gly Met Gly
35 40 45

Gly Ala Thr Gly
50

<210> 3148
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K832T"

<400> 3148
Trp Arg Lys Lys His Pro Phe Asp Lys Thr Ala Gly Glu Leu Asn Leu
1 5 10 15

Leu Asp Ser Asp Leu Asp Val Asp Thr Thr Thr Val Arg His Thr Trp
20 25 30

Ser Pro Gly Ala Leu Gln Tyr Tyr Gly Arg Ala Glu Leu Gln Ala Ser
35 40 45

Asp His Arg Pro
50

<210> 3149
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P1111fs"

<400> 3149
His Arg Ser Pro Ser Arg Ser Leu Ser Val Pro Asn Arg Pro Arg Pro
1 5 10 15

Pro Gln Pro Pro Gln Arg Pro Pro Pro Ser Asn Arg Phe Asn Gly Glu
20 25 30

Lys Val Gly Phe Arg Cys Val His Leu Leu Arg His Pro Trp Thr Val
35 40 45

Phe Asn Phe Ala Asp Gly Lys Thr Ser Thr Arg Ser Thr Ser Ala Thr
50 55 60

Ser Gln Gly Ser Asp Trp Asn Lys
65 70

<210> 3150
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R516Q"

<400> 3150
Arg Thr Val Ile Leu Gly Lys Lys Thr Glu Val Lys Ala Thr Arg Glu
1 5 10 15

Gln Glu Arg Asn Arg Pro Glu Thr Ile Gln Gln Thr Lys Pro Glu Glu
20 25 30

Lys Met Phe Asp Ser Lys Glu Lys Ala Ser Glu Glu Arg Asn Leu Arg
35 40 45

Trp Glu Glu Leu
50

<210> 3151
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.G619fs"

<400> 3151
Ser Ser His Leu Lys Gly Gln Ala Val Pro Ala Ser Lys Thr Gly Ile
1 5 10 15

Leu Glu Glu Ser Met Ala Arg Arg Gly Gln Pro Gln Ile His Val Tyr
20 25 30

Phe Arg Gly Glu Ala Gln Gly Asp Pro Glu Ser Arg Leu Ala Gly Ser
35 40 45

Gly Thr Asp Ser Gly
50

<210> 3152
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M1fs"

<400> 3152
Trp Leu Arg Ser Pro Pro Ala Gly Lys Asn Leu Met Lys Ser Pro Gln
1 5 10 15

Trp Trp Gly Ser Ser Val His Leu Ala Trp Ser Ser Gln Ser Leu Ser
20 25 30

Leu His Gly Ser Ala Val Arg Glu Asn His Pro Ser Leu Thr Arg Leu
35 40 45

Leu His Thr Ser Leu Cys Met Cys Leu Arg Glu Leu Ile Phe Thr Leu
50 55 60

Lys Thr
65

<210> 3153

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T349M"

<400> 3153
Thr Met Lys Arg Asn Leu Asn Pro Ile Phe Asn Glu Ser Phe Ala Phe
1 5 10 15

Asp Ile Pro Thr Glu Lys Leu Arg Glu Met Met Thr Ile Ile Ile Thr
20 25 30

Val Met Asp Lys Asp Lys Leu Ser Arg Asn Asp Val Ile Gly Lys Ile
35 40 45

Tyr Leu Ser Trp
50

<210> 3154
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R373W"

<400> 3154
Gly Ala Arg Ala Ser Gly Gln Pro Leu Gln His Trp Ala Asp Met Leu
1 5 10 15

Ala His Ala Arg Arg Pro Ile Ala Gln Trp Trp His Pro Leu Arg Pro
20 25 30

Ala Arg Glu Val Asp Arg Met Leu Ala Leu Gln Pro Arg Leu Arg Leu
35 40 45

Arg Leu Pro Leu
50

<210> 3155
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.I440M"

<400> 3155
Phe Pro Ile Asn Gly Leu His Ser His Ser Glu Val Leu Thr Ala Arg
1 5 10 15

Pro Gln Ser Met Glu Asn Ser Pro Thr Met Met Asn Glu Pro Lys Asp
20 25 30

Lys Ser Ser Glu Leu Thr Arg Leu Glu Ser Val Leu Pro Arg Ser Pro
35 40 45

Ala Asp Glu Leu
50

<210> 3156
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R211T"

<400> 3156
His Ile Pro Arg Tyr Ser Thr Asn Pro Ile Thr Val Thr Val Ser Gln
1 5 10 15

Asn Leu Pro Ser Gly Gln Thr Val Pro Thr Thr Ala Leu Gln Ile Leu
20 25 30

Pro Gln Ile Pro Ser Asn Leu Tyr Gly Ser Pro Gly Ser Ile Tyr Ile
35 40 45

Arg Gln Thr Ser
50

<210> 3157
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E67K"

<400> 3157
Ile Gly His His Arg Arg Tyr His Gly Tyr Gln Leu Val Asp Gly Gly
1 5 10 15

Arg Phe Thr Leu Trp Gly Pro Glu Ala Lys Lys Gly Gly Trp Thr Ser
20 25 30

Arg Glu Glu Gln Leu Leu Leu Asp Ala Ile Glu Gln Phe Gly Phe Gly
35 40 45

Asn Trp Glu Asp
50

<210> 3158
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R843W"

<400> 3158
Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys Ala
1 5 10 15

Phe Pro Ser His Ser Glu Ser Ser Ile Trp Trp Lys Arg Leu Lys Leu
20 25 30

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
35 40 45

Lys Ser Asp Phe
50

<210> 3159
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R172M"

<400> 3159
His Gly Met Leu Lys Asp Ala Lys Arg Asn Leu Ser Glu Ala Glu Thr
1 5 10 15

Trp Arg His Gly Glu Asn Thr Ser Ser Met Met Glu Ile Leu Ile Asn
20 25 30

Leu Ile Gln Ala Tyr Lys Gly Leu Leu Gln Tyr Tyr Thr Trp Ser Glu
35 40 45

Lys Lys Met Glu Leu
50

<210> 3160
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R292C"

<400> 3160
Gly Ile Glu Ser Trp Pro Asp Tyr Glu Asp Ile Tyr Lys Lys Thr Val
1 5 10 15

Glu Val Gly Thr Phe Leu Asp Leu Pro Cys Cys Phe Pro Asp Ile Thr

20 25 30

Glu Asp Cys Tyr Leu His Pro Asn Ile Leu Cys Met Lys Tyr Leu Met
35 40 45

Glu Val Asn Leu
50

<210> 3161
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K851fs"

<400> 3161
Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys Ser Lys Asp Arg Pro Arg
1 5 10 15

Arg Ile Arg Met Glu Asp Ile Lys Lys Pro Phe Leu Pro Ile Gln Lys
20 25 30

Ala Ala Ser Gly Arg Gly
35

<210> 3162
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S130A"

<400> 3162
Arg Gln Ser Lys Leu Arg Glu Ala Glu Glu Ala Leu Arg Arg Glu Ala
1 5 10 15

Gly Leu Leu Glu Glu Ala Val Ala Gly Ala Ala Gly Ala Pro Gly Glu
20 25 30

Val Asp Ser Ala Gly Ala Glu Val Thr Ser Ala Leu Leu Ser Arg Val
35 40 45

Thr Ala Ser Ala
50

<210> 3163
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S380L"

<400> 3163
Leu Asp Ser Pro Gly Lys Ala Ile Arg Gly Pro Gln Gln Pro Ile Trp
1 5 10 15

Lys Pro Phe Pro Asn Gln Asp Ser Asp Leu Leu Val Val Leu Ser Gly
20 25 30

Thr Asp Ser Glu Leu His Ile Pro Arg Val Cys Glu Phe Cys Gln Ala
35 40 45

Val Phe Pro Pro
50

<210> 3164
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.Q899fs"

<400> 3164
Gln Arg Val Glu Glu Glu Leu Leu Ala Leu Gln Thr Gly Arg Ser Glu
1 5 10 15

Arg Ile Arg Ser Leu Leu Glu Arg Gln Gly Pro
20 25

<210> 3165
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L782V"

<400> 3165
Val Leu Thr Glu Leu Ile Asn Leu His Leu Lys Val Gly Trp Lys Arg
1 5 10 15

Gly Asn Pro Ile Trp Arg Val Ile Ser Val Val Leu Lys Asn Ala Ser
20 25 30

Ile Gln His Leu Gln Glu Met Asp Ser Gly Gln Glu Pro Thr Val Gly
35 40 45

Ser Gln Ile Gln
50

<210> 3166
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E199K"

<400> 3166
Arg Gly Ser Glu Leu Pro Val Leu Glu Arg Ile Cys Gln Glu Leu Thr
1 5 10 15

Ala Ala Ala Arg Pro Phe Arg Arg Leu Lys Lys Ala Ser Arg Asp Gln
20 25 30

Leu Arg Gln Leu Phe Lys Asp Asn Pro Phe Lys Leu His Leu Ile Glu
35 40 45

Glu Lys Val Thr
50

<210> 3167
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G366D"

<400> 3167
Lys Gly Pro His Val Arg His Thr Gly Lys Ile Lys Thr Ile Lys Ile
1 5 10 15

Phe Lys Asn Ser Ser Thr Tyr Trp Glu Asp Asp Asn Pro Glu Met Glu
20 25 30

Thr Leu Gln Arg Ile Tyr Gly Ile Ser Phe Pro Asp Asn Lys Met Met
35 40 45

Arg Asp Trp Glu
50

<210> 3168
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R270C"

<400> 3168
Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg Leu Val Thr Ile
1 5 10 15

Val Asp Lys Leu Gln Gln Ser Thr Ala Cys Cys Val Val Val Val Phe

20 25 30

Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val Leu Arg Gln
35 40 45

Asn Phe Thr Gly
50

<210> 3169
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E525K"

<400> 3169
Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys Gly Phe His
1 5 10 15

Ser Cys Cys Tyr Asp Cys Val Asp Cys Lys Lys Ala Gly Ser Tyr Arg
20 25 30

Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp Glu Trp
35 40 45

Ser Pro Glu Arg
50

<210> 3170
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F183L"

<400> 3170
Lys Phe Phe Ser Gln Asn Ala Thr Ile Gln Lys Glu Asp Thr Leu Ala
1 5 10 15

Ile Gln Ile Phe Ser Phe Val Ala Glu Leu Leu Ser Val Pro Leu Leu
20 25 30

Ile Phe Leu Phe Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His
35 40 45

Thr Arg Gln Met
50

<210> 3171
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q177H"

<400> 3171
Ile Gln Leu Leu Thr Met Glu His Leu Pro Arg Asn Ser Thr Val Thr
1 5 10 15

Asp Lys Leu Glu Asn Phe His Gln Tyr His His Phe Gln Ala His Thr
20 25 30

Val Ala Leu Val Ile Pro Phe Ile Leu Phe Leu Ala Ser Thr Ile Phe
35 40 45

Leu Met Ala Ser
50

<210> 3172
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V231I"

<400> 3172
Gln Ile Gln His His Ser Thr Gly His Cys Asn Pro Ser Met Lys Ala
1 5 10 15

Arg Phe Thr Ala Leu Arg Ser Leu Ala Ile Ile Leu Phe Ile Val Phe
20 25 30

Thr Ser Tyr Phe Leu Thr Ile Leu Ile Thr Ile Ile Gly Thr Leu Phe
35 40 45

Asp Lys Arg Cys
50

<210> 3173
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L236fs"

<400> 3173
His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile Lys Ala
1 5 10 15

Leu Gln Thr Val Thr Ser Phe Leu Leu Val Met Cys His Leu Leu Ser
20 25 30

Val His Asp His Ile Ser Leu
35

<210> 3174
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I311T"

<400> 3174

Met Ala Ala Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn
1 5 10 15

Ala Lys Leu Arg Arg Ala Val Met Thr Thr Thr Leu Leu Trp Ala Gln
20 25 30

Ser Ser Leu Lys Val Arg Ala Asp His Lys Ala Asp Ser Arg Thr Leu
35 40 45

Cys

<210> 3175
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A255T"

<400> 3175
Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu Ile Leu Tyr Ala Leu
1 5 10 15

Ser Phe Leu Ser Leu Ile Ile Asp Ala Thr Thr Lys Phe Ile Ser Met
20 25 30

Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val Tyr Leu Cys Ile
35 40 45

Ser Val His Pro
50

<210> 3176
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.W98C"

<400> 3176
Pro Asp Val Tyr Thr Lys Asn Lys Gln Gln Ile Val Ile Phe Thr Phe
1 5 10 15

Trp Thr Phe Ala Asn Tyr Leu Asn Met Cys Cys Ile Thr Thr Cys Leu
20 25 30

Asn Val Phe Tyr Phe Leu Lys Ile Ala Ser Ser Ser His Pro Leu Phe
35 40 45

Leu Trp Leu Lys
50

<210> 3177
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E163Q"

<400> 3177
Phe Leu Ile Ser Leu Ile Ile Ser Val Pro Lys Asn Asp Asp Met Trp
1 5 10 15

Tyr His Leu Phe Lys Val Ser His Glu Gln Gln Asn Ile Thr Trp Lys
20 25 30

Phe Lys Val Ser Lys Ile Pro Gly Thr Phe Lys Gln Leu Thr Leu Asn
35 40 45

Leu Gly Val Met
50

<210> 3178
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R367H"

<400> 3178
Thr Leu Ser Phe Leu Lys Ser Asn Ala Asp Leu Cys Tyr Gly Ala Leu
1 5 10 15

Ala Ala Ile Pro Gly Leu Arg Pro Val His His Pro Ser Gly Ala Met
20 25 30

Tyr Leu Met Val Gly Ile Glu Met Glu His Phe Pro Glu Phe Glu Asn
35 40 45

Asp Val Glu Phe
50

<210> 3179
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S71F"

<400> 3179
Glu Val Arg Arg Leu Ser Arg Gln Ser Thr Arg Lys Glu Pro Val Thr
1 5 10 15

Lys Gln Val Arg Leu Cys Val Ser Pro Phe Phe Gly Leu Arg Cys Glu
20 25 30

Pro Glu Pro Gly Arg Ser Gln Gln Trp Asp Pro Leu Ile Tyr Ser Ser
35 40 45

Ile Phe Glu Cys
50

<210> 3180
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H277R"

<400> 3180
Asp Gly Gly Leu Arg Ser Ser Gly Phe Phe Ser Ser Phe Glu Glu Ser
1 5 10 15

Asp Ile Glu Asn His Leu Ile Ser Gly Arg Arg Asn Ile Val Gln Pro
20 25 30

Thr Asp Ile Glu Glu Asn Arg Thr Met Leu Phe Thr Ile Gly Gln Ser
35 40 45

Glu Val Tyr Leu
50

<210> 3181
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F608Y"

<400> 3181
Pro Asp Val Gly Tyr Val Gln Gly Met Ser Phe Ile Ala Ala Val Leu
1 5 10 15

Ile Leu Asn Leu Glu Glu Ala Asp Ala Tyr Tyr Ile Ala Phe Ala Asn
20 25 30

Leu Leu Asn Lys Pro Cys Gln Leu Ala Phe Phe Arg Val Asp His Ser
35 40 45

Met Met Leu Lys
50

<210> 3182
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R920Q"

<400> 3182
Ile Leu Asp Ala Arg Lys Leu Ile Ser Ile Ser Phe Gly Asp Leu Asn
1 5 10 15

Pro Phe Pro Leu Arg Gln Ile Arg Asn Gln Gln Arg Ala Tyr His Leu
20 25 30

Glu Lys Val Arg Leu Glu Leu Thr Glu Leu Glu Ala Ile Arg Glu Asp
35 40 45

Phe Leu Arg Glu
50

<210> 3183
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P1233T"

<400> 3183
Asp Trp Ala Ile Thr Phe Glu Gln Phe Leu Ala Ser Leu Leu Thr Glu
1 5 10 15

Pro Ala Leu Val Lys Tyr Phe Asp Lys Thr Thr Val Cys Met Met Ala
20 25 30

Arg Ile Thr Ser Ala Lys Asn Ile Arg Met Met Gly Lys Pro Leu Thr
35 40 45

Ser Ala Ser Asp
50

<210> 3184

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R476C"

<400> 3184
Asp Glu Lys Arg Gly Ala Cys Ser Val Gly Thr Asn Val Arg Asp Ala
1 5 10 15

Ala Cys Tyr Val Cys Trp Ala Phe Ala Cys Cys Ala Tyr Glu Pro Gln
20 25 30

Glu Leu Lys Pro Phe Val Thr Ala Ile Ser Ser Ala Leu Val Ile Ala
35 40 45

Ala Val Phe Asp
50

<210> 3185
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.N126fs"

<400> 3185
Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala Ala Ala Ala Ala
1 5 10 15

Ala Ala Ser Gln Gln Gly Ser Ala Lys Met Glu Lys Thr Gln Gln Met
20 25 30

Gly Arg Arg Met Glu His Ile Leu
35 40

<210> 3186
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H187Y"

<400> 3186
Arg Tyr Lys Phe His Asn Ser Arg Trp Met Val Ala Gly Lys Ala Asp
1 5 10 15

Pro Glu Met Pro Lys Arg Met Tyr Ile Tyr Tyr Pro Asp Ser Pro Ala
20 25 30

Thr Gly Glu Gln Trp Met Ser Lys Val Val Thr Phe His Lys Leu Lys
35 40 45

Leu Thr Asn Asn
50

<210> 3187
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S370fs"

<400> 3187
Leu Asp Leu Pro Cys Lys Arg Ser Tyr Leu Glu Ala Pro Ser Ser Val
1 5 10 15

Gly Glu Asp His Tyr Phe Arg Ser Pro Leu Pro Thr Thr Ser Lys Cys
20 25 30

<210> 3188
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E308K"

<400> 3188
Asp Leu Leu Ser Ala Phe Glu Ala Met Thr Ser Gln Ala Asn Pro Glu
1 5 10 15

Ala Leu Ser Ala Pro Ala Leu Gln Glu Lys Lys Ala Ala Phe Pro Gly
20 25 30

Arg Arg Val Asn Ala Lys Met Pro Val Tyr Ser Gly Ser Arg Pro Ala
35 40 45

Cys Gln Leu Gln
50

<210> 3189
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H140P"

<400> 3189
Gly Met Tyr Lys Glu Thr Val Tyr Ser Ala Phe Asn Leu Leu Met His
1 5 10 15

Tyr Pro Pro Pro Ser Gly Ala Gly Gln Pro Pro Pro Gln Pro Gln Pro
20 25 30

Pro Leu His Lys Ala Asn Gln Pro Pro His Gly Val Pro Gln Leu Ser
35 40 45

Leu Tyr Glu His
50

<210> 3190
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E172fs"

<400> 3190
Lys Leu Arg Glu Met Glu Leu Asp Leu His Gln Lys His Val Val Asn
1 5 10 15

Ser Trp Glu Met Gln Lys Glu Glu Lys Asn Ser Lys Lys Pro Pro Gln
20 25 30

Ser Lys Arg Thr Asn Gly Met Lys Met Asn Met Lys Gly Pro Glu Gly
35 40 45

Arg Arg
50

<210> 3191
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.K1366del"

<400> 3191
Gly Trp Glu Ser Arg Lys Arg Lys Leu Ser Gly Asp Gln Pro Ala Ala
1 5 10 15

Arg Thr Pro Arg Ser Lys Lys Lys Lys Leu Gly Ala Gly Glu Gly Gly
20 25 30

Glu Ala Ser Val Ser Pro Glu Lys Thr Ser Thr Thr Ser Lys Gly Lys
35 40 45

Ala Lys Arg Asp Lys
50

<210> 3192

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K264R"

<400> 3192
Ala Pro Ala Pro Gly Lys Val Gly Asp Val Thr Pro Gln Val Lys Gly
1 5 10 15

Gly Ala Leu Pro Pro Ala Lys Arg Ala Arg Arg Lys Pro Glu Glu Glu
20 25 30

Ser Glu Ser Ser Glu Glu Gly Ser Glu Ser Glu Glu Glu Ala Pro Ala
35 40 45

Gly Thr Arg Ser
50

<210> 3193
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S127I"

<400> 3193
Pro Glu His Gln Gln Lys Val Leu Asn His Leu Ser Pro Asp Leu Pro
1 5 10 15

Leu Ala Val Thr Ala Asn Leu Ile Asp Ile Ile Glu Asn Tyr Trp Leu
20 25 30

Arg Cys Cys Met His Arg Trp Pro Val Cys His Val Ala His His Gly
35 40 45

Gly Ser Trp Lys
50

<210> 3194
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S74L"

<400> 3194
His Ala Val Leu Lys Glu Glu Leu Ala Asn Ala Glu Tyr Ser Pro Glu
1 5 10 15

Glu Met Pro Gln Leu Thr Lys His Leu Leu Leu Glu Asn Ile Lys Asp
20 25 30

Lys Leu Lys Glu Met Gly Phe Asp Arg Tyr Lys Met Val Val Gln Val
35 40 45

Val Ile Gly Glu
50

<210> 3195
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q197H"

<400> 3195
Arg Val Pro Tyr Asn Arg Arg His Tyr Arg Asp Asn Phe Lys Gly Glu
1 5 10 15

Glu Asn Glu Leu Leu Leu Lys Ser Glu His His Glu Lys Thr Leu Leu
20 25 30

Glu Leu Val Glu Ala Trp Leu Glu Arg Thr Pro Gly Leu Glu Pro His
35 40 45

Gly Phe Asn Phe
    50

<210> 3196
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.W276C"

<400> 3196
Cys Leu Ala Glu Tyr His Leu Gly Asp Tyr Gly His Ala Trp Asn Arg
1   5   10   15

Cys Trp Val Leu Asp Arg Val Asp Thr Cys Cys Ala Val Val Met Phe
            20   25   30

Ile Asp Phe Gly Gln Leu Ala Thr Ile Pro Val Gln Ser Leu Arg Ser
        35   40   45

Leu Asp Ser Asp
    50

<210> 3197
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.S322L"

<400> 3197
Ser Leu Asp Ser Asp Asp Phe Trp Thr Ile Pro Pro Leu Thr Gln Pro
1   5   10   15

Phe Met Leu Glu Lys Asp Ile Leu Ser Leu Leu Tyr Glu Val Val His
            20   25   30

Arg Ile Leu Lys Gly Lys Ile Thr Gly Ala Leu Asn Ser Ala Val Thr
35 40 45

Ala Pro Ala Ser
50

<210> 3198
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P298fs"

<400> 3198
Asp Val Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu
1 5 10 15

Arg Glu Leu Tyr Asp Arg Gly Pro Pro Pro Cys Leu Leu Pro Gly Gln
20 25 30

Val Leu Gly Gly Pro Glu Leu Gly Pro Lys Trp
35 40

<210> 3199
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L29I"

<400> 3199
Lys Ala Phe Val Leu Leu Ala Ile Phe Ala Glu Ala Ser Ala Lys Ser
1 5 10 15

Cys Ala Pro Asn Lys Ala Asp Val Ile Ile Ile Val Phe Cys Tyr Pro
20 25 30

Lys Thr Ile Ile Thr Lys Ile Pro Glu Cys Pro Tyr Gly Trp Glu Val

35 40 45

His Gln Leu Ala
50

<210> 3200
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M166I"

<400> 3200
Leu Leu Val Leu Thr Ala Glu Leu Trp Ala Pro Asn Met Cys His Leu
1 5 10 15

Gln Leu Met Glu Thr Phe Leu Ile Leu Ile Ile Met Gly Ser Trp Leu
20 25 30

Met Gln Ala Gly Phe Ile Leu Tyr Arg Pro Val Ser Gly Tyr Pro Trp
35 40 45

Gln Asp Asp Asp
50

<210> 3201
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R401H"

<400> 3201
Leu Leu Glu Arg Ser Ile Met Ala Lys Glu Gly Pro Leu Lys Val Ala
1 5 10 15

Gln Thr Arg Leu Glu Cys Arg Thr Arg His His Pro Asn Met Glu Leu
20 25 30

Cys Arg Asp Ile Pro Gln Leu Lys Leu Val Asn Glu Val Phe Thr Ile
35 40 45

Asp Asp Thr Leu
50

<210> 3202
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T1472S"

<400> 3202
Ala Ala Val Arg Glu Ile Met Glu Asn Arg Tyr Gly Gln Lys Gly Asn
1 5 10 15

Ala Ile Arg Ile Glu Ile Val Val Tyr Ser Ser Gly Lys Glu Gly Lys
20 25 30

Ser Ser His Gly Cys Pro Ile Ala Lys Trp Val Leu Arg Arg Ser Ser
35 40 45

Asp Glu Glu Lys
50

<210> 3203
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1652Q"

<400> 3203
Ala Ser Ser Leu Gln Ile Leu Gln Glu Glu Thr Lys Val Cys Leu Asn
1 5 10 15

Ile Leu Pro Leu Phe Val Glu Ala Phe Gln Gln Arg Lys Gln Glu Cys
20 25 30

Ser Val Glu Gln Ile Leu Ile Ser Arg Glu Leu Leu Val Asp Gln Asn
35 40 45

Leu Trp Asn Asn
50

<210> 3204
<211> 162
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G482fs"

<400> 3204
Ser Leu Lys Pro Glu Gln Leu Asp Ile Glu Glu Glu Gly Arg Pro Gly
1 5 10 15

Ala Ala Thr Phe His Val Gly Gly Gly Thr Cys Pro Glu Cys Ser Pro
20 25 30

Ser Ala Ala Pro Cys Thr Ala Leu Arg Cys Pro Ser Gly Pro Ala Leu
35 40 45

Ser Gln Arg Pro Pro Gly Gly Pro Gly Arg Pro Leu Pro Pro Gly Ala
50 55 60

Gly Gly His Ser Asp Gly Gly Gly Gly Gly Gly Gly Gly Arg Thr Val
65 70 75 80

Gly Gly Cys Pro Val Pro Thr Ala Gly Cys Leu Arg Ser Pro Ala Leu
85 90 95

Phe Ser Val Pro Cys Cys Leu Gln Gly Gln Gln Pro Pro Gln Gln Leu
100 105 110

Gln His Gly Arg Gly Val Leu Ile Arg Pro His Pro Ser Pro Gly Thr
115 120 125

Phe Pro Pro Arg Lys Gly Gly Pro Val Arg Met Arg Pro Arg Leu Phe
130 135 140

Pro His Pro Pro Met Arg Leu Pro Cys Pro Gly Ile Leu Gly Glu Glu
145 150 155 160

Glu Met

<210> 3205
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.A382V"

<400> 3205
Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
1 5 10 15

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Val Val Arg Asn Arg Pro Pro
20 25 30

Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
35 40 45

<210> 3206
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R206C"

<400> 3206
Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn
1 5 10 15

Asn Phe Val Ser Arg Glu Asp Cys Lys Cys Cys Ala Cys Ala Lys Ala

20 25 30

Leu Lys Lys Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile
35 40 45

Arg Lys Ile Arg
50

<210> 3207
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R222C"

<400> 3207
Asn Phe Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu
1 5 10 15

Lys Lys Lys Lys Lys Met Pro Lys Leu Cys Cys Phe Ala Ser Arg Ile
20 25 30

Arg Lys Ile Arg Lys Lys Gln Phe
35 40

<210> 3208
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.S252C"

<400> 3208
Glu Ala Leu Asp Ser Ser Trp Val Ser Arg Gly Pro Asp Lys Leu Leu
1 5 10 15

Pro Tyr Pro Thr Leu Ala Ser Pro Ala Cys Cys Asp
20 25

<210> 3209
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S241L"

<400> 3209
Phe Gly Glu Val Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val
1 5 10 15

Lys Ile Phe Ser Ser Arg Glu Glu Arg Leu Leu Trp Phe Arg Glu Ala
20 25 30

Glu Ile Tyr Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe
35 40 45

Ile Ala Ala Asp
50

<210> 3210
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T358fs"

<400> 3210
Trp Asn Glu Ser Trp Phe Ala Arg Gln Asp Leu Gly Pro Ser Tyr Asn
1 5 10 15

Gly Trp Gln Val Leu Asp Ala Thr Pro Arg Arg Arg Val Lys Val Cys
20 25 30

Ser Gly Ala Ala Gln Pro Gln Ser Pro Pro Ser Ala Arg Val Met Cys
35 40 45

Thr Trp Leu Thr Met Ala Pro Ser Cys Leu Arg Arg Ser Thr Pro Thr
50 55 60

Thr Ser Pro Gly Cys Gly Thr Arg Met Arg Ala Gly Ser Val Tyr Thr
65 70 75 80

Gln Thr Arg Arg Arg Leu Gly Asp Ala Ser Ala Pro Arg Arg Trp Ala
85 90 95

Val Thr Pro Ala Trp Thr Ser Leu Thr Ser Thr Ser Ile Arg Lys Gly
100 105 110

Pro Gly Lys Arg Gly Arg Cys Thr Ala Arg Arg
115 120

<210> 3211
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S1941L"

<400> 3211
Arg Leu Leu Ala Phe Leu Glu Gly Lys Glu Gly Glu Asp Thr Leu Val
1 5 10 15

Leu Ser Val Trp Asp Ser Tyr Ala Glu Leu Leu Arg Gln Leu Thr Leu
20 25 30

Pro Arg Thr Glu Ala Ala Cys
35

<210> 3212
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.S287Y"

<400> 3212
Glu Glu Leu Asn Thr Asn Lys Glu Ser Val Ile Ala Ile Phe Val Pro
1 5 10 15

Ala Glu Asn Ser Lys Pro Ser Val Asn Tyr Tyr Phe Ile Ser Ala Gln
20 25 30

Lys Glu Thr Thr Glu Met Glu Asp Thr Asp Ile Glu Asp Ser Leu Tyr
35 40 45

Lys Asp Val Asp
50

<210> 3213
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L17R"

<400> 3213
Met Leu Arg Ser Cys Ala Ala Arg Leu Arg Thr Leu Gly Ala Leu Cys
1 5 10 15

Arg Arg Pro Pro Val Gly Arg Arg Leu Pro Gly Ser Glu Pro Arg Pro
20 25 30

Glu Leu Arg Ser Phe Ser Ser Glu Glu Val Ile
35 40

<210> 3214
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K551R"

<400> 3214
Tyr Lys Ala Val Gln Glu Lys Ser Ser Ser Pro Pro Pro Arg Lys Thr
1 5 10 15

Ser Glu Ser Arg Asp Lys Leu Gly Ala Arg Arg Gly Asp Phe Pro Thr
20 25 30

Gly Lys Ser Ser Phe Ser Ile Thr Arg Glu Ala Gln Val Asn Val Arg
35 40 45

Met Asp Ser Phe
50

<210> 3215
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R90C"

<400> 3215
Val Cys Asp Trp His Ser Asp Leu Phe Gln Trp Glu Val Ser Asp Trp
1 5 10 15

His His Cys Val Leu Val Pro Tyr Ala Cys Cys Gly Glu Val Lys Pro
20 25 30

Arg Thr Ala Glu Cys Val Thr Ala Gln His Gly Leu Gln His Arg Met
35 40 45

Val Arg Cys Ile
50

<210> 3216
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R90H"

<400> 3216
Val Cys Asp Trp His Ser Asp Leu Phe Gln Trp Glu Val Ser Asp Trp
1 5 10 15

His His Cys Val Leu Val Pro Tyr Ala His His Gly Glu Val Lys Pro
20 25 30

Arg Thr Ala Glu Cys Val Thr Ala Gln His Gly Leu Gln His Arg Met
35 40 45

Val Arg Cys Ile
50

<210> 3217
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E126K"

<400> 3217
Val Thr Ala Gln His Gly Leu Gln His Arg Met Val Arg Cys Ile Gln
1 5 10 15

Lys Leu Asn Arg Thr Val Val Ala Asn Lys Lys Ile Cys Glu His Phe
20 25 30

Ala Leu Gln Pro Pro Thr Glu Gln Ala Cys Leu Ile Pro Cys Pro Arg
35 40 45

Asp Cys Val Val
50

<210> 3218
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G247M"

<400> 3218
Gln Leu Ser Thr Cys Gln Arg Ala Asn Ser Leu Gly Asp Leu Tyr Ala
1 5 10 15

Gln Lys Asn Ser Gly Val Thr Ala Asn Met Met Gly Pro Gly Ser Lys
20 25 30

Phe Ala Gly Tyr Cys Arg Asn Leu Val Ser Asp Ile Pro Asn Leu Ala
35 40 45

Asn His Lys Met Pro
50

<210> 3219
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D43E"

<400> 3219
Gly Pro Ser Ala Phe Ala Asn Val Pro Pro Arg Leu Gln His Asp Thr
1 5 10 15

Ser Pro Leu Leu Leu Gly Arg Gly Gln Glu Glu Ala His Leu Gln Leu
20 25 30

Gln Leu Pro Arg Leu Ser Arg Arg His Leu Ser Leu Glu Pro Tyr Leu
35 40 45

Glu Lys Gly Ser
50

<210> 3220
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S312F"

<400> 3220
Val Glu Ser Phe Pro Ala His Pro Glu Val Lys Asn Leu Lys Ser Ile
1 5 10 15

Glu Leu Ala Phe Phe Pro Ser Cys Leu Phe Phe Ser Lys Cys Ile Ala
20 25 30

Met Lys Gln Gly Val Ile Lys Ser Leu Lys Ile Lys Tyr Arg His Cys
35 40 45

Leu Ile Lys Lys
50

<210> 3221
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.T152del"

<400> 3221
Val Arg Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala
1 5 10 15

Thr Thr Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln
20 25 30

Met Thr Thr Thr Pro Ala Ala Leu Pro Thr Thr Val Val Thr Thr Pro
35 40 45

Asp Leu Thr Thr Gly
50

<210> 3222

<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K83fs"

<400> 3222
Gly Phe Leu Ser Gly Leu Leu Asp Asn Val Lys Gln Glu Leu Ala Lys
1 5 10 15

Asn Lys Glu Met Lys Glu Ser Ile Lys Asn Ser Val Thr Arg Pro Glu
20 25 30

Gly

<210> 3223
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.A199fs"

<400> 3223
Tyr Gln Ser Lys His Tyr Ala Cys Ile Arg Gln Lys Gly Gly Tyr Cys
1 5 10 15

Ser Trp Tyr Arg Gly Trp Ala Pro Pro Gly
20 25

<210> 3224
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E403K"

<400> 3224
Met Gln Val Arg Glu Asp Phe Phe His Tyr Lys Thr Gly Ile Tyr Arg
1 5 10 15

His Val Thr Ser Thr Asn Lys Glu Ser Lys Lys Lys Tyr Arg Lys Leu
20 25 30

Gln Thr His Ala Val Lys Leu Thr Gly Trp Gly Thr Leu Arg Gly Ala
35 40 45

Gln Gly Gln Lys
50

<210> 3225
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P53Q"

<400> 3225
Cys Ala Gly Leu Asp Tyr Asp Tyr Thr Phe Asp Gly Asn Glu Glu Asp
1 5 10 15

Lys Thr Glu Thr Ile Asp Tyr Lys Asp Gln Gln Cys Lys Ala Ala Val
20 25 30

Phe Trp Gly Asp Ile Ala Leu Asp Asp Glu Asp Leu Asn Ile Phe Gln
35 40 45

Ile Asp Arg Thr
50

<210> 3226
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.T153M"

<400> 3226
Val Lys Gly Lys Val Pro Leu Gln Phe Ser Gly Gln Asn Glu Lys Asn
1 5 10 15

Arg Val Pro Arg Ala Ala Thr Ser Arg Met Met Glu Arg Ile Trp Pro
20 25 30

Gly Gly Val Ile Pro Tyr Val Ile Gly Gly Asn Phe Thr Gly Ser Gln
35 40 45

Arg Ala Met Phe
50

<210> 3227
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S872L"

<400> 3227
Leu Gly Arg Phe Cys Gly Ser Lys Lys Pro Asp Pro Thr Val Ala Ser
1 5 10 15

Gly Ser Ser Met Phe Leu Arg Phe Tyr Leu Leu Asp Ala Ser Val Gln
20 25 30

Arg Lys Gly Phe Gln Ala Val His Ser Thr Glu Cys Gly Gly Arg Leu
35 40 45

Lys Ala Glu Val
50

<210> 3228
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S208L"

<400> 3228
Arg Glu Gln Gly Val Asp Glu Asn Glu Thr Leu Leu Leu Arg Arg Lys
1 5 10 15

Phe Phe Tyr Ser Asp Gln Asn Val Asp Leu Leu Arg Asp Pro Val Gln
20 25 30

Leu Asn Leu Leu Tyr Val Gln Ala Arg Asp Asp Ile Leu Asn Gly Ser
35 40 45

His Pro Val Ser
50

<210> 3229
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.D327V"

<400> 3229
Arg Val Ile Asp Pro Gly Lys Val Glu Thr Leu Thr Ile Arg Arg Leu
1 5 10 15

His Ile Pro Arg Phe Tyr Leu Phe Tyr Val Val Leu Ser Thr Leu Tyr
20 25 30

Ser Leu Thr Glu Arg Val Lys Arg Ile Thr Val Glu Asn Ser Lys Val
35 40 45

Phe Leu Val Pro
50

<210> 3230

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L498V"

<400> 3230
Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu
1 5 10 15

Pro Asp Ile Phe Thr Glu Leu Arg Asn Val Val Thr Phe Leu Asp Leu
20 25 30

Ser Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu
35 40 45

Ser Ser Leu Gln
50

<210> 3231
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S15W"

<400> 3231
Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Trp Trp
1 5 10 15

Ala Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp
20 25 30

Ser Trp Thr Ile Val Gly Val Ala Ala
35 40

<210> 3232
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R91H"

<400> 3232
Arg Leu Asp Ser Val Glu Ser Val Leu Pro Tyr Glu Tyr Thr Ala Phe
1 5 10 15

Asp Phe Cys Gln Ala Ser Glu Gly Lys His His Pro Ser Glu Asn Leu
20 25 30

Gly Gln Val Leu Phe Gly Glu Arg Ile Glu Pro Ser Pro Tyr Lys Phe
35 40 45

Thr Phe Asn Lys
50

<210> 3233
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R276C"

<400> 3233
Asp Tyr Gly Ser Ser Glu Thr Pro Lys Met Thr Arg Gly Val Leu Ser
1 5 10 15

Arg Thr Ser Ser Ile Gln Pro Ser Phe Cys Cys His Arg Ser Asp Asp
20 25 30

Pro Val Gly Ser Leu Trp Gly Glu Asn Asp Tyr Pro Glu Gly Ile Glu
35 40 45

Met Ala Ser Met
50

<210> 3234
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R110H"

<400> 3234
Glu Gln Thr Ser Arg Asp Gly Asn Val Ala Glu Tyr Leu Lys Leu Val
1 5 10 15

Asn Asn Ala Asp Lys Gln Gln Ala Gly His His Ile Lys Gln Val Phe
20 25 30

Glu Lys Lys Asn Gln Lys Ser Ala His Ser Ile Ala Gln Leu Gln Lys
35 40 45

Lys Leu Glu Gln
50

<210> 3235
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S15fs"

<400> 3235
Met Ser Thr Ser Ser Ser Ser Ser Trp Asp Asn Leu Leu Glu Ser Leu
1 5 10 15

Ser Gln His Ser Met Glu Leu Asp Thr Ser Lys Phe Phe Gly Arg Asp
20 25 30

<210> 3236
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A110P"

<400> 3236
Ala Glu Leu Leu Leu Leu Arg Gly Gly Ile Arg Glu Gly Ser Leu Asp
1 5 10 15

Leu Gly His Ala Pro Leu Gly Pro Tyr Pro Pro Arg Gly Pro His Tyr
20 25 30

Asp Ala Gly Phe Thr Leu Leu Val Pro Met Phe Ser Leu Asp Gly Thr
35 40 45

Glu Leu Gln Leu
50

<210> 3237
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P299del"

<400> 3237
Phe Pro Pro Pro Ala Leu Ser Leu Glu Leu Gln Pro Pro Pro Pro Gln
1 5 10 15

Arg Asn Ser Val Pro Pro Pro Pro Pro Leu His Gly Pro Pro Gly Arg
20 25 30

Pro His Met Ser Ser Pro Thr Arg Asp Pro Leu Asp Thr
35 40 45

<210> 3238
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E1319Q"

<400> 3238
Ala His Ser Pro Leu Glu Gln His Pro Gln Pro Pro Leu Pro Pro Pro
1 5 10 15

Val Pro Gln Pro Gln Glu Pro Gln Pro Gln Gln Arg Leu Ser Pro Ala
20 25 30

Pro Leu Ala His Pro Ser His Pro Glu Arg Ala Ser Ser Ala Arg His
35 40 45

Ser Ser Glu Asp
50

<210> 3239
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R481C"

<400> 3239
Glu Ala Cys Asp Ala Val Phe Val Ala Gly Lys Glu Ser Arg Gly Ala
1 5 10 15

Arg Gly Val Arg Val Asp Phe Trp Trp Cys Cys Arg Leu Arg Ala Ser
20 25 30

Leu Arg Leu Thr Val Trp Ala Pro Leu Leu Pro Leu Arg Ile Glu Leu
35 40 45

Thr Asp Thr Thr
50

<210> 3240
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R578W"

<400> 3240
Gly Asp Ser Glu Glu Glu Glu Asp Asp Glu Arg Arg Gly Arg Gly Cys
1 5 10 15

Thr Leu Gln Tyr Gln His Ala Met Val Trp Trp Val Leu Thr Gln Phe
20 25 30

Val Ala Glu Ala Ala Gly Pro Gly Gly His Leu Ala His Leu Leu Gly
35 40 45

Ser Asp Trp Gln
50

<210> 3241
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P206fs"

<400> 3241
Ser Cys Arg Leu Gln Gly Asp Leu Gly Leu Cys Val Ala Glu Leu Glu
1 5 10 15

Leu Leu Ser Ser Trp Phe Ser Pro Pro Arg Trp Leu Pro Gly Gly Gly
20 25 30

Ser Pro Trp Thr Ser Arg Arg Gly Pro Pro Trp Ser Ser Thr Thr Pro
35 40 45

Cys Thr Gln Gly Val Arg Glu Gly Thr Ala Ser Gly Lys Thr Arg Gly
50 55 60

Glu Ala Met Gly Ser Gly Gln Ala Thr Val Thr Ser Met Ser Pro Gly
65 70 75 80

Pro Pro Cys Arg Gly Ser Gly Ala Ser Ser Phe Ile Arg His Thr Gly
85 90 95

Asn Pro Pro

<210> 3242
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A92V"

<400> 3242
Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp Leu Ile
1 5 10 15

Gly Leu Asn Leu Val Met Ser Arg Asn Val Val Gly Lys Gly Glu Tyr
20 25 30

Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile Met
35 40 45

Ser Arg Cys Ile
50

<210> 3243
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R81C"

<400> 3243

Ser Phe Val Thr Phe Leu Gln Pro Val Arg Glu Thr Gln Ile Ile Met
1 5 10 15

Arg Ile Phe Leu Asn Pro Ser Asn Phe Cys Cys Asn Phe Thr Arg Thr
20 25 30

Cys Gln Asp Ile Thr Gly Glu Phe Lys Met Cys Ser Ser Cys Leu Val
35 40 45

Cys Glu Ser Lys
50

<210> 3244
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L142P"

<400> 3244
Val Tyr Leu Val Thr Glu Val Tyr Tyr Asn Phe Met Lys Pro Thr Gln
1 5 10 15

Glu Met Asn Ile Ser Leu Val Trp Cys Pro Pro Leu Val Leu Ser Phe
20 25 30

Ala Ile Lys Val Leu Phe Ser Leu Thr Thr His Tyr Phe Lys Val Glu
35 40 45

Asp Gly Gly Glu
50

<210> 3245
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.R315Q"

<400> 3245
Lys Asp Tyr Ile Met Asn Pro Pro Leu Gly Lys Glu Ser Ile Pro Leu
1 5 10 15

Met Thr Glu Ala Thr Phe Asp Thr Leu Gln Gln Leu Trp Leu Ile Ile
20 25 30

Leu Leu Cys Ala Leu Arg Leu Ala Met Met Arg Ser His Leu Gln Ala
35 40 45

Tyr Leu Asn Leu
50

<210> 3246
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G331fs"

<400> 3246
Leu Asp Asn Asn Ala Val Asn Leu Phe Ser Ser Val Leu Ile Ala Leu
1 5 10 15

Leu Leu Pro Thr Ala Ala Trp Gly Phe Gly Pro Gly Gly Glu Leu Tyr
20 25 30

Phe Ile Ser Thr Gly
35

<210> 3247
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D140G"

<400> 3247
Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser Leu Leu Leu
1 5 10 15

Ser Gly Tyr Ile Ser Lys Gly Gly Ala Gly Gly Arg Ala Val Pro Val
20 25 30

Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His Leu Arg
35 40 45

Ile Ala Tyr Tyr
50

<210> 3248
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q128E"

<400> 3248
Glu Met Glu Leu Glu Lys Val Arg Met Glu Phe Glu Leu Thr Arg Leu
1 5 10 15

Lys Tyr Leu His Glu Lys Asn Gln Arg Glu Glu Arg Gln His Glu Val
20 25 30

Val Met Glu Gln Leu Gln Arg Glu Arg Gln His Glu Val Val Met Glu
35 40 45

Gln Leu Gln Gln
50

<210> 3249
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<223> /note="p.F156fs"

<400> 3249
Val Val Ser Tyr Phe Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val
1 5 10 15

Glu Glu Asn Arg Asn Ser Leu Phe Phe Ser Tyr Cys Phe
20 25

<210> 3250
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F230fs"

<400> 3250
Arg Ile Thr Pro Phe Leu Pro Asn Trp Phe Ile Asn Ile Thr Ser Pro
1 5 10 15

Val Ile Asn Val Pro Leu Lys Val Phe Leu Leu Val Leu Phe
20 25 30

<210> 3251
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="p.G87S"

<400> 3251
Ala Ser Leu Asp Ile Trp His Cys Glu Ser Thr Leu Ser Ser Asp Trp
1 5 10 15

Gln Ile Ala Thr Leu Ala Leu Leu Leu Ser Ser Gly Ala Ala Ile Ile
20 25 30

Leu Ile Ala Phe Leu Val Gly Leu Ile Ser Ile Cys Val Gly Ser Arg
35 40 45

Arg Arg Phe Tyr
50

<210> 3252
<211> 52
<212> PRT
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<220>
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<223> /note="p.R189Q"

<400> 3252
Met Glu Leu Arg Phe Asn Thr Leu Ala Lys Cys Pro His Cys Lys Lys
1 5 10 15

Ile Ser Ser Val Gly Ser Ala Leu Pro Gln Gln Arg Arg Cys Cys Ala
20 25 30

Tyr Ile Thr Ile Gly Met Ile Cys Ile Phe Ile Gly Val Gly Leu Thr
35 40 45

Val Gly Thr Pro
50

<210> 3253
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K77fs"

<400> 3253
Leu Ile Val Lys Met Ala Gly Arg Cys Lys Ser Gly Phe Asp Pro Arg
1 5 10 15

His Gly Ser His Asn Ile Lys Lys Lys Pro Gly Thr Ser Leu Gln Cys

20 25 30

Tyr Leu Asn
35

<210> 3254
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R63Q"

<400> 3254
Asp Ser Leu Asp Gly Tyr His Ser Phe Glu Cys Gly Ser Ile Asp Pro
1 5 10 15

Leu Thr Gly Ser His Tyr Thr Cys Arg Gln Gln Ser Pro Arg Leu Leu
20 25 30

Thr Asn Gly Tyr Tyr Ile Trp Thr Glu Asp Ser Phe Leu Cys Asp Lys
35 40 45

Asp Gly Asn Ile
50

<210> 3255
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R125Q"

<400> 3255
Cys Asn Cys Cys Ser Gln Glu Leu Glu Thr Ser Phe Thr Tyr Val Asp
1 5 10 15

Lys Asn Ile Asn Leu Glu Gln Arg Asn Gln Gln Ser Ser Pro Ser Ala
20 25 30

Lys Gly His Asn His Pro Gly Glu Leu Gly Trp Glu Asn Pro Asn Glu
35 40 45

Trp Ser Gln Glu
50

<210> 3256
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P161fs"

<400> 3256
Glu Arg Gln Pro Gln Glu Asp Leu Ile Val Arg Cys Glu Ala Gly Glu
1 5 10 15

Gly Glu Cys Arg Thr Phe Met Pro Pro Pro Gly His Pro Pro Arg Pro
20 25 30

His

<210> 3257
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S288L"

<400> 3257
Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp Ile Ala Val
1 5 10 15

Val Gln Val Ser Ser Arg Val Thr Phe Leu Leu Asp Asp Ile Arg Gln
20 25 30

Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu Thr Val
35 40 45

His Ile Thr Gly
50

<210> 3258
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G259C"

<400> 3258
Phe Thr Thr Tyr Lys Asn Pro Ala Arg Trp Thr Ala Ser Phe Gly Val
1 5 10 15

Thr Ile Lys Pro Ser Lys Met Lys Arg Cys Cys Leu Arg Arg Ile Ile
20 25 30

Val His Glu Lys Tyr Lys His Pro Ser His Asp Tyr Asp Ile Ser Leu
35 40 45

Ala Glu Leu Ser
50

<210> 3259
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R274Q"

<400> 3259
Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly
1 5 10 15

Ala Thr Ile Thr Pro Pro Ala Val Lys Gln Gln Asn Val Arg Lys Ile
20 25 30

Ile Leu His Glu Asn Tyr His Arg Glu Thr Asn Glu Asn Asp Ile Ala
35 40 45

Leu Val Gln Leu
50

<210> 3260
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R16Q"

<400> 3260
Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Gln
1 5 10 15

Gln Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro
20 25 30

Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
35 40

<210> 3261
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V302I"

<400> 3261
Ile Thr Ser Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val
1 5 10 15

Leu Ala Ser Gly Ala Ile Met Ala Val Ile Ile Trp Lys Lys Gly Leu

20 25 30

His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe
35 40 45

Gln Ala Cys Glu
50

<210> 3262
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T409R"

<400> 3262
Arg Thr Gln Leu Pro Ser Thr Glu Asn Ile Val Val Leu Ser Leu Ser
1 5 10 15

Leu Leu Ile Ile Pro Phe Val Pro Ala Arg Arg Asn Leu Phe Phe Tyr
20 25 30

Val Gly Phe Val Ile Ala Glu Arg Val Leu Tyr Ile Pro Ser Met Gly
35 40 45

Phe Cys Leu Leu
50

<210> 3263
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R611C"

<400> 3263
Glu Ala Ala Glu Gln Ser Tyr Arg Thr Ala Ile Lys His Arg Arg Lys
1 5 10 15

Tyr Pro Asp Cys Tyr Tyr Asn Leu Gly Cys Cys Leu Tyr Ala Asp Leu
20 25 30

Asn Arg His Val Asp Ala Leu Asn Ala Trp Arg Asn Ala Thr Val Leu
35 40 45

Lys Pro Glu His
50

<210> 3264
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R151C"

<400> 3264
Ala His Arg Val Ser Gly Ala Leu Ile Arg Pro Leu Pro Ser Gln Gln
1 5 10 15

Met Phe Glu His Met Gln Lys Arg His Cys Cys Val Phe Phe Val Tyr
20 25 30

Val Gly Gly Glu Ser Pro Leu Lys Glu Lys Tyr Ile Asp Ala Ala Ser
35 40 45

Glu Leu Ile Val
50

<210> 3265
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L47F"

<400> 3265
Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe Leu Ser Leu Phe Ser
1 5 10 15

Phe Leu Ile Val Ala Gly Ala Thr Thr Phe Phe Phe Cys Leu Leu His
20 25 30

Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro Arg Asp Leu Ser
35 40 45

Leu Ile Ser Pro
50

<210> 3266
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A232T"

<400> 3266
Ser Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala
1 5 10 15

Arg His Ala Trp Gln Leu Thr Gln Gly Thr Thr Thr Val Leu Gly Leu
20 25 30

Phe Arg Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser
35 40 45

Glu

<210> 3267
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<221> source
<223> /note="p.R73G"

<400> 3267
Leu Arg Ala Arg Leu Ala Ala Leu Glu Gly Asp Ala Ala Pro Ser Leu
1 5 10 15

Val Asp Ala Leu Leu Glu Gln Val Ala Gly Gly Phe Arg Glu Gln Leu
20 25 30

Arg Arg Gln Glu Gly Gly Ala Ala Glu Ala Gln Met Arg Gln Glu Ile
35 40 45

Glu Arg Leu Thr
50

<210> 3268
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A139T"

<400> 3268
Gln Pro Gln His Glu Arg Glu Lys Glu Val Val Leu Leu Arg Arg Ser
1 5 10 15

Met Ala Glu Gly Glu Arg Ala Arg Ala Thr Thr Ser Asp Val Leu Cys
20 25 30

Arg Ser Leu Ala Asn Glu Thr His Gln Leu Arg Arg Thr Leu Thr Ala
35 40 45

Thr Ala His Met
50

<210> 3269
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.P632fs"

<400> 3269
Pro Thr Arg Ala Leu Pro Arg Pro Leu His Pro Thr Pro Val Val Asp
1 5 10 15

Trp Asp Ala Arg Pro Leu Pro Pro Pro Ala Arg Leu
20 25

<210> 3270
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T619fs"

<400> 3270
His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu Leu Leu
1 5 10 15

Gln His Gly Ala Asp Pro Thr Lys Lys Lys Gln Gly Trp Lys Tyr Ser
20 25 30

Phe Gly Ser Cys
35

<210> 3271
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L692I"

<400> 3271
Ser Ala Val Met Asn Ser Gln Gln Ser Val Pro Ala Thr Met Asn Ala
1 5 10 15

Arg Thr Glu Leu Asp Ser Pro Arg Asp Ile Ile Met Val Thr Ala Ser
20 25 30

Ser Glu Thr Ser Ile Ser Leu Ile Trp Thr Lys Ala Ser Gly Pro Ile
35 40 45

Asp His Tyr Arg
50

<210> 3272
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P183S"

<400> 3272
Gly Gln Pro Ser Gln Arg Arg Tyr Val His Tyr Phe Ser Gly Leu Leu
1 5 10 15

Ser Gly Ser Ile Lys Met Asn Asn Lys Ser Ser Leu Phe Leu His His
20 25 30

Val Ile Met His Gly Ile Pro Asn Phe Glu Ser Lys Gly Gly Cys Arg
35 40 45

Pro Phe Leu Arg
50

<210> 3273
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V706fs"

<400> 3273
Glu Glu Pro Pro Ala Ser Ala Cys Pro Gly Gly Cys Gly Pro Arg Glu
1 5 10 15

Leu Cys Arg Ala Gly Gln Cys Val Cys Arg Gly Leu Pro Arg Pro
20 25 30

<210> 3274
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R736L"

<400> 3274
Asn Glu Arg Ser Ile Pro Ser Met Val Asp Gly Leu Lys Pro Gly Gln
1 5 10 15

Arg Lys Val Leu Phe Thr Cys Phe Lys Leu Leu Asn Asp Lys Arg Glu
20 25 30

Val Lys Val Ala Gln Leu Ala Gly Ser Val Ala Glu Met Ser Ser Tyr
35 40 45

His His Gly Glu
50

<210> 3275
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K1199E"

<400> 3275
Phe Ile Glu Glu Leu Glu Ala Val Glu Ala Lys Glu Lys Gln Asp Glu
1 5 10 15

Gln Val Gly Leu Pro Gly Lys Gly Gly Glu Glu Ala Lys Gly Lys Lys
20 25 30

Thr Gln Met Ala Glu Val Leu Pro Ser Pro Arg Gly Gln Arg Val Ile
35 40 45

Pro Arg Ile Thr
50

<210> 3276
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R656H"

<400> 3276
Ile Lys Tyr Tyr Lys Gly Leu Gly Thr Ser Thr Ala Lys Glu Ala Lys
1 5 10 15

Glu Tyr Phe Ala Asp Met Glu Arg His His His Ile Leu Phe Arg Tyr
20 25 30

Ala Gly Pro Glu Asp Asp Ala Ala Ile Thr Leu Ala Phe Ser Lys Lys
35 40 45

Lys Ile Asp Asp
50

<210> 3277
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I1381fs"

<400> 3277
Ile Leu Asp Val Leu Thr Gly Ile Asn Val Gln Gln Arg Arg Leu Ala

1 5 10 15

Leu Ala Ala Met Arg Trp Arg Lys Lys Ser Ser Lys Asp Lys Asn Leu
20 25 30

Ala Leu Leu Arg Glu His Leu Val Gly Gly Arg Leu Phe Tyr Met Trp
35 40 45

Ile Ser Leu Glu Lys Gln Ala Ser Asn Ala Phe Phe Ser Gln Glu Glu
50 55 60

Gln Arg Cys Tyr Leu Val Ile Leu Tyr Leu Tyr Leu Lys Arg Pro His
65 70 75 80

Ile Phe Phe Leu Thr
85

<210> 3278
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G146R"

<400> 3278
Pro Ser Asp Lys Val Gly Arg Ala Asp Ala His Leu Gly Ser Ser Ser
1 5 10 15

Val Ala Leu Pro Lys Glu Ala Ser Asp Arg Arg Thr Gly Ala Ser Gln
20 25 30

Glu Pro Pro Thr Thr Asp Ser Gln Glu Ala Gln Ser Pro Gly His Ser
35 40 45

Ser Ala Gly Gln
50

<210> 3279
<211> 39
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.F13L"

<400> 3279
Met Leu Arg Gly Pro Trp Arg Gln Leu Trp Leu Phe Leu Leu Leu Leu
1 5 10 15

Leu Leu Pro Gly Ala Pro Glu Pro Arg Gly Ala Ser Arg Pro Trp Glu
20 25 30

Gly Thr Asp Glu Pro Gly Ser
35

<210> 3280
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S354L"

<400> 3280
Arg Ala Ser Leu Val Ser Lys Ser Tyr Ser Glu Pro Val Asp Val Lys
1 5 10 15

Thr Ser Gln Pro Pro Gln Leu Ile Asn Leu Leu Lys Pro Ser Val Phe
20 25 30

His Gly Pro Ser Gln Ala His Ser Ala Leu Tyr Leu Ser Ser His Tyr
35 40 45

His Gln Gln Pro
50

<210> 3281
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R337L"

<400> 3281
Thr Ser Ser Ser Pro Gln Pro Lys Lys Lys Pro Leu Asp Gly Glu Tyr
1 5 10 15

Phe Thr Leu Gln Ile Arg Gly Arg Glu Leu Leu Phe Glu Met Phe Arg
20 25 30

Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly Lys Glu
35 40 45

Pro Gly Gly Ser
50

<210> 3282
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P58fs"

<400> 3282
Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
1 5 10 15

Asp Ile Glu Gln Trp Phe Thr Glu Asp Gln Val Gln Met Lys Leu Pro
20 25 30

Glu Cys Gln Arg Leu Leu Pro Pro Trp Pro Leu His Gln Gln Leu Leu
35 40 45

His Arg Arg Pro Leu His Gln Pro Pro Pro Gly Pro Cys His Leu Leu
50 55 60

Ser Leu Pro Arg Lys Pro Thr Arg Ala Ala Thr Val Ser Val Trp Ala
65 70 75 80

Ser Cys Ile Leu Gly Gln Pro Ser Leu
85

<210> 3283
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P72fs"

<400> 3283
Asp Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala
1 5 10 15

Pro Arg Met Pro Glu Ala Ala Pro Pro Trp Pro Leu His Gln Gln Leu
20 25 30

Leu His Arg Arg Pro Leu His Gln Pro Pro Pro Gly Pro Cys His Leu
35 40 45

Leu Ser Leu Pro Arg Lys Pro Thr Arg Ala Ala Thr Val Ser Val Trp
50 55 60

Ala Ser Cys Ile Leu Gly Gln Pro Ser Leu
65 70

<210> 3284
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G105C"

<400> 3284
Pro Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser
1 5 10 15

Ser Val Pro Ser Gln Lys Thr Tyr Gln Cys Cys Ser Tyr Gly Phe Arg

20 25 30

Leu Gly Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr
35 40 45

Ser Pro Ala Leu
50

<210> 3285
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G108fs"

<400> 3285
Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser Val Pro
1 5 10 15

Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Val Ser Val Trp Ala Ser Cys
20 25 30

Ile Leu Gly Gln Pro Ser Leu
35

<210> 3286
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R110fs"

<400> 3286
Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser Val Pro Ser Gln
1 5 10 15

Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Val Trp Ala Ser Cys Ile Leu
20 25 30

Gly Gln Pro Ser Leu
35

<210> 3287
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R110L"

<400> 3287
Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser Val Pro Ser Gln
1 5 10 15

Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Leu Leu Leu Gly Phe Leu His
20 25 30

Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro Ala Leu Asn
35 40 45

Lys Met Phe Cys
50

<210> 3288
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K132N"

<400> 3288
Tyr Gly Phe Arg Leu Gly Phe Leu His Ser Gly Thr Ala Lys Ser Val
1 5 10 15

Thr Cys Thr Tyr Ser Pro Ala Leu Asn Asn Asn Met Phe Cys Gln Leu
20 25 30

Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser Thr Pro Pro Pro
35 40 45

Gly Thr Arg Val
50

<210> 3289
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K132N"

<400> 3289
Tyr Gly Phe Arg Leu Gly Phe Leu His Ser Gly Thr Ala Lys Ser Val
1 5 10 15

Thr Cys Thr Tyr Ser Pro Ala Leu Asn Asn Asn Met Phe Cys Gln Leu
20 25 30

Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser Thr Pro Pro Pro
35 40 45

Gly Thr Arg Val
50

<210> 3290
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C141G"

<400> 3290
Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro Ala Leu Asn
1 5 10 15

Lys Met Phe Cys Gln Leu Ala Lys Thr Gly Gly Pro Val Gln Leu Trp
20 25 30

Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile
35 40 45

Tyr Lys Gln Ser
50

<210> 3291
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C141Y"

<400> 3291
Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro Ala Leu Asn
1 5 10 15

Lys Met Phe Cys Gln Leu Ala Lys Thr Tyr Tyr Pro Val Gln Leu Trp
20 25 30

Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile
35 40 45

Tyr Lys Gln Ser
50

<210> 3292
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V143M"

<400> 3292
Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro Ala Leu Asn Lys Met

1 5 10 15

Phe Cys Gln Leu Ala Lys Thr Cys Pro Met Met Gln Leu Trp Val Asp
20 25 30

Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys
35 40 45

Gln Ser Gln His
50

<210> 3293
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P151T"

<400> 3293
Tyr Ser Pro Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys
1 5 10 15

Pro Val Gln Leu Trp Val Asp Ser Thr Thr Thr Pro Pro Gly Thr Arg
20 25 30

Val Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val
35 40 45

Val Arg Arg Cys
50

<210> 3294
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P152fs"

<400> 3294
Ser Pro Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro
1 5 10 15

Val Gln Leu Trp Val Asp Ser Thr Pro Arg Pro Ala Pro Ala Ser Ala
20 25 30

Pro Trp Pro Ser Thr Ser Ser His Ser Thr
35 40

<210> 3295
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G154V"

<400> 3295
Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
1 5 10 15

Leu Trp Val Asp Ser Thr Pro Pro Pro Val Val Thr Arg Val Arg Ala
20 25 30

Met Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg
35 40 45

Cys Pro His His
50

<210> 3296
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T155N"

<400> 3296
Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu
1 5 10 15

Trp Val Asp Ser Thr Pro Pro Pro Gly Asn Asn Arg Val Arg Ala Met
20 25 30

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
35 40 45

Pro His His Glu
50

<210> 3297
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V157F"

<400> 3297
Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val
1 5 10 15

Asp Ser Thr Pro Pro Pro Gly Thr Arg Phe Phe Arg Ala Met Ala Ile
20 25 30

Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His
35 40 45

His Glu Arg Cys
50

<210> 3298
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.R158H"

<400> 3298
Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp
1 5 10 15

Ser Thr Pro Pro Pro Gly Thr Arg Val His His Ala Met Ala Ile Tyr
20 25 30

Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His
35 40 45

Glu Arg Cys Ser
50

<210> 3299
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R158L"

<400> 3299
Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp
1 5 10 15

Ser Thr Pro Pro Pro Gly Thr Arg Val Leu Leu Ala Met Ala Ile Tyr
20 25 30

Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His
35 40 45

Glu Arg Cys Ser
50

<210> 3300
<211> 52
<212> PRT
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<220>
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<220>
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<223> /note="p.A159P"

<400> 3300
Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser
1 5 10 15

Thr Pro Pro Pro Gly Thr Arg Val Arg Pro Pro Met Ala Ile Tyr Lys
20 25 30

Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu
35 40 45

Arg Cys Ser Asp
50

<210> 3301
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A159V"

<400> 3301
Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser
1 5 10 15

Thr Pro Pro Pro Gly Thr Arg Val Arg Val Val Met Ala Ile Tyr Lys
20 25 30

Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu
35 40 45

Arg Cys Ser Asp
50

<210> 3302
<211> 52
<212> PRT
<213> Artificial Sequence

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.Y163C"

<400> 3302
Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser Thr Pro Pro Pro
1 5 10 15

Gly Thr Arg Val Arg Ala Met Ala Ile Cys Cys Lys Gln Ser Gln His
20 25 30

Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser Asp
35 40 45

Ser Asp Gly Leu
50

<210> 3303
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V173M"

<400> 3303
Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr
1 5 10 15

Lys Gln Ser Gln His Met Thr Glu Val Met Met Arg Arg Cys Pro His
20 25 30

His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu
35 40 45

Ile Arg Val Glu
50

<210> 3304
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V173L"

<400> 3304
Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr
1 5 10 15

Lys Gln Ser Gln His Met Thr Glu Val Leu Leu Arg Arg Cys Pro His
20 25 30

His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu
35 40 45

Ile Arg Val Glu
50

<210> 3305
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R175G"

<400> 3305
Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln
1 5 10 15

Ser Gln His Met Thr Glu Val Val Arg Gly Gly Cys Pro His His Glu
20 25 30

Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg
35 40 45

Val Glu Gly Asn
50

<210> 3306
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R175C"

<400> 3306
Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln
1 5 10 15

Ser Gln His Met Thr Glu Val Val Arg Cys Cys Cys Pro His His Glu
20 25 30

Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg
35 40 45

Val Glu Gly Asn
50

<210> 3307
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R175H"

<400> 3307
Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln
1 5 10 15

Ser Gln His Met Thr Glu Val Val Arg His His Cys Pro His His Glu
20 25 30

Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg
35 40 45

Val Glu Gly Asn

50

<210> 3308
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C176Y"

<400> 3308
Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln Ser
1 5 10 15

Gln His Met Thr Glu Val Val Arg Arg Tyr Tyr Pro His His Glu Arg
20 25 30

Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg Val
35 40 45

Glu Gly Asn Leu
50

<210> 3309
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C176F"

<400> 3309
Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln Ser
1 5 10 15

Gln His Met Thr Glu Val Val Arg Arg Phe Phe Pro His His Glu Arg
20 25 30

Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg Val
35 40 45

Glu Gly Asn Leu
    50

<210> 3310
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="p.H179Y"

<400> 3310
Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met
1   5   10   15

Thr Glu Val Val Arg Arg Cys Pro His Tyr Tyr Glu Arg Cys Ser Asp
            20   25   30

Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn
        35   40   45

Leu Arg Val Glu
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<210> 3311
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.H179R"

<400> 3311
Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met
1   5   10   15

Thr Glu Val Val Arg Arg Cys Pro His Arg Arg Glu Arg Cys Ser Asp
            20   25   30

Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn
35 40 45

Leu Arg Val Glu
50

<210> 3312
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H179L"

<400> 3312
Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met
1 5 10 15

Thr Glu Val Val Arg Arg Cys Pro His Leu Leu Glu Arg Cys Ser Asp
20 25 30

Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn
35 40 45

Leu Arg Val Glu
50

<210> 3313
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P191del"

<400> 3313
Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg
1 5 10 15

Cys Ser Asp Ser Asp Gly Leu Ala Pro Gln His Leu Ile Arg Val Glu
20 25 30

Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His
35 40 45

Ser Val Val Val Pro
50

<210> 3314
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H193Y"

<400> 3314
His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser
1 5 10 15

Asp Ser Asp Gly Leu Ala Pro Pro Gln Tyr Tyr Leu Ile Arg Val Glu
20 25 30

Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His
35 40 45

Ser Val Val Val
50

<210> 3315
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H193R"

<400> 3315
His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser

1 5 10 15

Asp Ser Asp Gly Leu Ala Pro Pro Gln Arg Arg Leu Ile Arg Val Glu
20 25 30

Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His
35 40 45

Ser Val Val Val
50

<210> 3316
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H193L"

<400> 3316
His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser
1 5 10 15

Asp Ser Asp Gly Leu Ala Pro Pro Gln Leu Leu Leu Ile Arg Val Glu
20 25 30

Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His
35 40 45

Ser Val Val Val
50

<210> 3317
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L194R"

<400> 3317
Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser Asp
1 5 10 15

Ser Asp Gly Leu Ala Pro Pro Gln His Arg Arg Ile Arg Val Glu Gly
20 25 30

Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His Ser
35 40 45

Val Val Val Pro
50

<210> 3318
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I195T"

<400> 3318
Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser Asp Ser
1 5 10 15

Asp Gly Leu Ala Pro Pro Gln His Leu Thr Thr Arg Val Glu Gly Asn
20 25 30

Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His Ser Val
35 40 45

Val Val Pro Tyr
50

<210> 3319
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R196P"

<400> 3319
Glu Val Val Arg Arg Cys Pro His His Glu Arg Cys Ser Asp Ser Asp
1 5 10 15

Gly Leu Ala Pro Pro Gln His Leu Ile Pro Pro Val Glu Gly Asn Leu
20 25 30

Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His Ser Val Val
35 40 45

Val Pro Tyr Glu
50

<210> 3320
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G199V"

<400> 3320
Arg Arg Cys Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala
1 5 10 15

Pro Pro Gln His Leu Ile Arg Val Glu Val Val Asn Leu Arg Val Glu
20 25 30

Tyr Leu Asp Asp Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr
35 40 45

Glu Pro Pro Glu
50

<210> 3321
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.Y205C"

<400> 3321
Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile
1 5 10 15

Arg Val Glu Gly Asn Leu Arg Val Glu Cys Cys Leu Asp Asp Arg Asn
20 25 30

Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly
35 40 45

Ser Asp Cys Thr
50

<210> 3322
<211> 30
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R209fs"

<400> 3322
Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg Val Glu Gly
1 5 10 15

Asn Leu Arg Val Glu Tyr Leu Asp Asp Lys His Phe Ser Thr
20 25 30

<210> 3323
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.H214R"

<400> 3323
Ala Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu
1 5 10 15

Tyr Leu Asp Asp Arg Asn Thr Phe Arg Arg Arg Ser Val Val Val Pro
20 25 30

Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn
35 40 45

Tyr Met Cys Asn
50

<210> 3324
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S215I"

<400> 3324
Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr
1 5 10 15

Leu Asp Asp Arg Asn Thr Phe Arg His Ile Ile Val Val Val Pro Tyr
20 25 30

Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr
35 40 45

Met Cys Asn Ser
50

<210> 3325
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S215R"

<400> 3325
Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr
1 5 10 15

Leu Asp Asp Arg Asn Thr Phe Arg His Arg Arg Val Val Val Pro Tyr
20 25 30

Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr
35 40 45

Met Cys Asn Ser
50

<210> 3326
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V216M"

<400> 3326
Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu
1 5 10 15

Asp Asp Arg Asn Thr Phe Arg His Ser Met Met Val Val Pro Tyr Glu
20 25 30

Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met
35 40 45

Cys Asn Ser Ser
50

<210> 3327
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.Y220S"

<400> 3327
Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn
1 5 10 15

Thr Phe Arg His Ser Val Val Val Pro Ser Ser Glu Pro Pro Glu Val
20 25 30

Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser
35 40 45

Cys Met Gly Gly
50

<210> 3328
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.Y220C"

<400> 3328
Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn
1 5 10 15

Thr Phe Arg His Ser Val Val Val Pro Cys Cys Glu Pro Pro Glu Val
20 25 30

Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser
35 40 45

Cys Met Gly Gly
50

<210> 3329
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.Y234C"

<400> 3329
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
1 5 10 15

Val Gly Ser Asp Cys Thr Thr Ile His Cys Cys Asn Tyr Met Cys Asn
20 25 30

Ser Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile
35 40 45

Thr Leu Glu Asp
50

<210> 3330
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.Y236D"

<400> 3330
Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly
1 5 10 15

Ser Asp Cys Thr Thr Ile His Tyr Asn Asp Asp Met Cys Asn Ser Ser
20 25 30

Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu
35 40 45

Glu Asp Ser Ser
50

<210> 3331

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y236C"

<400> 3331
Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly
1 5 10 15

Ser Asp Cys Thr Thr Ile His Tyr Asn Cys Cys Met Cys Asn Ser Ser
20 25 30

Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu
35 40 45

Glu Asp Ser Ser
50

<210> 3332
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M237I"

<400> 3332
Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser
1 5 10 15

Asp Cys Thr Thr Ile His Tyr Asn Tyr Ile Ile Cys Asn Ser Ser Cys
20 25 30

Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu
35 40 45

Asp Ser Ser Gly
50

<210> 3333
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M237I"

<400> 3333
Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser
1 5 10 15

Asp Cys Thr Thr Ile His Tyr Asn Tyr Ile Ile Cys Asn Ser Ser Cys
20 25 30

Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu
35 40 45

Asp Ser Ser Gly
50

<210> 3334
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.C238Y"

<400> 3334
Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp
1 5 10 15

Cys Thr Thr Ile His Tyr Asn Tyr Met Tyr Tyr Asn Ser Ser Cys Met
20 25 30

Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp
35 40 45

Ser Ser Gly Asn
50

<210> 3335
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C238F"

<400> 3335
Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp
1 5 10 15

Cys Thr Thr Ile His Tyr Asn Tyr Met Phe Phe Asn Ser Ser Cys Met
20 25 30

Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp
35 40 45

Ser Ser Gly Asn
50

<210> 3336
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S241Y"

<400> 3336
Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr
1 5 10 15

Ile His Tyr Asn Tyr Met Cys Asn Ser Tyr Tyr Cys Met Gly Gly Met
20 25 30

Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly
35 40 45

Asn Leu Leu Gly
50

<210> 3337
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S241F"

<400> 3337
Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr
1 5 10 15

Ile His Tyr Asn Tyr Met Cys Asn Ser Phe Phe Cys Met Gly Gly Met
20 25 30

Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly
35 40 45

Asn Leu Leu Gly
50

<210> 3338
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.S241fs"

<400> 3338
Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile
1 5 10 15

His Tyr Asn Tyr Met Cys Asn Ser Ser Ala Trp Ala Ala

20 25

<210> 3339
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C242F"

<400> 3339
Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile
1 5 10 15

His Tyr Asn Tyr Met Cys Asn Ser Ser Phe Phe Met Gly Gly Met Asn
20 25 30

Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn
35 40 45

Leu Leu Gly Arg
50

<210> 3340
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 3340
Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr
1 5 10 15

Asn Tyr Met Cys Asn Ser Ser Cys Met Cys Cys Gly Met Asn Arg Arg
20 25 30

Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu
35 40 45

Gly Arg Asn Ser
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<210> 3341
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G244D"

<400> 3341
Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr
1 5 10 15

Asn Tyr Met Cys Asn Ser Ser Cys Met Asp Asp Gly Met Asn Arg Arg
20 25 30

Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu
35 40 45

Gly Arg Asn Ser
50

<210> 3342
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G245S"

<400> 3342
Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn
1 5 10 15

Tyr Met Cys Asn Ser Ser Cys Met Gly Ser Ser Met Asn Arg Arg Pro
20 25 30

Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly
35 40 45

Arg Asn Ser Phe
50

<210> 3343
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G245D"

<400> 3343
Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn
1 5 10 15

Tyr Met Cys Asn Ser Ser Cys Met Gly Asp Asp Met Asn Arg Arg Pro
20 25 30

Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly
35 40 45

Arg Asn Ser Phe
50

<210> 3344
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G245V"

<400> 3344
Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn
1 5 10 15

Tyr Met Cys Asn Ser Ser Cys Met Gly Val Val Met Asn Arg Arg Pro
20 25 30

Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly
35 40 45

Arg Asn Ser Phe
50

<210> 3345
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R248W"

<400> 3345
Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys
1 5 10 15

Asn Ser Ser Cys Met Gly Gly Met Asn Trp Trp Arg Pro Ile Leu Thr
20 25 30

Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser
35 40 45

Phe Glu Val Arg
50

<210> 3346
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> source
<223> /note="p.R248Q"

<400> 3346
Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys

1 5 10 15

Asn Ser Ser Cys Met Gly Gly Met Asn Gln Gln Arg Pro Ile Leu Thr
20 25 30

Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser
35 40 45

Phe Glu Val Arg
50

<210> 3347
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R248P"

<400> 3347
Pro Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys
1 5 10 15

Asn Ser Ser Cys Met Gly Gly Met Asn Pro Pro Arg Pro Ile Leu Thr
20 25 30

Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser
35 40 45

Phe Glu Val Arg
50

<210> 3348
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R249G"

<400> 3348
Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn
1 5 10 15

Ser Ser Cys Met Gly Gly Met Asn Arg Gly Gly Pro Ile Leu Thr Ile
20 25 30

Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe
35 40 45

Glu Val Arg Val
50

<210> 3349
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R249M"

<400> 3349
Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn
1 5 10 15

Ser Ser Cys Met Gly Gly Met Asn Arg Met Met Pro Ile Leu Thr Ile
20 25 30

Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe
35 40 45

Glu Val Arg Val
50

<210> 3350
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R249S"

<400> 3350
Glu Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn
1 5 10 15

Ser Ser Cys Met Gly Gly Met Asn Arg Ser Ser Pro Ile Leu Thr Ile
20 25 30

Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe
35 40 45

Glu Val Arg Val
50

<210> 3351
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P250L"

<400> 3351
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
1 5 10 15

Ser Cys Met Gly Gly Met Asn Arg Arg Leu Leu Ile Leu Thr Ile Ile
20 25 30

Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu
35 40 45

Val Arg Val Cys
50

<210> 3352
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.I255F"

<400> 3352
Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met Gly Gly
1 5 10 15

Met Asn Arg Arg Pro Ile Leu Thr Ile Phe Phe Thr Leu Glu Asp Ser
20 25 30

Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala
35 40 45

Cys Pro Gly Arg
50

<210> 3353
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D259Y"

<400> 3353
Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met Gly Gly Met Asn Arg Arg
1 5 10 15

Pro Ile Leu Thr Ile Ile Thr Leu Glu Tyr Tyr Ser Ser Gly Asn Leu
20 25 30

Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg
35 40 45

Asp Arg Arg Thr
50

<210> 3354
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G262V"

<400> 3354
Met Cys Asn Ser Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu
1 5 10 15

Thr Ile Ile Thr Leu Glu Asp Ser Ser Val Val Asn Leu Leu Gly Arg
20 25 30

Asn Ser Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg
35 40 45

Thr Glu Glu Glu
50

<210> 3355
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G266R"

<400> 3355
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
1 5 10 15

Leu Glu Asp Ser Ser Gly Asn Leu Leu Arg Arg Arg Asn Ser Phe Glu
20 25 30

Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu
35 40 45

Asn Leu Arg Lys
50

<210> 3356
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G266E"

<400> 3356
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
1 5 10 15

Leu Glu Asp Ser Ser Gly Asn Leu Leu Glu Glu Arg Asn Ser Phe Glu
20 25 30

Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu
35 40 45

Asn Leu Arg Lys
50

<210> 3357
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.G266V"

<400> 3357
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
1 5 10 15

Leu Glu Asp Ser Ser Gly Asn Leu Leu Val Val Arg Asn Ser Phe Glu
20 25 30

Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu
35 40 45

Asn Leu Arg Lys
50

<210> 3358
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R267P"

<400> 3358
Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu
1 5 10 15

Glu Asp Ser Ser Gly Asn Leu Leu Gly Pro Pro Asn Ser Phe Glu Val
20 25 30

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
35 40 45

Leu Arg Lys Lys
50

<210> 3359
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E271K"

<400> 3359
Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser
1 5 10 15

Gly Asn Leu Leu Gly Arg Asn Ser Phe Lys Lys Val Arg Val Cys Ala
20 25 30

Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys
35 40 45

Gly Glu Pro His
50

<210> 3360
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V272M"

<400> 3360
Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly
1 5 10 15

Asn Leu Leu Gly Arg Asn Ser Phe Glu Met Met Arg Val Cys Ala Cys
20 25 30

Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly
35 40 45

Glu Pro His His
50

<210> 3361
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R273C"

<400> 3361
Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn
1 5 10 15

Leu Leu Gly Arg Asn Ser Phe Glu Val Cys Cys Val Cys Ala Cys Pro
20 25 30

Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu

35 40 45

Pro His His Glu
50

<210> 3362
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R273H"

<400> 3362
Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn
1 5 10 15

Leu Leu Gly Arg Asn Ser Phe Glu Val His His Val Cys Ala Cys Pro
20 25 30

Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu
35 40 45

Pro His His Glu
50

<210> 3363
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R273L"

<400> 3363
Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn
1 5 10 15

Leu Leu Gly Arg Asn Ser Phe Glu Val Leu Leu Val Cys Ala Cys Pro
20 25 30

Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu
35 40 45

Pro His His Glu
50

<210> 3364
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V274F"

<400> 3364
Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu
1 5 10 15

Leu Gly Arg Asn Ser Phe Glu Val Arg Phe Phe Cys Ala Cys Pro Gly
20 25 30

Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro
35 40 45

His His Glu Leu
50

<210> 3365
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.C275Y"

<400> 3365
Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu
1 5 10 15

Gly Arg Asn Ser Phe Glu Val Arg Val Tyr Tyr Ala Cys Pro Gly Arg
20 25 30

Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro His
35 40 45

His Glu Leu Pro
50

<210> 3366
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C275F"

<400> 3366
Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu
1 5 10 15

Gly Arg Asn Ser Phe Glu Val Arg Val Phe Phe Ala Cys Pro Gly Arg
20 25 30

Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro His
35 40 45

His Glu Leu Pro
50

<210> 3367
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C277F"

<400> 3367

Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg
1 5 10 15

Asn Ser Phe Glu Val Arg Val Cys Ala Phe Phe Pro Gly Arg Asp Arg
20 25 30

Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu
35 40 45

Leu Pro Pro Gly
50

<210> 3368
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P278S"

<400> 3368
Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn
1 5 10 15

Ser Phe Glu Val Arg Val Cys Ala Cys Ser Ser Gly Arg Asp Arg Arg
20 25 30

Thr Glu Glu Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu
35 40 45

Pro Pro Gly Ser
50

<210> 3369
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.D281N"

<400> 3369
Thr Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu
1 5 10 15

Val Arg Val Cys Ala Cys Pro Gly Arg Asn Asn Arg Arg Thr Glu Glu
20 25 30

Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly
35 40 45

Ser Thr Lys Arg
50

<210> 3370
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R282W"

<400> 3370
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
1 5 10 15

Arg Val Cys Ala Cys Pro Gly Arg Asp Trp Trp Arg Thr Glu Glu Glu
20 25 30

Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser
35 40 45

Thr Lys Arg Ala
50

<210> 3371
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E285K"

<400> 3371
Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys
1 5 10 15

Ala Cys Pro Gly Arg Asp Arg Arg Thr Lys Lys Glu Glu Asn Leu Arg
20 25 30

Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg
35 40 45

Ala Leu Pro Asn
50

<210> 3372
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E286K"

<400> 3372
Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala
1 5 10 15

Cys Pro Gly Arg Asp Arg Arg Thr Glu Lys Lys Glu Asn Leu Arg Lys
20 25 30

Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala
35 40 45

Leu Pro Asn Asn
50

<210> 3373
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S315fs"

<400> 3373
Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala
1 5 10 15

Leu Pro Asn Asn Thr Ser Ser Ser Pro Ala Lys Glu Glu Thr Thr Gly
20 25 30

Trp Arg Ile Phe His Pro Ser Asp Pro Trp Ala
35 40

<210> 3374
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.L174fs"

<400> 3374
Val Leu Ala Arg Met His Asp Glu Asp Leu Ile His Gly Asp Leu Thr
1 5 10 15

Thr Ser Asn Met Leu Leu Lys Pro Pro Trp Asn Ser
20 25

<210> 3375
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S398T"

<400> 3375

Ala Ala Cys Ala Pro Glu Pro Gly Ile Pro Gly Glu Thr Arg Gly Pro
1 5 10 15

Cys Phe Leu Ala Gly Asp Gly Arg Ala Thr Thr Glu Val Pro Ser Leu
20 25 30

Thr Ala Leu His Thr Leu Trp Leu Arg Glu His Asn Arg Leu Ala Ala
35 40 45

Ala Leu Lys Ala
50

<210> 3376
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E558K"

<400> 3376
Gly Gly Leu Asp Pro Leu Ile Arg Gly Leu Leu Ala Arg Pro Ala Lys
1 5 10 15

Leu Gln Val Gln Asp Gln Leu Met Asn Lys Lys Glu Leu Thr Glu Arg
20 25 30

Leu Phe Val Leu Ser Asn Ser Ser Thr Leu Asp Leu Ala Ser Ile Asn
35 40 45

Leu Gln Arg Gly
50

<210> 3377
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.A826T"

<400> 3377
Ala Asp Gly Ala His Pro Pro Cys His Ala Ser Ala Arg Cys Arg Asn
1 5 10 15

Thr Lys Gly Gly Phe Gln Cys Leu Cys Thr Thr Asp Pro Tyr Glu Leu
20 25 30

Gly Asp Asp Gly Arg Thr Cys Val Asp Ser Gly Arg Leu Pro Arg Val
35 40 45

Thr Trp Ile Ser
50

<210> 3378
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R30K"

<400> 3378
Ala Lys Pro Ala Lys Ala Ala Asn Arg Thr Pro Pro Lys Ser Pro Gly
1 5 10 15

Asp Pro Ser Lys Asp Arg Ala Ala Lys Lys Lys Leu Ser Leu Glu Ser
20 25 30

Glu Gly Ala Gly Glu Gly Ala Ala Ala Ser Pro Glu Leu Ser Ala Leu
35 40 45

Glu Glu Ala Phe
50

<210> 3379
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S2155L"

<400> 3379
Glu Asp Arg Thr Val Pro Ser Thr Pro Thr Leu Val Val Pro His Arg
1 5 10 15

Thr Asp Gly Phe Ala Glu Ala Ile His Leu Leu Pro Gln Val Ala Gly
20 25 30

Val Pro Arg Phe Arg Phe Gly Pro Pro Glu Asp Met Pro Gln Thr Ser
35 40 45

Ser Ser His Ser
50

<210> 3380
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S200P"

<400> 3380
Asn Pro Gly Pro Ile Pro Gly Pro Asn Pro Gly Pro Ile Pro Gly Pro
1 5 10 15

Ile Ser Gly Pro Ile Pro Gly Pro Ile Pro Pro Val Pro Ile Pro Gly
20 25 30

Pro Ile Pro Gly Pro Ile Ser Gly Pro Ile Ser Gly Pro Asn Pro Gly
35 40 45

Pro Ile Pro Gly
50

<210> 3381
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S423L"

<400> 3381
Ala Gln Val Lys His Leu Tyr Asn Trp Asn Leu Pro Pro Arg Arg Ile
1 5 10 15

Leu Phe Ile Lys His Phe Ile Ile Tyr Leu Leu Ile Pro Arg Tyr Val
20 25 30

Arg Asp Leu Lys Ile Gln Ile Glu Met Glu Lys Lys Val Val Phe Ser
35 40 45

Thr Ile Ser Leu
50

<210> 3382
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.M541I"

<400> 3382
Asp Asn Leu His Lys Gln Lys Ala Arg Arg Ile Tyr Pro Ser Asp Phe
1 5 10 15

Ala Val Glu Ile Leu Phe Gly Glu Lys Ile Ile Thr Ser Ser Asp Val
20 25 30

Val Ala Gly Ser Asp
35

<210> 3383
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R258Q"

<400> 3383
Phe Pro Ser Ser Gly Arg Gln Ser Phe Tyr Arg Asn Pro Ile Glu Glu
1 5 10 15

Val Val Arg Phe Leu Asp Lys Lys His Gln Gln Asn His Tyr Arg Val
20 25 30

Tyr Asn Leu Cys Ser Glu Arg Ala Tyr Asp Pro Lys His Phe His Asn
35 40 45

Arg Val Ser Arg
50

<210> 3384
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S9F"

<400> 3384
Met Glu Ser Ser Lys Lys Met Asp Phe Phe Pro Gly Ala Leu Gln Thr
1 5 10 15

Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val
20 25 30

Phe Val Pro
35

<210> 3385
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R11H"

<400> 3385
Met Ser Ser Gly Lys Ser Ala Arg Tyr Asn His His Phe Ser Gly Gly
1 5 10 15

Pro Ser Asn Leu Pro Thr Pro Asp Val Thr Thr Gly Thr Arg Met Glu
20 25 30

Thr Thr Phe Gly Pro
35

<210> 3386
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.D627N"

<400> 3386
Asp Pro Arg Pro Gly Val Val Thr Lys Gly Phe Arg Thr Leu Asp Val
1 5 10 15

Asp Leu Asp Glu Val Tyr Cys Leu Asn Asn Asn Phe Glu Glu Asp Asp
20 25 30

Thr Gly Asp His Ile Ser Leu Pro Arg Leu Ala Thr Ser Thr Pro Val
35 40 45

Gln His Pro Glu
50

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<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.E41Q"

<400> 3387
His Glu Phe Val Leu Gln Asn His Ala Asp Ile Val Ser Cys Val Ala
1 5 10 15

Met Val Phe Leu Leu Gly Leu Met Phe Gln Gln Ile Thr Ala Lys Ala
20 25 30

Ser Ile Ile Phe Val Thr Leu Gln Tyr Asn Val Thr Leu Pro Ala Thr
35 40 45

Glu Glu Gln Ala
50

<210> 3388
<211> 38
<212> PRT
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<223> /note="p.R345fs"

<400> 3388
Leu Gln Arg Trp Val Glu Asp Ser Asn Ile Gln Ala Ser Cys Met Lys
1 5 10 15

Lys Lys Arg Ser Arg Ser Ser Lys Lys Glu Gln Lys Thr Glu Trp Glu
20 25 30

Trp Lys Leu Gln Ile Glu
35

<210> 3389
<211> 52
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<220>
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<220>
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<223> /note="p.E846K"

<400> 3389
Tyr Asn Ile Ser Arg Arg Leu Ser Lys Leu Arg Val Leu Pro Trp Ser
1 5 10 15

Ile His Glu Leu Tyr Gly Asp Glu Ile Lys Lys Asp Phe Thr Gln Ala
20 25 30

Glu Leu Ala Leu Leu Met Lys Cys Ile Asn Asp Pro Asn Ser Met Phe
35 40 45

Leu Thr Gly Asp
50

<210> 3390
<211> 42
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.K133fs"

<400> 3390
Trp Gln Asn Val Leu Lys Ala His Ser Ser Val Asp Trp Leu Ile Val
1 5 10 15

Ile Val Glu Asn Asp Ala Lys Lys Lys Lys Gln Asn Gln His Pro Ser
20 25 30

Pro Asn Leu Tyr Cys Gly Gln Asn Lys Lys
35 40

<210> 3391
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="p.R568Q"

<400> 3391
Met Asn Glu Ser Pro Asp Pro Glu Pro Asp Cys Asp Ile Leu Ala Val
1 5 10 15

Lys Thr Ala Gln Lys Leu Trp Ala Asp Gln Gln Ile Ser Leu Ala Gly
20 25 30

Ser Asn Ile Phe Thr Ile Gly Val Gln Asp Phe Val Pro Phe Val Gln
35 40 45

Cys Lys Ala Lys
50

<210> 3392
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.*730Y"

<400> 3392
Pro Phe Thr Pro Ala Asp Arg Pro Gly Glu Ser Ser Gly Gln Ala Asn
1 5 10 15

Ser Pro Gly Gln Lys Gln Gln Gly Gln Tyr Tyr Thr His Met Tyr Asp
20 25 30

Pro Tyr Lys Cys Phe Lys Ile Leu Lys Met
35 40

<210> 3393
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R396Q"

<400> 3393
Gln Gln Gln Phe Thr Glu Val Ala Asp His Ile Gln Leu Asp Ala Ser
1 5 10 15

Ile Pro Val Thr Phe Thr Lys Asp Asn Gln Gln Val His Ile Gly Pro
20 25 30

Lys Met Glu Ile Arg Val Val Thr Leu Gly Leu Asp Gly Ala Gly Lys
35 40 45

Thr Thr Ile Leu
50

<210> 3394
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R289Q"

<400> 3394
Ile Val Glu Asp Gly Ile Gly Met Ala His Thr Glu His Val Pro Gly
1 5 10 15

Thr Ala Glu Asn Ala Arg Ser Cys Ile Gln Gln Ala Tyr Phe Tyr Asp
20 25 30

Leu His Glu Thr Leu Cys Arg Gln Glu Glu Met Ala Leu Ser Val Val
35 40 45

Asp Ala His Val
50

<210> 3395
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R398L"

<400> 3395
Asn Val Phe Thr Ser Gly Lys His Tyr Trp Glu Val Glu Ser Arg Asp
1 5 10 15

Ser Leu Glu Val Ala Val Gly Val Cys Leu Leu Glu Asp Val Met Gly
20 25 30

Ile Thr Asp Arg Ser Lys Met Ser Pro Asp Val Gly Ile Trp Ala Ile
35 40 45

Tyr Trp Ser Ala
50

<210> 3396
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q127K"

<400> 3396
Thr Phe His Lys Gly Arg Leu Arg Ser Ile His Thr Ser Ser Lys Thr
1 5 10 15

Ala Leu Arg Thr Gly Ser Ser Asp Thr Lys Lys Val Asp Glu Val Lys
20 25 30

Ser Ile Pro Ala Asn Ser His Leu Val Asn His Leu Asn Cys Pro Met
35 40 45

Cys Ser Arg Leu
50

<210> 3397
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3397
Cys Phe Glu Cys Ile Lys Thr Ile Gln Gln Arg Asn Leu Lys Thr Asn
1 5 10 15

Ile Arg Leu Lys Lys Met Ala Ser Leu Asp Asp Arg Lys Ala Ser Leu
20 25 30

Trp Leu Phe Leu Ser Ser Glu Glu Gln Met Cys Gly Ile His Arg Glu
35 40 45

Thr Lys Lys Met
50

<210> 3398
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K98N"

<400> 3398
Ser Leu Thr Glu Ile Ala Lys Gln Leu Gln Ile Arg Ser Lys Lys Arg
1 5 10 15

Lys Arg Gln Glu Glu Lys His Val Cys Asn Asn Lys His Asn Gln Val
20 25 30

Leu Thr Phe Phe Cys Gln Lys Asp Leu Glu Leu Leu Cys Pro Arg Cys
35 40 45

Ser Leu Ser Thr
50

<210> 3399
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.L332I"

<400> 3399
Met Lys Asn Lys Val Trp Asn Val Ser Leu Lys Thr Phe Val Leu Lys
1 5 10 15

Gly Met Leu Lys Lys Phe Lys Glu Asp Ile Ile Arg Gly Glu Leu Glu
20 25 30

Lys Glu Glu Lys Val Glu Leu Thr Leu Asp Pro Asp Thr Ala Asn Pro
35 40 45

Arg Leu Ile Leu
50

<210> 3400
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R337S"

<400> 3400
Phe Glu Ala Cys Leu Val Ala Gln Cys Asp Ala Leu Ile Asp Ala Leu
1 5 10 15

Asn Arg Arg Lys Ala Gln Leu Leu Ala Ser Ser Val Asn Lys Glu His
20 25 30

Glu His Lys Leu Lys Val Val Arg Asp Gln Ile Ser His Cys Thr Val
35 40 45

Lys Leu Arg Gln
50

<210> 3401

<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3401
Asp Leu Phe Ser Leu Ile Gly Leu Lys Ile Gly Asp Asp Tyr Ser Leu
1 5 10 15

Trp Val Ser Ser Pro Leu Lys Gly Gln Gln Gln Val Arg Glu Pro Val
20 25 30

Cys Lys Val Gly Val Phe Leu Asp Tyr Glu Ser Gly His Ile Ala Phe
35 40 45

Tyr Asn Gly Thr
50

<210> 3402
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R661W"

<400> 3402
Gln Thr Gly Glu Cys Asp Pro Glu Glu Ile Tyr Gln Ala Ala His Gln
1 5 10 15

Leu Glu Asp Arg Ile Gln Asp Phe Val Trp Trp Arg Val Glu Gln Arg
20 25 30

Lys Ile Leu Leu Asp Met Ser Val Ser Phe His Thr His Val Lys Glu
35 40 45

Leu Trp Thr Trp
50

<210> 3403
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H1300R"

<400> 3403
Asp Leu Pro Pro Pro Arg Arg Leu Ala Gln Arg Gln Pro Gly Pro Gln
1 5 10 15

Ala Gln Cys Ser Ser Gly Gly Arg Thr Arg Arg Ser Pro Gly Arg Ala
20 25 30

Glu Val Glu Arg Leu Phe Gly Gln Glu Arg Arg Lys Ser Glu Ala Ala
35 40 45

Gly Ala Phe Gln
50

<210> 3404
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K541fs"

<400> 3404
Asp Gln Leu Ser Lys Gln Gln Asn Glu Gly Asp Ser Ile Ile Ser Lys
1 5 10 15

Leu Lys Gln Asp Leu Asn Asp Glu Lys Arg Glu Phe Ile Asn Leu Lys
20 25 30

Met Ile Lys Trp Thr Leu Leu Lys Ser
35 40

<210> 3405
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1775P"

<400> 3405
Lys Leu Met Ala Lys Ala Ile Met Asp Phe Arg Leu Val Asp Leu Pro
1 5 10 15

Leu Gly Leu Pro Phe Tyr Lys Trp Met Pro Pro Arg Gln Glu Thr Ser
20 25 30

Leu Thr Ser His Asp Leu Phe Asp Ile Asp Pro Val Val Ala Arg Ser
35 40 45

Val Tyr His Leu
50

<210> 3406
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S244I"

<400> 3406
Ala Leu Ala Ala Arg Gly Phe Ser Glu Leu Ser Thr Leu Glu Val Leu
1 5 10 15

Pro Gln Val Tyr Asn Val Arg Thr Val Ile Ile Leu Pro Pro Pro Asp
20 25 30

Leu Gly Thr Gly Thr Asp Gly Pro Ala Gly Ser Asp Thr Ser Pro Phe
35 40 45

Arg Ser Gly Thr
50

<210> 3407
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K54N"

<400> 3407
Thr Glu Asp Phe Lys Glu Ser Leu Lys Val Val Phe Glu Gly Ser Ala
1 5 10 15

Tyr Gly Leu Gln Asn Phe Asn Lys Gln Asn Asn Lys Leu Lys Arg Cys
20 25 30

Asp Asp Met Asp Thr Phe Phe Leu His Tyr Ala Ala Ala Glu Gly Gln
35 40 45

Ile Glu Leu Met
50

<210> 3408
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T673fs"

<400> 3408
Asp Lys Ser Cys Arg Asp Tyr Tyr Ile Glu Tyr Asn Phe Lys Tyr Leu
1 5 10 15

Gln Cys Pro Leu Glu Phe Thr Lys Lys His Leu His Arg Met Leu Tyr
20 25 30

Met Asn Arg Leu Gln Pro Ser Thr Gln Trp Tyr Lys Ile Thr Ala

35 40 45

<210> 3409
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S490L"

<400> 3409
Pro Arg Glu Glu Trp Glu Met Trp His Pro Thr Leu Ile Ala Glu Ala
1 5 10 15

Leu Phe Ala Ile Ser Asn Ile Leu Ser Leu Leu Leu Arg Leu Ile Ser
20 25 30

Leu Phe Thr Ala Asn Ser His Leu Gly Pro Leu Gln Ile Ser Leu Gly
35 40 45

Arg Met Leu Leu
50

<210> 3410
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R429W"

<400> 3410
Thr Arg Thr Gln Ala Gln His Leu Phe Ile Ile Leu Met Glu Cys Met
1 5 10 15

Lys Lys Lys Glu Leu Ile Thr Val Phe Trp Trp Met Gly Ser Glu Gly
20 25 30

His Gln Asp Ile Asp Leu Ala Ile Leu Thr Ala Leu Leu Lys Gly Ala
35 40 45

Asn Ala Ser Ala
50

<210> 3411
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G298W"

<400> 3411
Gln Thr Met Ser Asn Pro Met Ser Lys Leu Thr Val Leu Asn Ser Met
1 5 10 15

His Ser His Phe Ile Leu Ala Asp Asn Trp Trp Thr Thr Gly Lys Tyr
20 25 30

Gly Ala Glu Val Lys Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu
35 40 45

Gln Lys Ile Asn
50

<210> 3412
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R995H"

<400> 3412
Ile Ala Lys Met Thr Ala Asn Met Phe Tyr Ile Val Ile Ile Met Ala
1 5 10 15

Ile Val Leu Leu Ser Phe Gly Val Ala His His Lys Ala Ile Leu Ser
20 25 30

Pro Lys Glu Pro Pro Ser Trp Ser Leu Ala Arg Asp Ile Val Phe Glu
35 40 45

Pro Tyr Trp Met
50

<210> 3413
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R843Q"

<400> 3413
Val Arg Ile Leu Asp Ser Asn Glu Gly Lys Asn Glu Met Glu Ile Gln
1 5 10 15

Met Lys Ser Lys Lys Leu Pro Ile Thr Gln Gln Lys Phe Tyr Ala Phe
20 25 30

Tyr His Ala Pro Ile Val Lys Phe Trp Phe Asn Thr Leu Ala Tyr Leu
35 40 45

Gly Phe Leu Met
50

<210> 3414
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1862C"

<400> 3414
Pro Gln Asp Glu Pro Ser Asp Leu Asn Leu Gln Pro Gly Asn Ser Thr
1 5 10 15

Lys Glu Ser Glu Ser Thr Asn Ser Val Cys Cys Leu Met Leu
20 25 30

<210> 3415
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H765fs"

<400> 3415
Val Phe Tyr Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met
1 5 10 15

Asp Phe His Ser Val Pro His Pro Pro Arg Ala Gly Pro Val Leu Ala
20 25 30

Gly Leu Cys Pro Leu Leu
35

<210> 3416
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1125W"

<400> 3416
Ile Glu Lys Tyr Gln Tyr Pro Leu Phe Gly Leu Pro Phe Val His Asn
1 5 10 15

Asp Phe Gln Ser Glu Ala Asp Trp Leu Trp Trp Phe Trp Ser Lys Tyr
20 25 30

Lys Leu Ser Val Pro Gly Asn Pro His Tyr Leu Ser His Val Pro Gly
35 40 45

Leu Pro Asn Pro

50

<210> 3417
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L627del"

<400> 3417
Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe Gln Glu Gln Leu His
1 5 10 15

Phe Arg Gly Met Val Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr
20 25 30

Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Met Ser Glu Thr Val Asn
35 40 45

Ser Val Ala Thr Asp
50

<210> 3418
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A218E"

<400> 3418
Phe Ala Glu Glu Asn Asp Ile Leu Gly Arg Phe Ile Asn Ala Glu Tyr
1 5 10 15

Thr Glu Glu Ala Tyr Glu Gly Gln Thr Glu Glu Leu Asn Ile Ala Ile
20 25 30

Glu Arg Arg Gln Gly Asp Ile Ala Ala Leu Leu Ile Ala Ala Gly Ala
35 40 45

Asp Val Asn Ala
50

<210> 3419
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R492H"

<400> 3419
Tyr Phe Thr Arg Gly Phe Gln Met Leu Gly Pro Phe Thr Ile Met Ile
1 5 10 15

Gln Lys Met Ile Phe Gly Asp Leu Met His His Phe Cys Trp Leu Met
20 25 30

Ala Val Val Ile Leu Gly Phe Ala Ser Ala Phe Tyr Ile Ile Phe Gln
35 40 45

Thr Glu Asp Pro
50

<210> 3420
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R3515W"

<400> 3420
Thr His Tyr Tyr Ile Lys Ile Ala Arg Phe Met Pro Arg Val Glu Ile
1 5 10 15

Val Gln Lys His Asn Thr Ala Ala Arg Trp Trp Leu Tyr Ile Arg Gly
20 25 30

His Asn Gly Lys Ile Tyr Pro Tyr Leu Val Met Asn Asp Ala Cys Leu
35 40 45

Thr Glu Ser Arg
50

<210> 3421
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A973S"

<400> 3421
Asp Cys Leu Lys Ser Ala Asn Thr Glu Pro Tyr Tyr Arg Arg Gln Ala
1 5 10 15

Trp Glu Val Ile Lys Cys Phe Leu Val Ser Ser Met Met Ser Leu Glu
20 25 30

Asp Asn Lys His Ala Leu Tyr Gln Leu Leu Ala His Pro Asn Phe Thr
35 40 45

Glu Lys Thr Ile
50

<210> 3422
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G378C"

<400> 3422
Cys Gly Met Thr Thr Pro Pro Thr Ser Pro Gly Asn Val Pro Pro Asp
1 5 10 15

Leu Ser His Pro Tyr Ser Lys Val Phe Cys Cys Thr Thr Ala Gly Gly
20 25 30

Lys Gly Thr Pro Leu Gly Thr Pro Ala Thr Ser Pro Pro Pro Ala Pro
35 40 45

Leu Cys His Ser
50

<210> 3423
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A419T"

<400> 3423
Ala Gln Pro Ser Ser Thr Gly Ala Ala Ala Ser Pro Ala Thr Ala Ala
1 5 10 15

Thr Leu Pro Val Gly Thr Gly Gln Asn Thr Thr Ser Ser Val Gly Ala
20 25 30

Gln Leu Met Gly Ala Ser Ser Gln Pro Ser Glu Ala Met Ala Pro Arg
35 40 45

Thr Gly Pro Ala
50

<210> 3424
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K265R"

<400> 3424
Trp Arg Met Lys Glu Glu Met Asp Arg Ala Gln Ala Glu Leu Asn Ala

1 5 10 15

Leu Lys Arg Thr Glu Glu Asp Leu Lys Arg Arg Gly His Gln Lys Leu
20 25 30

Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val Ala Glu Val Asp Lys
35 40 45

Asn Ile Glu Leu
50

<210> 3425
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R276S"

<400> 3425
Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly
1 5 10 15

His Gln Lys Leu Glu Glu Met Val Thr Ser Ser Leu Asp Gln Glu Val
20 25 30

Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
35 40 45

Leu Ser Ser Ala
50

<210> 3426
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K501N"

<400> 3426
Glu Asp Ser Leu Glu Lys Phe Glu Pro Ser Thr Leu Tyr Pro Tyr Leu
1 5 10 15

Arg Glu Glu Asp Leu Asp Asp Ser Pro Asn Asn Gly Gly Leu Asp Ile
20 25 30

Leu Lys Ser Leu Glu Asn Thr Val Ser Thr Ala Ile Ser Lys Ala Gln
35 40 45

Asn Gly Ala Pro
50

<210> 3427
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R881M"

<400> 3427
Gln Ala Gln Phe Ala Ser Ser Leu Arg Glu Thr Thr Glu Gly Lys Tyr
1 5 10 15

Ile Met Ser Asp Leu Gly Pro Gln Glu Met Met Val His Ile Ser Lys
20 25 30

Phe Thr Gly Leu Ser Met Thr Thr Ile Ser His Trp Leu Ala Asn Val
35 40 45

Lys Tyr Gln Leu
50

<210> 3428
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A222T"

<400> 3428
Leu Tyr Arg Gln Ser Ser Lys Met Cys Gly Thr Val Phe Thr Gly Ala
1 5 10 15

Ser Arg Phe Arg Cys Arg Gln Cys Ser Thr Thr Ala Tyr Asp Thr Leu
20 25 30

Val Glu Leu Thr Val His Met Asn Glu Thr Gly His Tyr Gln Asp Asp
35 40 45

Asn Arg Lys Lys
50

<210> 3429
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G677V"

<400> 3429
Glu Pro Ile Lys Met Glu Ala Ser Ser Asp Gly Gly Phe Arg Ser Gln
1 5 10 15

Glu Asn Ser Pro Ser Pro Pro Arg Asp Val Val Cys Lys Asp Gly Ser
20 25 30

Pro Leu Ala Glu Pro Val Glu Asn Gly Lys Glu Leu Val Lys Pro Leu
35 40 45

Ala Ser Ser Leu
50

<210> 3430
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.E513K"

<400> 3430
Cys Pro Ser Cys Gln Arg Leu His Lys Lys Ile Leu Glu Leu Glu Arg
1 5 10 15

Gln Ala Leu Ala Lys His Val Arg Ala Lys Lys Ala Leu Ser Ser Thr
20 25 30

Leu Arg Leu Ala Gln Asp Glu Ala Leu Arg Ala Lys Asn Leu Leu Leu
35 40 45

Thr Asp Lys Met
50

<210> 3431
<211> 52
<212> PRT
<213> Artificial Sequence

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<400> 3431
Ile Gly Phe Val Gly Cys Leu Gly Ala Ile Lys Glu Asn Lys Cys Leu
1 5 10 15

Leu Leu Thr Phe Phe Leu Leu Leu Leu Val Val Val Phe Leu Leu Glu
20 25 30

Ala Thr Ile Ala Ile Leu Phe Phe Ala Tyr Thr Asp Lys Ile Asp Arg
35 40 45

Tyr Ala Gln Gln
50

<210> 3432
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

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<223> /note="p.E301K"

<400> 3432
Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Ser Ser
1 5 10 15

Arg Gly Thr Glu Pro Leu Trp Thr Pro Lys Lys Pro Gly Ser Asp Lys
20 25 30

Lys Ser Ala Thr Lys Leu Glu Pro Glu Gly Glu Ala Gln Pro Gln Ala
35 40 45

Gln Pro Glu Thr
50

<210> 3433
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="p.C83W"

<400> 3433
Lys Gln Val Leu Lys Met Glu Val Ala Val Leu Lys Lys Leu Gln Gly
1 5 10 15

Lys Asp His Val Cys Arg Phe Ile Gly Trp Trp Gly Arg Asn Asp Arg
20 25 30

Phe Asn Tyr Val Val Met Gln Leu Gln Gly Arg Asn Leu Ala Asp Leu
35 40 45

Arg Arg Ser Gln
50

<210> 3434
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S270Y"

<400> 3434
Glu Ser Asn Ile Asp Ala Cys Gln Ile Leu Thr Val His Glu Leu Ala
1 5 10 15

Arg Glu Gly Asn Met Thr Thr Val Ser Tyr Tyr Leu Lys Thr Gln Lys
20 25 30

Ala Thr Asn His Val Arg Asn Leu Ile Lys Ala Leu Glu Thr Arg Glu
35 40 45

Pro Glu Asn Pro
50

<210> 3435
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K336fs"

<400> 3435
Arg Pro Ala Val Gly Leu His Gly Glu Thr Ala Gly Ile Pro Ala Pro
1 5 10 15

Ala Tyr Lys Asn Lys Ser Lys Lys Lys Arg Lys Ser Pro Ile Thr Arg
20 25 30

Asn Leu Arg Gln Trp Pro Cys Leu Arg Ala Ser Arg Val His Thr Leu
35 40 45

Lys Asp His Arg Trp Ala Val Arg Leu Gly Leu Trp Lys Ala Val Gln
50 55 60

Leu Leu Lys Gly Ser Arg Asn Pro Thr Val Gln Arg Arg Ser Leu Arg
65 70 75 80

Lys Gly Ser Leu Arg Leu Ser Lys Gly His Glu Cys Leu Val Met Ile
85 90 95

Phe Gln Cys Pro Val Arg Thr Leu Arg Ala His Ser Leu Ile Gln
100 105 110

<210> 3436
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q530R"

<400> 3436
Ile Lys Asp Arg Ala Thr Ser Thr Ile Lys Arg Met Tyr Arg Asp Asp
1 5 10 15

Leu Glu Arg Phe Lys Glu Phe Lys Ala Arg Arg Gly Val Ala Ile Lys
20 25 30

Phe Gly Lys Phe Ser Val Lys Glu Asn Lys Gln Leu Glu Lys Asn Val
35 40 45

Glu Asp Phe Leu
50

<210> 3437
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R761S"

<400> 3437

Leu Asp Glu Ala His Asn Val Lys Asn Pro Arg Val Gln Thr Ser Ile
1 5 10 15

Ala Val Cys Lys Leu Gln Ala Cys Ala Ser Ser Trp Ala Val Thr Gly
20 25 30

Thr Pro Ile Gln Asn Asn Leu Leu Asp Met Tyr Ser Leu Leu Lys Phe
35 40 45

Leu Arg Cys Ser
50

<210> 3438
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R707H"

<400> 3438
Cys Gly Tyr Asp Ser Leu Gln His Leu Ile Asn Gln Asn Ser Asp Tyr
1 5 10 15

Leu Val Asn Gly Ile Ser Leu Asn Leu His His His Leu Ala Leu His
20 25 30

Pro His Thr Pro Lys Val Leu Glu Val Met Leu Arg Asn Ser Asp Ala
35 40 45

Asn Leu Leu Pro
50

<210> 3439
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.122_123insKA"

<400> 3439
Ser Glu Leu Ala Ala Arg Trp Glu Ala Glu Ala Val Ala Ala Ala Lys
1 5 10 15

Ala Ala Ala Lys Ala Glu Ala Glu Ala Lys Ala Lys Ala Thr Ala Glu
20 25 30

Thr Val Ala Glu Gln Val Arg Val Asp Ala Gly Ala Ala Gly Glu Pro
35 40 45

Glu Cys Lys Ala Gly Glu Glu Gln Pro Lys
50 55

<210> 3440
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R751H"

<400> 3440
Leu Ile Lys Leu Asp Ser Val Lys Gln Arg Lys Val Leu Asp Ile Val
1 5 10 15

Lys Thr Ser Ile Arg Thr Val Leu Pro His His Ile Trp Lys Val Pro
20 25 30

Asp Val Glu Glu Val Asn Leu Tyr Arg Ile Phe Asn Arg Val Phe Asn
35 40 45

Arg Leu Leu Trp
50

<210> 3441
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L146F"

<400> 3441
Glu Asp Gly Val Val Gly Leu Asn Tyr Ser Cys Gly Asn Leu Gly Arg
1 5 10 15

Arg Val Asn Gly Glu Leu Gln Leu Gly Phe Phe Leu Ala Ile Ile Asn
20 25 30

<210> 3442
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q176fs"

<400> 3442
Ser Leu Leu Met Glu Arg Leu Ser Val Asp Tyr Gly Lys Lys Ser Lys
1 5 10 15

Leu Glu Phe Ala Ile Tyr Pro Ala Pro Pro Gly Leu His Gly Arg Gly
20 25 30

Gly Ala Leu Gln Leu His Pro Asp His Pro His Asp Pro Gly Thr Phe
35 40 45

<210> 3443
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R243Q"

<400> 3443
Asp Ile Glu Arg Pro Thr Tyr Thr Asn Leu Asn Arg Leu Ile Gly Gln
1 5 10 15

Ile Val Ser Ser Ile Thr Ala Ser Leu Gln Gln Phe Asp Gly Ala Leu
20 25 30

Asn Val Asp Leu Thr Glu Phe Gln Thr Asn Leu Val Pro Tyr Pro Arg
35 40 45

Ile His Phe Pro
50

<210> 3444
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V102M"

<400> 3444
Thr Tyr His Gly Asp Ser His Leu Gln Leu Glu Arg Ile Asn Val His
1 5 10 15

His His Glu Ala Ser Gly Gly Arg Tyr Met Met Pro Arg Ala Val Leu
20 25 30

Val Asp Leu Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro Phe
35 40 45

Gly Gln Val Leu
50

<210> 3445
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R119H"

<400> 3445

His Glu Ala Ser Gly Gly Arg Tyr Val Pro Arg Ala Val Leu Val Asp
1 5 10 15

Leu Glu Pro Gly Thr Met Asp Ser Val His His Ser Gly Pro Phe Gly
20 25 30

Gln Val Leu Arg Pro Asp Asn Phe Ile Phe Gly Glu Leu Arg Ala Arg
35 40 45

Thr Gly Val Arg
50

<210> 3446
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A200V"

<400> 3446
Tyr Gly Thr Gly Glu Val Ile Val Gln Asn Tyr Asn Ser Ile Leu Thr
1 5 10 15

Leu Ser His Leu Tyr Arg Ser Ser Asp Val Val Leu Leu Leu His Glu
20 25 30

Asn Asp Ala Ile His Lys Ile Cys Ala Lys Leu Met Asn Ile Lys Gln
35 40 45

Ile Ser Phe Ser
50

<210> 3447
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.A340T"

<400> 3447
Lys Ser Gln Gln Arg Lys Val Arg Gln Met Ile Glu Gln Leu Gln Asn
1 5 10 15

Ser Lys Ala Val Ile Gln Ser Lys Asp Thr Thr Thr Ile Gln Glu Leu
20 25 30

Lys Glu Lys Ile Ala Tyr Leu Glu Ala Glu Asn Leu Glu Met His Asp
35 40 45

Arg Met Glu His
50

<210> 3448
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L101F"

<400> 3448
His Ser Ala Gly His Ser Leu Ala Ser Glu Leu Val Glu Ser His Asp
1 5 10 15

Gly His Glu Glu Ile Ile Lys Val Tyr Phe Phe Lys Gly Arg Ser Gly
20 25 30

Asp Lys Met Ile His Glu Lys Asn Ile Asn Gln Leu Lys Ser Glu Val
35 40 45

Gln Tyr Ile Gln
50

<210> 3449
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H306Q"

<400> 3449
Lys Lys Lys His Gln Glu Val Gln Asp Gln Asp Pro Val Phe Gln Gly
1 5 10 15

Ser Asp Ser Ser Gly Tyr Gln Ser Asp Gln Gln Lys Lys Lys Lys Lys
20 25 30

Lys Arg Lys His Ser Glu Glu Ala Glu Phe Thr Pro Pro Leu Lys Cys
35 40 45

Ser Pro Lys Arg
50

<210> 3450
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<221> source
<223> /note="p.R343Q"

<400> 3450
Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu Phe Phe Leu
1 5 10 15

Ile Ser Phe Ile Met Tyr Ala Thr Ile Gln Gln Thr Glu Ser Ile Arg
20 25 30

Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu
35 40

<210> 3451
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R234C"

<400> 3451
Ala Glu Arg Ser Glu Pro Thr Gln Ala Leu Glu Leu Thr Glu Asp Asp
1 5 10 15

Ile Lys Glu Asp Gly Ile Val Pro Leu Cys Cys Tyr Val Lys Phe Gln
20 25 30

Asn Val Asn Ser Val Thr Ile Phe Val Gln Ser Asn Gln Gly Glu Glu
35 40 45

Glu Thr Thr Arg
50

<210> 3452
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T352fs"

<400> 3452
Pro Glu Pro Gln Asp Val Ala Gln Cys Leu Glu Val Gly Leu Phe Asp
1 5 10 15

Thr Pro Pro Phe Tyr Ser Asn Ser Thr Val Ser Glu Thr Gln Trp Lys
20 25 30

Val Thr Val Thr Pro Arg Glu Ser Met Thr Leu Leu Phe Glu Val Phe
35 40 45

Thr Ile Trp Leu Ile Tyr Ser
50 55

<210> 3453
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.S34Y"

<400> 3453
Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser Phe Tyr Phe Lys Ile
1 5 10 15

Gly Ala Cys Arg His Gly Asp Arg Cys Tyr Tyr Arg Leu His Asn Lys
20 25 30

Pro Thr Phe Ser Gln Thr Ile Ala Leu Leu Asn Ile Tyr Arg Asn Pro
35 40 45

Gln Asn Ser Ser
50

<210> 3454
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S34F"

<400> 3454
Phe Gly Thr Glu Lys Asp Lys Val Asn Cys Ser Phe Tyr Phe Lys Ile
1 5 10 15

Gly Ala Cys Arg His Gly Asp Arg Cys Phe Phe Arg Leu His Asn Lys
20 25 30

Pro Thr Phe Ser Gln Thr Ile Ala Leu Leu Asn Ile Tyr Arg Asn Pro
35 40 45

Gln Asn Ser Ser
50

<210> 3455
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G684fs"

<400> 3455
Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr
1 5 10 15

Leu His Leu Val Leu Arg Leu Arg Gly Val Ser Lys Phe Pro Leu Leu
20 25 30

Arg Phe Gln Gln Ile Ser Leu His Phe Pro Phe Asn Lys Val Val Ala
35 40 45

Phe

<210> 3456
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I191T"

<400> 3456
Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys
1 5 10 15

Ile Gln Asp Lys Glu Gly Ile Pro Pro Thr Thr Ser Arg Gly Ser Ser
20 25 30

Leu Gln Ala Ser Ser Trp Lys Met Ala Val Leu Phe Leu Thr Thr Thr
35 40 45

Ser Arg Arg Ser
50

<210> 3457
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G193W"

<400> 3457
Lys Gln Lys Gln Lys Ala Gln Asp Glu Leu Ser Ser Arg Pro Gln Thr
1 5 10 15

Leu Pro Leu Pro Asp Val Val Pro Asp Trp Trp Glu Thr His Leu Val
20 25 30

Gln Asn Gly Ile Gln Leu Leu Asn Gly His Ala Pro Gly Ala Val Pro
35 40 45

Asn Leu Ala Gly
50

<210> 3458
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G131D"

<400> 3458
Leu Glu Gly Asn Val Cys Leu Asn Ile Leu Arg Glu Asp Trp Lys Pro
1 5 10 15

Val Leu Thr Ile Asn Ser Ile Ile Tyr Asp Asp Leu Gln Tyr Leu Phe
20 25 30

Leu Glu Pro Asn Pro Glu Asp Pro Leu Asn Lys Glu Ala Ala Glu Val
35 40 45

Leu Gln Asn Asn
50

<210> 3459
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R86I"

<400> 3459
Glu Glu Tyr Pro Met Ala Ala Pro Lys Val Arg Phe Met Thr Lys Ile
1 5 10 15

Tyr His Pro Asn Val Asp Lys Leu Glu Ile Ile Ile Ser Leu Asp Ile
20 25 30

Leu Lys Asp Lys Trp Ser Pro Ala Leu Gln Ile Arg Thr Val Leu Leu
35 40 45

Ser Ile Gln Ala
50

<210> 3460
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1118fs"

<400> 3460
Tyr Glu Asn Ser Arg Cys Tyr Asn Glu Met Ala Leu Ile Arg Val Val
1 5 10 15

Gln Ser Met Thr Gln Leu Val Arg Arg Ala Pro Arg Gly Leu
20 25 30

<210> 3461
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A97T"

<400> 3461
Ala Tyr Arg Ser His Gly Val Leu Asp Pro Arg Leu Leu Val Gly Cys
1 5 10 15

Ala Val Ala Val Leu Ala Val His Gly Thr Thr Gly Asn Leu Val Asn
20 25 30

Thr Tyr Tyr Asp Phe Ser Lys Gly Ile Asp His Lys Lys Ser Asp Asp
35 40 45

Arg Thr Leu Val
50

<210> 3462
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S417L"

<400> 3462
Leu Pro Thr Thr Ser Glu His Thr Ala Lys Lys Met Lys Ala Thr Asn
1 5 10 15

Glu Pro Ser Leu Thr His Met Asp Cys Leu Leu Thr Gly Pro Leu Ser
20 25 30

His Glu Gln Lys Leu Ser Gln Ser Leu Glu Ile Ala Leu Ala Ser Thr
35 40 45

Leu Gly Ser Met
50

<210> 3463

<211> 95
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A523fs"

<400> 3463
Pro Ile Gly Pro Ile Val Pro Phe Thr Pro Ile Gly Pro Ile Gly Pro
1 5 10 15

Ile Gly Pro Thr Gly Pro Ala Ala Pro Leu Ala Pro Pro Ala Leu Val
20 25 30

Ala Pro Arg Gly Leu Leu Cys Pro Ala Leu His Leu Val Lys Pro Arg
35 40 45

Val Leu His Gln Asn Leu Asp Pro Thr Ser Ser Ser Phe Ser Lys Trp
50 55 60

Cys Arg Pro Trp Leu Glu Gln Met Leu His Ser Cys Arg Ile Gln Lys
65 70 75 80

Ser Asp Phe Ser Asn Asn Trp Asn Ser Ser Thr Gln Trp Gly Ser
85 90 95

<210> 3464
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G1647W"

<400> 3464
Lys His Pro Val Leu Cys Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln
1 5 10 15

Asn Ile Cys Cys Gln Glu Ile Val Asn Trp Trp Glu Glu Val Gly Ala
20 25 30

Cys Ile Phe His Ala Leu His Cys Gly Ala Gly Val Cys Ile Phe Leu
35 40 45

Lys Ile Arg Glu
50

<210> 3465
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P2802fs"

<400> 3465
Thr Ala Glu Asn Val Asn Asn Gly Asn Pro Ser Pro Leu Glu Ala Leu
1 5 10 15

Leu Ala Gly Ala Glu Gly Phe Pro Pro Cys Trp Thr Ser His Leu Met
20 25 30

Gln Met Thr Arg Pro Trp Leu Asn
35 40

<210> 3466
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K2120fs"

<400> 3466
Glu Val Leu Pro Thr Lys Met Ser Tyr Ala Ala Asn Leu Lys Asn Val
1 5 10 15

Met Asn Met Gln Asn Arg Gln Lys Lys Lys Gly Lys Asn Ser Pro Cys
20 25 30

Cys Gln Lys Lys Leu Arg Val Gln Asn Gln Gly His Leu Leu Met Ile
35 40 45

Leu Leu His Asn
50

<210> 3467
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R2517S"

<400> 3467
Leu Asp Asp Thr Asp Asp Gly Asp Asp Asn Ala Pro Leu Phe Tyr Gln
1 5 10 15

Pro Gly Lys Arg Gly Phe Tyr Thr Pro Ser Ser Pro Gly Lys Asn Thr
20 25 30

Glu Ala Arg Leu Asn Cys Phe Arg Asn Ile Gly Arg Ile Leu Gly Leu
35 40 45

Cys Leu Leu Gln
50

<210> 3468
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A276V"

<400> 3468
Leu Asp Gln Val Thr Gly Phe Leu Gly Glu His Gly Gln Leu Asp Gly
1 5 10 15

Leu Ser Ser Ser Pro Pro Lys Lys Cys Val Val Arg Ser Glu Ser Leu
20 25 30

Ile Asp Ala Ser Glu Asp Ser Gln Leu Glu Ala Ala Ile Arg Ala Ser
35 40 45

Leu Gln Glu Thr
50

<210> 3469
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D262H"

<400> 3469
Ala Ser Phe Tyr Asn Ser Gly Leu Leu Asp Thr Phe Ile Gly Glu Gly
1 5 10 15

Lys Glu Tyr Ile Phe Val Ser Asn Ile His His Asn Leu Gly Ala Thr
20 25 30

Val Asp Leu Tyr Ile Leu Asn His Leu Met Asn Pro Pro Asn Gly Lys
35 40 45

Arg Cys Glu Phe
50

<210> 3470
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T4A"

<400> 3470
Met Ala Arg Ala Ala Gly Trp Thr Ser Pro Ile Pro Leu Cys Val Ser

1 5 10 15

Leu Leu Leu Thr Cys Gly Phe Ala Glu Ala Gly Lys Leu Leu
20 25 30

<210> 3471
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N97fs"

<400> 3471
Glu Ile Tyr Arg Val Pro Phe Gly Lys Glu Arg Ile Glu Gly Val Ile
1 5 10 15

Lys Asp Phe Val Leu Thr Trp Leu Glu Ile Asp His Leu Leu Gln Pro
20 25 30

Phe Gly Asp Ser Ile Arg Arg Trp Pro Lys
35 40

<210> 3472
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R447I"

<400> 3472
Ser Thr Asp Leu Leu Asn Ala Leu Lys Thr Val Ile Asn Asp Pro Leu
1 5 10 15

Tyr Lys Glu Asn Ile Met Lys Leu Ser Ile Ile Ile Gln His Asp Gln
20 25 30

Pro Val Lys Pro Leu Asp Arg Ala Val Phe Trp Ile Glu Phe Val Met
35 40 45

Pro His Lys Gly
50

<210> 3473
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P289H"

<400> 3473
Phe Gln Phe Pro His Pro Phe Leu Pro Asn Ile Asp Phe Val Gly Gly
1 5 10 15

Leu His Cys Lys Pro Ala Lys Pro Leu His His Lys Glu Met Glu Glu
20 25 30

Phe Val Gln Ser Ser Gly Glu Asn Gly Val Val Val Phe Ser Leu Gly
35 40 45

Ser Val Ile Ser
50

<210> 3474
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M214I"

<400> 3474
Phe Pro Pro Ser Tyr Val Pro Val Val Met Ser Glu Leu Thr Asp Gln
1 5 10 15

Met Thr Phe Met Glu Arg Val Lys Asn Ile Ile Ile Tyr Val Leu Tyr
20 25 30

Phe Asp Phe Trp Phe Glu Ile Phe Asp Met Lys Lys Trp Asp Gln Phe
35 40 45

Tyr Ser Glu Val
50

<210> 3475
<211> 52
<212> PRT
<213> Artificial Sequence

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<220>
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<223> /note="p.E102K"

<400> 3475
Phe Asn Ser Thr Thr Ser Asp Ala Phe Leu Gln Ser Lys Met Arg Asn
1 5 10 15

Ile Phe Ser Gly Arg Leu Thr Ala Ile Lys Lys Leu Phe Asp Ile Leu
20 25 30

Asp His Tyr Thr Lys Asn Cys Asp Leu Met Val Gly Asn His Ala Leu
35 40 45

Ile Gln Gly Leu
50

<210> 3476
<211> 44
<212> PRT
<213> Artificial Sequence

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<223> /note="p.I1330fs"

<400> 3476
Glu Ile Pro Val Val Val Pro Met Gln Ile Glu Leu Leu Asn Ser Ser
1 5 10 15

Ile Thr Leu Lys Asp Asp Ile Pro Pro Ser Ile Gln His Leu Gln Ala
20 25 30

Pro Ser Pro Ser Leu Trp Pro Trp Asn Met Leu Cys
35 40

<210> 3477
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.M559I"

<400> 3477
Cys Gln Cys Arg Thr Thr Arg Asp Ala Thr Pro Ser Arg Ala Gly Arg
1 5 10 15

Ala Cys Glu Gly Asp Leu Val Ser Pro Ile Ile Gly Gly Gly Leu Ser
20 25 30

Ala Ala Thr Gly Val Thr Val Pro Gly Leu Gly Thr Gly Thr Ala Ala
35 40 45

Leu Gly Leu Glu
50

<210> 3478
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V445A"

<400> 3478
Leu Thr Met Val Ala Tyr Gly Leu Val Glu Cys Val Glu Ser Lys Asn
1 5 10 15

Pro Ile Arg Pro His Ala Pro Gly Gln Ala Ala Asn Gln Ala Glu Asp

20 25 30

Glu Glu Ile Gln Thr Lys Met
35

<210> 3479
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V498M"

<400> 3479
Tyr His Trp Trp Gln Ala Val Ala Ile Phe Thr Val Tyr Leu Gly Ser
1 5 10 15

Ser Leu His Met Lys Ala Lys Leu Ala Met Met Leu Leu Val Thr Leu
20 25 30

Val Ala Ala Ala Val Ser Tyr Leu Arg Met Glu Gln Lys Leu Arg Arg
35 40 45

Gly Val Ala Pro
50

<210> 3480
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P49fs"

<400> 3480
Asp Phe Asn Ile Ser Ser Leu Ser Gly Leu Leu Ser Pro Ala Leu Thr
1 5 10 15

Glu Ser Leu Leu Val Ala Leu Pro Pro Val Thr Ser Gln Glu Ala Met
20 25 30

Pro His

<210> 3481
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G272fs"

<400> 3481
Gln Ile Thr Gln Glu Ala Val Pro Lys Ser Leu Gly Ala Ser Glu Ser
1 5 10 15

Ser Tyr Thr Ser Val Asn Arg Gly Pro Ala Thr Gly Gln Gly
20 25 30

<210> 3482
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.S6A"

<400> 3482
Met Leu Ser Val Ala Ala Ala Arg Ser Gly Pro Phe Ala Pro Val Leu
1 5 10 15

Ser Ala Thr Ser Arg Gly Val Ala Gly Ala Leu Arg Pro Leu Val Gln
20 25 30

<210> 3483
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I83V"

<400> 3483
Gln Ala Val Arg Arg Pro Leu Val Ala Ser Val Gly Leu Asn Val Pro
1 5 10 15

Ala Ser Val Cys Tyr Ser His Thr Asp Val Val Lys Val Pro Asp Phe
20 25 30

Ser Glu Tyr Arg Arg Leu Glu Val Leu Asp Ser Thr Lys Ser Ser Arg
35 40 45

Glu Ser Ser Glu
50

<210> 3484
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G639fs"

<400> 3484
His Phe Leu Arg Glu Met Gly Gln Phe Tyr Glu Ala Glu Ser Cys Leu
1 5 10 15

Val Glu Ala Gly Arg Leu Pro Ala Gly Pro Glu Ala Phe Cys Pro Leu
20 25 30

Pro Arg Leu Gly Leu Gly Ala Ala Ala Asp Arg Ala Ala Ser Gly Ala
35 40 45

Asn Arg Trp Glu His Ala Glu His Ala Arg Pro Leu Gly His Arg Ala
50 55 60

Pro Glu Gly Ala Ala Arg Pro Thr Gly Glu Thr Val Lys Ala Gly Gly
65 70 75 80

Ser Val Asn Arg Arg Gly Ala Arg His Gly Gln Val His Thr Pro Gln
85 90 95

His His Val Trp Ala Ala Val Cys His Arg Glu Glu Leu Arg Ser Ser
100 105 110

Arg Gly Leu His Ala Ala His His Ser Gly
115 120

<210> 3485
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S13fs"

<400> 3485
Met Glu Ala Pro Thr Val Glu Thr Pro Pro Asp Pro Ser Pro Pro Phe
1 5 10 15

Gly Pro Gly Pro Cys Pro Gly Ser Val Ala Arg Pro Gly Cys Gly Ala
20 25 30

Ala Ala Arg Gly Ala Gly Lys Gly Gly His
35 40

<210> 3486
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R52Q"

<400> 3486
Asp Pro Thr Ser Val Ala Ile Ala Ser Ile Gln Ser Ala Ala Thr Phe
1 5 10 15

Pro Asp Pro Asn Val Lys Tyr Val Phe Gln Gln Thr Glu Asn Gly Gly

20 25 30

Gln Val Met Tyr Arg Val Ile Gln Val Ser Glu Gly Gln Leu Asp Gly
35 40 45

Gln Thr Glu Gly
50

<210> 3487
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R3719H"

<400> 3487
Asn Ser Thr Thr Val Glu Leu Tyr Trp Ser Leu Pro Glu Lys Pro Asn
1 5 10 15

Gly Leu Val Ser Gln Tyr Gln Leu Ser His His Asn Gly Asn Leu Leu
20 25 30

Phe Leu Gly Gly Ser Glu Glu Gln Asn Phe Thr Asp Lys Asn Leu Glu
35 40 45

Pro Asn Ser Arg
50

<210> 3488
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F2369L"

<400> 3488
Lys Ala His Val Arg Trp Glu Ala Pro Phe Arg Pro Asn Gly Leu Leu
1 5 10 15

Thr His Ser Val Leu Phe Thr Gly Ile Leu Leu Tyr Val Asp Pro Val
20 25 30

Gly Asn Asn Tyr Thr Leu Leu Asn Val Thr Lys Val Met Tyr Ser Gly
35 40 45

Glu Glu Thr Asn
50

<210> 3489
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.A286T"

<400> 3489
Val Leu Asp Ala Ala Leu Glu Thr Gly Gln Leu Ile Ile Met Glu Thr
1 5 10 15

Arg Lys Lys Asp Gly Thr Trp Pro Ser Thr Thr Gln Leu His Val Met
20 25 30

Asn Asn Asn Met Ser Glu Glu Asp Glu Asp Phe Lys Gly Gln Pro Gly
35 40 45

Ile Cys Gly Leu
50

<210> 3490
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.K782fs"

<400> 3490
Lys Lys Arg Tyr Phe Asp Glu Asn Ala Ala Glu Asp Phe Glu Lys His
1 5 10 15

Glu Ser Val Glu Tyr Lys Pro Pro Lys Asn Pro Leu
20 25

<210> 3491
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R455Q"

<400> 3491
Asp Ile Pro Ser Gly Thr Ser Lys His Leu Gln Lys Lys Ala Lys Lys
1 5 10 15

Gln Ala Lys Lys Gln Ala Lys Asn Gln Gln Gln Arg Gln Gln Lys Ile
20 25 30

Gln Gly Lys Val Leu His Leu Asn Asp Ile Cys Thr Ile Asp His Pro
35 40 45

Glu Asp Ser Glu
50

<210> 3492
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R873H"

<400> 3492
Phe Lys Ala Ile Lys Leu Glu Tyr Ala Arg Leu Val Lys Leu Ala Gln
1 5 10 15

Glu Asp Thr Pro Pro Glu Thr Asp Tyr His His Leu His His Val Val
20 25 30

Val Tyr Phe Ile Gln Asn Gln Ala Pro Lys Lys Ile Ile Glu Lys Thr
35 40 45

Leu Leu Glu Gln
50

<210> 3493
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1119Q"

<400> 3493
Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu Arg
1 5 10 15

Phe Ala Arg Ile Met Leu Ser Leu Ser Gln Gln Thr Pro Ala Asp Gly
20 25 30

Arg

<210> 3494
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R861Q"

<400> 3494
Thr Leu Lys Ser Gly His Tyr Ile Cys Asp Ala Tyr Asp Phe Glu Lys
1 5 10 15

Gln Ile Trp Phe Thr Tyr Asp Asp Met Gln Gln Val Leu Gly Ile Gln

20 25 30

Glu Ala Gln Met Gln Glu Asp Arg Arg Cys Thr Gly Tyr Ile Phe Phe
35 40 45

Tyr Met His Asn
50

<210> 3495
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.F81L"

<400> 3495
Asn Ile Arg Ser Val Val Leu Arg His Cys Lys Lys Arg Gln Ser His
1 5 10 15

Leu Arg Leu Thr Leu Lys Asn Asn Val Leu Leu Leu Phe Ile Asp Lys
20 25 30

Leu Ser Tyr Arg Asp Ala Lys Gln Leu Asn Met Phe Leu Asp Ile Ile
35 40 45

His Gln Asn Lys
50

<210> 3496
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D391N"

<400> 3496
Leu Thr Glu Met Tyr Tyr Asp Gly Phe His Arg Ser Phe Cys Asp Thr
1 5 10 15

Asp Asp Leu Glu Thr Val His Glu Ser Asn Asn Cys Ile Phe Ala Phe
20 25 30

Glu Thr Pro Glu Ile Phe Arg Pro Glu Gly Ile Leu Ser Gln Arg Gly
35 40 45

Ile His Leu Asn
50

<210> 3497
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R36Q"

<400> 3497
Leu Thr Leu Lys Val Leu Pro His Phe Glu Ser Leu Gly Lys Gln Glu
1 5 10 15

Lys Ile Pro Asn Lys Met Ser Ala Phe Gln Gln Asn His Cys Pro His
20 25 30

Leu Asp Ser Val Gly Glu Ile Thr Lys Glu Asp Leu Ile Gln Lys Ser
35 40 45

Leu Gly Thr Cys
50

<210> 3498
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L259V"

<400> 3498
Ser Thr Ala Pro Ser Arg Asn Phe Thr Thr Ser Pro Lys Ser Ser Ala
1 5 10 15

Ser Pro Tyr Ser Ser Val Ser Ala Ser Val Val Ile Ala Asn Gly Asp
20 25 30

Ser Thr Ser Thr Cys Gly Met His Ser Ser Gly Val Ser Arg Gly Gly
35 40 45

Ser Gly Phe Ser
50

<210> 3499
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S851L"

<400> 3499
Asp Ser Tyr Thr Leu Lys Glu Ala Glu Leu Lys Met Gly Ser Ser Leu
1 5 10 15

Gly Leu Cys Leu Gly Lys Ala Pro Ser Leu Leu Ser Gln Leu Phe Leu
20 25 30

Phe Phe Ala Met Gly Ser Asp Val Gln Pro Gly Thr Glu Met Glu Ile
35 40 45

Val Val Glu Glu
50

<210> 3500
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<223> /note="p.R779P"

<400> 3500
Ser Pro Ala Ala Glu Ser Leu Glu Glu Pro Asp Ala Ala Ala Gly Leu
1 5 10 15

Ser Ser Thr Lys Lys Ala Pro Pro Pro Pro Pro Asp Pro Gly Thr Pro
20 25 30

Ala Thr Lys Glu Gly Ala Trp Glu Ala Met Ala Val Ala Pro Glu Glu
35 40 45

Pro Pro Pro Ser
50

<210> 3501
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q137R"

<400> 3501
Leu Phe Asp Asn Tyr Met Gln Gln Asp Ala His Glu Phe Leu Asn Tyr
1 5 10 15

Leu Leu Asn Thr Ile Ala Asp Ile Leu Arg Arg Glu Glu Lys Lys Gln
20 25 30

Glu Lys Gln Asn Gly Lys Leu Lys Asn Gly Asn Met Asn Glu Pro Ala
35 40 45

Glu Asn Asn Lys
50

<210> 3502
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V148I"

<400> 3502
Glu Glu Ile Glu Arg Ile His Arg Glu Val Ala Phe Asn Lys Thr Ala
1 5 10 15

Gln Val Leu Ser Lys Trp Asp Pro Val Ile Ile Leu Lys Asn Arg Gln
20 25 30

Ala Glu Gln Leu Val Phe Pro Leu Glu Lys Glu Glu Pro Ala Ile Ala
35 40 45

Pro Ile Glu His
50

<210> 3503
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E81del"

<400> 3503
Ser Arg Ala Ala Leu Ala Lys Gly Trp Asn Glu Val Gln Ser Gly Asp
1 5 10 15

Glu Glu Asp Gly Glu Glu Glu Glu Glu Val Leu Ala Leu Asp Met Asp
20 25 30

Asp Glu Asp Asp Glu Asp Gly Gly Asn Ala Gly Glu Glu Glu Glu Glu
35 40 45

Glu Asn Ala Asp Asp
50

<210> 3504
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.A289E"

<400> 3504
Val Leu Leu Phe Trp Ala Cys Phe Leu Pro Phe Trp Leu Trp Gln Leu
1 5 10 15

Leu Ala Gln Tyr His Gln Ala Pro Leu Glu Glu Pro Arg Thr Ala Arg
20 25 30

Ile Val Asn Tyr Leu Thr Thr Cys Leu Thr Tyr Gly Asn Ser Cys Ala
35 40 45

Asn Pro Phe Leu
50

<210> 3505
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.V100L"

<400> 3505
Gln Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg
1 5 10 15

Ile Leu Ile Thr Gly Gly Ala Gly Phe Leu Leu Gly Ser His Leu Thr
20 25 30

Asp Lys Leu Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe
35 40 45

Phe Thr Gly Arg
50

<210> 3506
<211> 53
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.P51S"

<400> 3506
Glu Ala Gly Glu Gly Pro Gly Trp Gly Gly Ala His Pro Arg Ile Cys
1 5 10 15

Leu Gln Pro Pro Pro Thr Ser Arg Thr Ser Ser Phe Pro Pro Pro Arg
20 25 30

Leu Pro Ala Leu Glu Gln Gly Pro Gly Gly Leu Trp Val Trp Gly Ala
35 40 45

Thr Ala Val Ala Gln
50

<210> 3507
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.G3fs"

<400> 3507
Met Pro Gly Gly Arg Arg Trp Leu Gly Val Ala Ala Ala Val Pro Leu
1 5 10 15

Gln Arg Pro Leu Arg Pro Pro Pro Pro Leu Gly Ser Gly Val Trp Arg
20 25 30

Pro Ala Lys Glu Pro Gln Pro Arg Glu Met Arg Ser Gln Lys Arg Lys
35 40 45

Gly Lys Arg Thr Cys Glu Thr Glu Ala Ser Pro Ser Leu Ser Thr Gly
50 55 60

Val Gly Tyr Leu Trp Met Arg Pro Pro Gly Lys Gly Cys Gly Asn Thr
65 70 75 80

Trp Pro Arg Ser Thr Pro Met Glu Arg Arg Trp Arg Asn Gly Ser Val
85 90 95

Gly Pro Gln Thr Cys Pro Arg Ser Pro Tyr Arg Val Cys Leu Arg Ser
100 105 110

Ser Arg Leu His Leu Ser Leu Ser Ala Trp Lys Leu Cys Ser Ala Thr
115 120 125

Ser Glu Ser Cys Ser Thr Ile Thr Gln Gly His Ser Ser Leu Lys Leu
130 135 140

Arg Arg Ala Asp Leu
145

<210> 3508
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E685K"

<400> 3508
Cys Val Pro Lys Pro Val Asp Tyr Ser Cys Gln Pro Trp Tyr Ala Gly
1 5 10 15

Ala Met Glu Arg Leu Gln Ala Glu Thr Lys Lys Leu Ile Asn Arg Val
20 25 30

Asn Ser Thr Tyr Leu Val Arg His Arg Thr Lys Glu Ser Gly Glu Tyr
35 40 45

Ala Ile Ser Ile
50

<210> 3509
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R1125H"

<400> 3509
His Ser Val Ser Tyr Pro Pro Gly Ala Val Thr Glu His Lys Val Lys
1 5 10 15

Thr Asp Glu Val Val Thr Leu Thr Pro His His Ile Gly Pro Lys Val
20 25 30

Ser Leu Ser Pro Gly Pro Glu Gln Lys Tyr Glu Thr Glu Gly Ser Ser
35 40 45

Thr Thr Gly Phe
50

<210> 3510
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S1308C"

<400> 3510
Ser Ser Pro Pro Ala Thr Gln Pro Thr Arg Pro Pro Thr Val Glu Asp
1 5 10 15

Lys Glu Ala Phe Gly Pro Gln Ala Leu Cys Cys Thr Pro Gln Pro Pro
20 25 30

Ala Ser Thr Lys Phe His Pro Asp Ile Asn Val Tyr Ile Ile Glu Val
35 40 45

Arg Glu Asn Lys
50

<210> 3511
<211> 54

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.355_356insN"

<400> 3511
Glu Thr Ser Asn Gln Lys Gln Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Gln Gln His Asn Asn Val Thr Ser Trp Pro
20 25 30

Gly Lys Gln Val Glu Thr Leu Arg Leu Trp Glu Glu Ala Val Lys Ala
35 40 45

Arg Lys Lys Glu Ala Ala
50

<210> 3512
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G39S"

<400> 3512
Gly Ala Glu Glu Ala Gly Val Glu Glu Tyr Gly Pro Glu Glu Asp Gly
1 5 10 15

Gly Glu Glu Ser Gly Ala Glu Glu Ser Ser Ser Pro Glu Glu Ser Gly
20 25 30

Pro Glu Glu Leu Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg
35 40 45

Pro Val Leu Arg
50

<210> 3513
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P45L"

<400> 3513
Val Glu Glu Tyr Gly Pro Glu Glu Asp Gly Gly Glu Glu Ser Gly Ala
1 5 10 15

Glu Glu Ser Gly Pro Glu Glu Ser Gly Leu Leu Glu Glu Leu Gly Ala
20 25 30

Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg Ser Val
35 40 45

Asn Ser Arg Glu
50

<210> 3514
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S65L"

<400> 3514
Pro Glu Glu Ser Gly Pro Glu Glu Leu Gly Ala Glu Glu Glu Met Glu
1 5 10 15

Ala Gly Arg Pro Arg Pro Val Leu Arg Leu Leu Val Asn Ser Arg Glu
20 25 30

Pro Ser Gln Val Ile Phe Cys Asn Arg Ser Pro Arg Val Val Leu Pro
35 40 45

Val Trp Leu Asn
    50

<210> 3515
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V74D"

<400> 3515
Gly Ala Glu Glu Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg
1   5   10   15

Ser Val Asn Ser Arg Glu Pro Ser Gln Asp Asp Ile Phe Cys Asn Arg
            20   25   30

Ser Pro Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro
        35   40   45

Gln Pro Tyr Pro
    50

<210> 3516
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.N78D"

<400> 3516
Glu Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg Ser Val Asn Ser
1   5   10   15

Arg Glu Pro Ser Gln Val Ile Phe Cys Asp Asp Arg Ser Pro Arg Val
            20   25   30

Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln Pro Tyr Pro

35 40 45

Thr Leu Pro Pro
50

<210> 3517
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R79P"

<400> 3517
Met Glu Ala Gly Arg Pro Arg Pro Val Leu Arg Ser Val Asn Ser Arg
1 5 10 15

Glu Pro Ser Gln Val Ile Phe Cys Asn Pro Pro Ser Pro Arg Val Val
20 25 30

Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln Pro Tyr Pro Thr
35 40 45

Leu Pro Pro Gly
50

<210> 3518
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R82P"

<400> 3518
Gly Arg Pro Arg Pro Val Leu Arg Ser Val Asn Ser Arg Glu Pro Ser
1 5 10 15

Gln Val Ile Phe Cys Asn Arg Ser Pro Pro Pro Val Val Leu Pro Val
20 25 30

Trp Leu Asn Phe Asp Gly Glu Pro Gln Pro Tyr Pro Thr Leu Pro Pro
35 40 45

Gly Thr Gly Arg
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<210> 3519
<211> 52
<212> PRT
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<400> 3519
Leu Arg Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn
1 5 10 15

Arg Ser Pro Arg Val Val Leu Pro Val Leu Leu Leu Asn Phe Asp Gly
20 25 30

Glu Pro Gln Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile
35 40 45

His Ser Tyr Arg
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<210> 3520
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<400> 3520
Arg Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg
1 5 10 15

Ser Pro Arg Val Val Leu Pro Val Trp His His Asn Phe Asp Gly Glu
20 25 30

Pro Gln Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His
35 40 45

Ser Tyr Arg Gly
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<210> 3521
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<212> PRT
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<400> 3521
Arg Ser Val Asn Ser Arg Glu Pro Ser Gln Val Ile Phe Cys Asn Arg
1 5 10 15

Ser Pro Arg Val Val Leu Pro Val Trp Pro Pro Asn Phe Asp Gly Glu
20 25 30

Pro Gln Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His
35 40 45

Ser Tyr Arg Gly
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<210> 3522
<211> 52
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<213> Artificial Sequence

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<400> 3522

Arg Val Val Leu Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln Pro
1 5 10 15

Tyr Pro Thr Leu Pro Pro Gly Thr Gly Pro Pro Arg Ile His Ser Tyr
20 25 30

Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu
35 40 45

Leu Val Asn Gln
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<210> 3523
<211> 52
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<220>
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<400> 3523
Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln Pro Tyr Pro Thr Leu
1 5 10 15

Pro Pro Gly Thr Gly Arg Arg Ile His Asn Asn Tyr Arg Gly His Leu
20 25 30

Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu Leu Val Asn Gln
35 40 45

Thr Glu Leu Phe
50

<210> 3524
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S111R"

<400> 3524
Pro Val Trp Leu Asn Phe Asp Gly Glu Pro Gln Pro Tyr Pro Thr Leu
1 5 10 15

Pro Pro Gly Thr Gly Arg Arg Ile His Arg Arg Tyr Arg Gly His Leu
20 25 30

Trp Leu Phe Arg Asp Ala Gly Thr His Asp Gly Leu Leu Val Asn Gln
35 40 45

Thr Glu Leu Phe
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<210> 3525
<211> 52
<212> PRT
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<220>
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<220>
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<400> 3525
Asn Phe Asp Gly Glu Pro Gln Pro Tyr Pro Thr Leu Pro Pro Gly Thr
1 5 10 15

Gly Arg Arg Ile His Ser Tyr Arg Gly Asn Asn Leu Trp Leu Phe Arg
20 25 30

Asp Ala Gly Thr His Asp Gly Leu Leu Val Asn Gln Thr Glu Leu Phe
35 40 45

Val Pro Ser Leu
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<210> 3526
<211> 66
<212> PRT
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<223> /note="p.L116fs"

<400> 3526
Asp Gly Glu Pro Gln Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg
1 5 10 15

Arg Ile His Ser Tyr Arg Gly His Leu Gly Ser Ser Glu Met Gln Gly
20 25 30

His Thr Met Gly Phe Trp Leu Thr Lys Leu Asn Tyr Leu Cys His Leu
35 40 45

Ser Met Leu Thr Asp Ser Leu Phe Leu Pro Ile Ser His Cys Gln Cys
50 55 60

Ile Leu
65

<210> 3527
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D121Y"

<400> 3527
Gln Pro Tyr Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser
1 5 10 15

Tyr Arg Gly His Leu Trp Leu Phe Arg Tyr Tyr Ala Gly Thr His Asp
20 25 30

Gly Leu Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val
35 40 45

Asp Gly Gln Pro
50

<210> 3528
<211> 59
<212> PRT

<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.G123fs"

<400> 3528
Pro Thr Leu Pro Pro Gly Thr Gly Arg Arg Ile His Ser Tyr Arg Gly
1 5 10 15

His Leu Trp Leu Phe Arg Asp Ala Gly His Thr Met Gly Phe Trp Leu
20 25 30

Thr Lys Leu Asn Tyr Leu Cys His Leu Ser Met Leu Thr Asp Ser Leu
35 40 45

Phe Leu Pro Ile Ser His Cys Gln Cys Ile Leu
50 55

<210> 3529
<211> 52
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.L128H"

<400> 3529
Pro Gly Thr Gly Arg Arg Ile His Ser Tyr Arg Gly His Leu Trp Leu
1 5 10 15

Phe Arg Asp Ala Gly Thr His Asp Gly His His Leu Val Asn Gln Thr
20 25 30

Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly Gln Pro Ile Phe Ala
35 40 45

Asn Ile Thr Leu
50

<210> 3530
<211> 52
<212> PRT
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<400> 3530
His Ser Tyr Arg Gly His Leu Trp Leu Phe Arg Asp Ala Gly Thr His
1 5 10 15

Asp Gly Leu Leu Val Asn Gln Thr Glu Phe Phe Phe Val Pro Ser Leu
20 25 30

Asn Val Asp Gly Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr
35 40 45

Thr Leu Lys Glu
50

<210> 3531
<211> 52
<212> PRT
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<220>
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<223> /note="p.I151T"

<400> 3531
Asp Gly Leu Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn
1 5 10 15

Val Asp Gly Gln Pro Ile Phe Ala Asn Thr Thr Thr Leu Pro Val Tyr
20 25 30

Thr Leu Lys Glu Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro
35 40 45

Glu Asn Tyr Arg

50

<210> 3532
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3532
Leu Leu Val Asn Gln Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp
1 5 10 15

Gly Gln Pro Ile Phe Ala Asn Ile Thr Pro Pro Pro Val Tyr Thr Leu
20 25 30

Lys Glu Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn
35 40 45

Tyr Arg Arg Leu
50

<210> 3533
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3533
Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly Gln Pro Ile Phe
1 5 10 15

Ala Asn Ile Thr Leu Pro Val Tyr Thr Val Val Lys Glu Arg Cys Leu
20 25 30

Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg Arg Leu Asp
35 40 45

Ile Val Arg Ser
    50

<210> 3534
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.L158P"

<400> 3534
Thr Glu Leu Phe Val Pro Ser Leu Asn Val Asp Gly Gln Pro Ile Phe
1   5   10   15

Ala Asn Ile Thr Leu Pro Val Tyr Thr Pro Pro Lys Glu Arg Cys Leu
            20   25   30

Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg Arg Leu Asp
        35   40   45

Ile Val Arg Ser
    50

<210> 3535
<211> 29
<212> PRT
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<220>
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<400> 3535
Leu Asn Val Asp Gly Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val
1   5   10   15

Tyr Thr Leu Lys Glu Arg Cys Leu Gln Leu Ser Gly Ala
            20   25

<210> 3536
<211> 52
<212> PRT
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<220>
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<400> 3536
Gly Gln Pro Ile Phe Ala Asn Ile Thr Leu Pro Val Tyr Thr Leu Lys
1 5 10 15

Glu Arg Cys Leu Gln Val Val Arg Ser Pro Pro Val Lys Pro Glu Asn
20 25 30

Tyr Arg Arg Leu Asp Ile Val Arg Ser Leu Tyr Glu Asp Leu Glu Asp
35 40 45

His Pro Asn Val
50

<210> 3537
<211> 52
<212> PRT
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<223> /note="p.L184P"

<400> 3537
Lys Glu Arg Cys Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn
1 5 10 15

Tyr Arg Arg Leu Asp Ile Val Arg Ser Pro Pro Tyr Glu Asp Leu Glu
20 25 30

Asp His Pro Asn Val Gln Lys Asp Leu Glu Arg Leu Thr Gln Glu Arg
35 40 45

Ile Ala His Gln
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<210> 3538
<211> 52
<212> PRT
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<220>
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<223> /note="p.L188P"

<400> 3538
Leu Gln Val Val Arg Ser Leu Val Lys Pro Glu Asn Tyr Arg Arg Leu
1   5   10   15

Asp Ile Val Arg Ser Leu Tyr Glu Asp Pro Pro Glu Asp His Pro Asn
            20   25   30

Val Gln Lys Asp Leu Glu Arg Leu Thr Gln Glu Arg Ile Ala His Gln
        35   40   45

Arg Met Gly Asp
    50

<210> 3539
<211> 52
<212> PRT
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<223> /note="p.R231H"

<400> 3539
Ile Pro Ile Ser Trp Val Cys Asp Asp Asp Ala Asp Cys Ser Asp Gln
1   5   10   15

Ser Asp Glu Ser Leu Glu Gln Cys Gly His His Gln Pro Val Ile His
            20   25   30

Thr Lys Cys Pro Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile

35 40 45

His Lys Lys Trp
50

<210> 3540
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3540
Ala Gln Arg Gln Lys Leu His His Lys Ser Glu Met Gly Thr Pro Gln
1 5 10 15

Gly Glu Asn Trp Leu Ser Trp Met Phe Gln Gln Lys Leu Val Val Val
20 25 30

Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser Met Ala Gln Ser
35 40 45

Tyr Ala Lys Arg
50

<210> 3541
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.R802Q"

<400> 3541
Ala Arg Leu Gln Lys Ala Asp Val Val Ala Gln Ser Arg Ile Ser Phe
1 5 10 15

Pro Glu Lys Glu Leu Leu Leu Leu Ile Gln Gln Asn His Leu Ile Ser
20 25 30

Lys Gly Leu Gly Glu Thr Ala Thr Val Leu Thr Lys Glu Ala Asp Leu
35 40 45

Pro Met Thr Ala
50

<210> 3542
<211> 40
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.K939fs"

<400> 3542
Cys Asn Gly Arg Lys Ile Arg Val Leu Arg Gln Lys Ser Asp His Gly
1 5 10 15

Ala Tyr Ser Gln Ser Pro Ala Ile Lys Asn Ser Trp Thr Asp Ile Phe
20 25 30

Leu Pro His Leu Arg Trp Thr Val
35 40

<210> 3543
<211> 44
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.F2883fs"

<400> 3543
Ile Leu Gly Leu Asp Val Leu Gly Asn Pro Phe Gly Leu Ile Arg Glu
1 5 10 15

Phe Ser Glu Gly Val Glu Ala Phe Phe Met Asn Leu Thr Arg Glu Pro
20 25 30

Ser Arg Val Leu Lys Ser Leu Trp Lys Glu Trp His
35 40

<210> 3544
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R692Q"

<400> 3544
Ile Met Gly Glu Lys Asn Ser Ser Asn Phe Met Asn Thr Thr Asn Phe
1 5 10 15

Gln Ser Leu Arg Pro Leu Pro Ser Ile Gln Gln Ile Leu Val Asp Lys
20 25 30

Ile Asn Leu Glu His Ser Val Pro Met Tyr Ala Glu Gln Leu Val His
35 40 45

Val Val Ser Ser
50

<210> 3545
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.G2575W"

<400> 3545
Ala Gln Ala Asp Cys Lys Leu Leu Glu Cys Arg Asn Val Thr Met Gln
1 5 10 15

Ser Val Val Lys Pro Phe Ser Ile Phe Trp Trp Gln Met Ala Val Ser
20 25 30

Ser Asp Val Val Glu Lys Leu Leu Asp Cys Thr Val Ile Val Asp Ser
35 40 45

Val Phe Val Asn
50

<210> 3546
<211> 52
<212> PRT
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<220>
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<223> /note="p.D1359Y"

<400> 3546
Ser Trp Tyr His Lys Val Pro Val Val Glu Ile Lys Gly His Leu Asp
1 5 10 15

Ser Met Asn Val Ser Leu Asn Gln Glu Tyr Tyr Leu Asn Leu Leu Phe
20 25 30

Arg Ile Leu Thr Glu Asn Leu Cys Glu Gly Thr Glu Asp Leu Asp Lys
35 40 45

Val Lys Pro Arg
50

<210> 3547
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G317D"

<400> 3547
Arg Thr Thr Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys Gln Asn Gly
1 5 10 15

Gly Thr Cys Val Pro Glu Gly Leu Asp Asp Asp Tyr Gln Cys Leu Cys

20 25 30

Pro Leu Ala Phe Gly Gly Glu Ala Asn Cys Ala Leu Lys Leu Ser Leu
35 40 45

Glu Cys Arg Val
50

<210> 3548
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V955I"

<400> 3548
Leu Glu Lys Val Leu Arg Arg Tyr Val Gln Arg Leu Gln Trp Leu Leu
1 5 10 15

Ser Gly Ser Arg Arg Leu Phe Gly Thr Ile Ile Leu Glu Ser Lys Val
20 25 30

Cys Ile Leu Leu Asp Thr Ser Gly Ser Met Gly Pro Tyr Leu Gln Gln
35 40 45

Val Lys Thr Glu
50

<210> 3549
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R557L"

<400> 3549
Gln Phe Ile Gln Glu Gln Leu Lys Tyr Lys Ser Lys Phe Asn Phe Val
1 5 10 15

Lys Phe Asp Gly Gln Ala Val Ala Trp Leu Leu Glu Gln Leu Ala Glu
20 25 30

Val Asn Glu Asp Asn Leu Glu Gln Ala Gln Ser Trp Ile Arg Asp Ile
35 40 45

Lys Ile Gly Ser
50

<210> 3550
<211> 52
<212> PRT
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<220>
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<220>
<221> source
<223> /note="p.V792G"

<400> 3550
Phe Ser Leu Thr Ser Asn Leu Ser Arg Ala His Leu Glu Leu Asn Glu
1 5 10 15

Ser Ala Trp Gly Arg Leu Trp Leu Glu Gly Gly Pro Asp Ser Ala Ala
20 25 30

Pro Asp Ser Val Val Met Val Thr Val Thr Ala Gly Gly Arg Glu Ala
35 40 45

Asn Pro Val Pro
50

<210> 3551
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K1720N"

<400> 3551
Leu Leu Asp Gly Ser Ser Ser Phe Pro Ala Ser Tyr Phe Asp Glu Met
1 5 10 15

Lys Ser Phe Ala Lys Ala Phe Ile Ser Asn Asn Ala Asn Ile Gly Pro
20 25 30

Arg Leu Thr Gln Val Ser Val Leu Gln Tyr Gly Ser Ile Thr Thr Ile
35 40 45

Asp Val Pro Trp
50

<210> 3552
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R522fs"

<400> 3552
Gly Phe Asp Asp Leu Ser Glu Ser Glu Asp Asp Glu Asp Asp Asp Cys
1 5 10 15

Gln Val Glu Arg Lys Thr Ser Lys Lys Glu Leu Lys Gln Leu His His
20 25 30

Pro Pro Cys Ser Leu Pro Gln Lys Ala Met Ile Ile Pro Arg Thr Val
35 40 45

Ser Leu Val Leu Thr Met Gln Arg Thr Cys Leu Val Cys Leu Lys Val
50 55 60

<210> 3553
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.P305fs"

<400> 3553
Glu His Glu Tyr Arg Pro Pro Ser Ala Ser Ala Arg His Met Ala Leu
1 5 10 15

Asn Arg Pro Gln Gln Pro Pro Pro Pro Ala Ser Pro Ser Gly Pro Arg
20 25 30

Gly Val Pro Gly Leu Cys Thr Asp Gly Ser Ser Arg Leu Arg Asp Ala
35 40 45

Pro Ser Ala Asp Asn
50

<210> 3554
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G175S"

<400> 3554
Ala Pro Arg Glu Val Val Asp Pro Ser Gly Gly Arg Ala Thr Leu Leu
1 5 10 15

Glu Ser Ile Arg Gln Ala Gly Gly Ile Ser Ser Lys Ala Lys Leu Arg
20 25 30

Ser Met Lys Glu Arg Lys Leu Glu Lys Lys Gln Gln Lys Glu Gln Glu
35 40 45

Gln Val Arg Ala
50

<210> 3555
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L187V"

<400> 3555
Ala Thr Leu Leu Glu Ser Ile Arg Gln Ala Gly Gly Ile Gly Lys Ala
1 5 10 15

Lys Leu Arg Ser Met Lys Glu Arg Lys Val Val Glu Lys Lys Gln Gln
20 25 30

Lys Glu Gln Glu Gln Val Arg Ala Thr Ser Gln Gly Gly His Leu Met
35 40 45

Ser Asp Leu Phe
50

<210> 3556
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P138fs"

<400> 3556
Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala Tyr Glu Asp Val Val
1 5 10 15

His Arg Pro Gly Thr Pro Pro Pro Pro Leu Tyr Cys Gly Pro Arg Pro
20 25 30

Pro Leu Asp Cys Phe Gln
35

<210> 3557
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R228C"

<400> 3557
Leu Glu Glu Tyr Val His Lys Arg Tyr Pro Gly Leu Val Lys Val Val
1 5 10 15

Arg Asn Gln Lys Arg Glu Gly Leu Ile Cys Cys Ala Arg Ile Glu Gly
20 25 30

Trp Lys Val Ala Thr Gly Gln Val Thr Gly Phe Phe Asp Ala His Val
35 40 45

Glu Phe Thr Ala
50

<210> 3558
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L1842fs"

<400> 3558
Phe Ile Phe Gly Val Pro Ala Ser Ser Gly Thr Val Val Ser Ser Ile
1 5 10 15

His Asn Val Cys Thr Glu Ala Val Phe Tyr Tyr Trp Glu Cys Ser Ala
20 25 30

Ala Cys

<210> 3559
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P278S"

<400> 3559
Ser Glu Ser Leu Ser Cys Ile Thr Thr Phe Asn Leu Pro Ser Ala Ala
1 5 10 15

Ala Ser Val Gln Cys Leu Ala Trp Val Ser Ser Ser Ala Pro Gly Met
20 25 30

Phe Ile Thr Gly Asp Ser Gln Val Gly Val Leu Arg Ile Trp Asn Val
35 40 45

Ser Arg Thr Thr
50

<210> 3560
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E841K"

<400> 3560
Lys Ser Ser Glu Leu Glu Glu Ser Leu Leu Val Leu Pro Phe Ser Tyr
1 5 10 15

Val Pro Asp Ile Leu Lys Leu Phe Asn Lys Lys Phe Ile Gln Leu Gly
20 25 30

Ser Asp Val Glu Leu Ile Cys Arg Cys Leu Phe Phe Leu Leu Arg Ile
35 40 45

His Phe Gly Gln
50

<210> 3561
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.W60G"

<400> 3561
Pro Gly Pro Leu Gln Asp Glu Thr Leu Gly Val Ala Ser Val Pro Ser
1 5 10 15

Gln Trp Arg Ala Val Gln Gly Ile Arg Gly Gly Glu Thr Lys Ser Cys
20 25 30

Gln Thr Ala Ser Ile Ala Thr Ala Ser Ala Ser Ala Gln Ala Arg Asn
35 40 45

His Val Asp Ala
50

<210> 3562
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.N214fs"

<400> 3562
Asp Gly Leu Cys Arg Ile Trp Asp Thr Ala Ser Gly Gln Cys Leu Lys
1 5 10 15

Thr Leu Ile Asp Asp Asp Asn Pro Pro Cys Leu Leu
20 25

<210> 3563
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R837S"

<400> 3563
Glu His Leu Ser Ser Pro Trp Gly Glu Ser Ser Pro Glu Glu Leu Arg
1 5 10 15

Phe Gly Ser Leu Thr Tyr Ser Asp Pro Ser Ser Glu Arg Glu Arg Asp
20 25 30

Gln His Asp Lys Asn Lys Arg Leu Leu Asp Pro Ala Asn Thr Gln Gln
35 40 45

Phe Asp Asp Phe
50

<210> 3564
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.N160fs"

<400> 3564
Ile Lys Asp Thr Arg Lys Pro Thr Val Ala Leu Ser Ala Val Ala Gly
1 5 10 15

Ala Ser Gln Val Lys Trp Asn Lys Lys Met Leu Thr Ala Leu Pro Pro
20 25 30

Ala Met Thr Ala Met Cys Gly Tyr Gly Ile Arg Gly Asn Pro Val Gln
35 40 45

Gln Trp Asn Ile
50

<210> 3565
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q412fs"

<400> 3565
Asp Gly Asp Asp Asp Glu Ser Ser Asn Glu Pro Glu Ser Arg Glu Lys
1 5 10 15

Leu Glu Glu Leu Pro Leu Ala Gln Lys Arg Lys Tyr Lys Lys Phe Lys
20 25 30

Glu Leu Leu Met Gln Lys Met Lys Gly Leu Ala Ser Tyr Leu
35 40 45

<210> 3566
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.G262fs"

<400> 3566
Arg Val Phe Asp Ala Gly Asp Tyr Ser Leu Leu Cys Ser Gly Pro Ser
1 5 10 15

Glu Asn Gly Gln Thr Trp Thr Gly Gly Thr Leu Ser His Gln Ile Lys
20 25 30

Ser Ser Phe Gly Gln Lys Met Gly Lys Val Ile Phe Thr Asn Tyr Leu
35 40 45

Pro Val Ala Phe Gln Leu Val Ile His Ser Ala Val Met Trp Gly Arg
50 55 60

Gln Leu Lys Ile
65

<210> 3567
<211> 68
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.DGTRSQ315del"

<400> 3567
Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val Tyr Asp Ala
1 5 10 15

Thr Ser Trp Asp Gly Thr Arg Ser Gln Val Glu Pro Leu Phe Thr His
20 25 30

Arg Gly His Ile Phe Leu Asp Gly Asn Gly Met Asp Pro Ala Pro Leu
35 40 45

Val Thr Thr His Thr Trp His Pro Cys Arg Pro Arg Thr Leu Leu Ser
50 55 60

Ala Thr Asn Asp
65

<210> 3568
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P287Q"

<400> 3568
Ser Leu Leu Ser Gly Gly Arg Glu Ser Val Leu Val Glu Trp Arg Asp
1 5 10 15

Ala Thr Glu Lys Asn Lys Glu Phe Leu Gln Gln Arg Leu Gly Ala Thr
20 25 30

Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu Phe Cys Thr Ser
35 40 45

His Ser Asp Asn
50

<210> 3569
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.N110K"

<400> 3569
Asn Gln Ser Arg Met Ala Val Ser Lys Thr Val Leu Ile Pro Pro Glu
1 5 10 15

Leu Lys Thr Val Glu Lys Pro Asn Pro Lys Lys Ile Lys Thr Thr Gln
20 25 30

Val Phe Asp Ile Asn Gly Thr Asp Val Thr Pro Arg Pro Leu Tyr His
35 40 45

Pro Asp Pro Leu
50

<210> 3570
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G100W"

<400> 3570
Lys His Gln Val Pro Glu Lys Leu Ile Trp Gly Asp Gln Asp Pro Leu
1 5 10 15

Ser Lys Ile Pro Phe Lys Ile Leu Ser Trp Trp His Glu His Ala Val
20 25 30

Ser Thr Cys His Phe Cys Val Asp Asp Thr Lys Leu Leu Ser Gly Ser
35 40 45

Tyr Asp Cys Thr

50

<210> 3571
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M287fs"

<400> 3571
Arg Leu Arg Val Leu Val Ala Thr Tyr Val Thr Phe Ser Pro Asn Gly
1 5 10 15

Thr Glu Leu Leu Val Asn Met Gly Gly Gly Thr Gly Leu Phe Val
20 25 30

<210> 3572
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K418fs"

<400> 3572
Tyr Ile Asp Lys Gln Pro Glu Glu Ala Leu Ser Gln Ala Lys Lys Ser
1 5 10 15

Val Ala Ser Lys Thr Glu Val Lys Lys Asn Pro Thr Thr Lys Ile Cys
20 25 30

Ala Glu Tyr Ser Ala Arg Thr Asp Gln Cys Arg Gly Gly Gly Leu Leu
35 40 45

Thr Leu Lys Tyr
50

<210> 3573
<211> 77

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G606fs"

<400> 3573
Cys Glu Thr Asp Gly Tyr Leu Ser Ser Ser Gly Phe Leu Asp Ala Ser
1 5 10 15

Asp Pro Ala Leu Gln Pro Pro Gly Gly Cys His Pro Ala Trp Leu Ser
20 25 30

Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe His Val Leu
35 40 45

Ala Leu Glu Val Thr Phe Pro Pro Gly Thr Ala Met Pro Gln Met Gln
50 55 60

Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp Lys
65 70 75

<210> 3574
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W167fs"

<400> 3574
Ser Glu Gly Ser Ile Glu Ser Cys Thr Cys Asp Tyr Arg Arg Arg Gly
1 5 10 15

Pro Gly Gly Pro Asp Trp His Trp Gly Ala Ala Ala Thr Thr Leu Thr
20 25 30

Ser Ala Ala Ser Ser Ala Gly Ser Ser Trp Thr Pro Gly Arg Arg Gly
35 40 45

Gly Thr Cys Ala Ser Ser
    50

<210> 3575
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="p.C344Y"

<400> 3575
Asn Pro Tyr Thr Asp Arg Val Val Glu Arg Cys His Cys Lys Tyr His
1   5   10   15

Trp Cys Cys Tyr Val Thr Cys Arg Arg Tyr Tyr Glu Arg Thr Val Glu
            20   25   30

Arg Tyr Val Cys Lys
        35

<210> 3576
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.W165fs"

<400> 3576
Gly Asn Met Thr Glu Cys Ser Cys Asp Thr Thr Leu Gln Asn Gly Gly
1   5   10   15

Ser Ala Ser Glu Gly Trp His Trp Gly Ala Ala Pro Met Met Ser Ser
            20   25   30

Met Ala Cys Gly Ser Ala Glu Ser Ser
        35   40

<210> 3577
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K327E"

<400> 3577
Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu Leu Met
1 5 10 15

Cys Cys Gly Arg Gly Tyr Asn Gln Phe Glu Glu Ser Val Gln Val Glu
20 25 30

Arg Cys His Cys Lys Phe His Trp Cys Cys Phe Val Arg Cys Lys Lys
35 40 45

Cys Thr Glu Ile
50

<210> 3578
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S381fs"

<400> 3578
His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val Arg Arg Val Pro
1 5 10 15

Gly Val Ala Pro Thr Leu Val Arg Ser Gly Arg His Leu Arg Pro Val
20 25 30

Arg Asn Ala Pro Ser Cys Val Leu Thr Gln Ala Ala Ile Arg Asp Ile
35 40 45

Leu Ser Cys Pro Thr Tyr Arg Cys Thr Ala Gly Ser Thr Leu Val Arg

50 55 60

Asn His Thr Ser Val Thr Ser Arg Thr Val Asn Glu Gly Phe Leu Val
65 70 75 80

Gln Thr Ser Ser Lys Asp Thr Lys Gly Asp Ile Gln Val
85 90

<210> 3579
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G458A"

<400> 3579
Glu Asp Pro Arg Thr Gln Gly Met Ile Gln Glu Pro Ala Leu Pro Pro
1 5 10 15

Gly Trp Glu Met Lys Tyr Thr Ser Glu Ala Ala Val Arg Tyr Phe Val
20 25 30

Asp His Asn Thr Arg Thr Thr Thr Phe Lys Asp Pro Arg Pro Gly Phe
35 40 45

Glu Ser Gly Thr
50

<210> 3580
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E782K"

<400> 3580
Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu Leu
1 5 10 15

Glu Gln Arg Ala Glu Gln Leu Ala Ala Lys Lys Ala Glu Arg Asp Gln
20 25 30

Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser
35 40 45

Arg Glu Glu Leu
50

<210> 3581
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P410S"

<400> 3581
Met Asp His Thr Phe Phe Pro Gly Tyr Arg Lys Thr Leu Leu Ser Pro
1 5 10 15

Glu Glu Ile Leu Leu Ser Ile Glu Ile Ser Ser Tyr Ser Arg Glu Gly
20 25 30

Glu Tyr Phe Ser Ala Phe Lys Gln Ala Ser Arg Arg Glu Asp Asp Ile
35 40 45

Ala Lys Val Thr
50

<210> 3582
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D2439N"

<400> 3582
Gly Lys Thr Gly Val Leu Pro Pro Thr Leu Pro Lys Pro Lys Leu
1 5 10 15

Pro Lys His Ile Lys Asp Asn Lys Asn Asn Asn Phe Ser Pro Lys Val
20 25 30

Glu Leu Ala Thr Ser Leu Ser Asp Met Glu Cys Lys Ile Thr Thr Ser
35 40 45

Lys Asp Gln Lys
50

<210> 3583
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V3008E"

<400> 3583
Ile Pro Gly Trp Leu Ile Ser Glu Asp Lys Arg Glu Tyr Ala Val His
1 5 10 15

Ile Ala Met Glu Asn Asn Leu Glu Lys Glu Glu Lys Glu Glu Ile Thr
20 25 30

His Ile Lys Thr Gln Ala Glu Asp Met Leu Val Ser Tyr Glu Asn Ile
35 40 45

Ile Gln Thr Ala
50

<210> 3584
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R268Q"

<400> 3584
Ser Val Ile His Leu Leu Gln Met Gly Gln Val Trp Arg Tyr Ile Arg
1 5 10 15

Thr Met Tyr Leu Gly Ile Gln Ser Gln Gln Gln Arg Lys Glu His Gln
20 25 30

Arg Arg Phe Tyr Trp Ala Met Met Tyr Glu Tyr Ala Asp Val Asn Met
35 40 45

Leu Arg Leu Leu
50

<210> 3585
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E571K"

<400> 3585
Gln Tyr Pro Arg Phe Leu Arg Ala His Trp Lys Phe Leu Lys Thr Val
1 5 10 15

Val Asn Lys Leu Phe Glu Phe Met His Lys Lys Thr His Asp Gly Val
20 25 30

Gln Asp Met Ala Cys Asp Thr Phe Ile Lys Ile Ala Gln Lys Cys Arg
35 40 45

Arg His Phe Val
50

<210> 3586
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R541W"

<400> 3586
Glu Pro Gln His Ile Pro Cys Val Leu Met Ala Phe Leu Asp His Arg
1 5 10 15

Gly Leu Arg His Ser Ser Ala Lys Val Trp Trp Ser Arg Thr Ala Tyr
20 25 30

Leu Phe Ser Arg Phe Val Lys Ser Leu Asn Lys Gln Met Asn Pro Phe
35 40 45

Ile Glu Asp Ile
50

<210> 3587
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S87F"

<400> 3587
Thr Ser Pro Val Leu Met Trp Val Gln Ala Leu Asp Ile Ile Leu Glu
1 5 10 15

Lys Met Lys Ala Ser Gly Phe Asp Phe Phe Phe Gln Val Leu Ala Leu
20 25 30

Ser Gly Ala Gly Gln Gln His Gly Ser Ile Tyr Trp Lys Ala Gly Ala
35 40 45

Gln Gln Ala Leu
50

<210> 3588
<211> 102
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Y526fs"

<400> 3588
Arg Lys Phe Glu Ser Thr Val Asn Gln Glu Val Leu Glu Ile Leu Asp
1 5 10 15

Phe His Leu Tyr Gly Ser Tyr Pro Pro Ala Arg Gln Pro Ser Arg Pro
20 25 30

Thr Gly Arg Thr Pro Thr Thr Arg Leu Met Ala Pro Val Gly Ser Val
35 40 45

Met Ser Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr
50 55 60

Met Pro Pro Leu Leu His Pro Gln Trp Ala Pro His Ser Ala Gly Leu
65 70 75 80

Ser Pro Gly Ala Cys Arg Pro Ala Cys Thr Cys Ile Ser Met Thr Thr
85 90 95

Ile Ser Arg Ala Thr Trp
100

<210> 3589
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P250L"

<400> 3589
Gly Ala Gly Glu Gln Gly Arg Pro Val Arg Gln Asn Met Tyr Arg Gly
1 5 10 15

Tyr Arg Pro Arg Phe Arg Arg Gly Pro Leu Leu Arg Gln Arg Gln Pro
20 25 30

Arg Glu Asp Gly Asn Glu Glu Asp Lys Glu Asn Gln Gly Asp Glu Thr
35 40 45

Gln Gly Gln Gln
50

<210> 3590
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P226fs"

<400> 3590
Ser Ala Gly Thr Gly Pro Gly Ser Lys Gly Glu Arg Ala Glu Asp Ser
1 5 10 15

Gly Gln Arg Pro Arg Arg Trp Cys Pro His Pro Ser Ser Thr Asp Gly
20 25 30

Gly Leu Cys Glu Ala Pro Gly Leu Pro Thr Ser Ser Ser Leu
35 40 45

<210> 3591
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R131fs"

<400> 3591
Leu Gly Leu Leu Val Phe Pro Tyr Thr His Gln Asn Trp Glu Val Gln
1 5 10 15

Tyr Ser Arg Asp Ala Pro Leu Pro Pro Gly Lys Thr Ser Thr Pro Leu
20 25 30

Thr Ser Ile Ser Pro Arg Trp Pro Ser Leu Leu Thr Cys Ser Trp Leu
35 40 45

Gly Trp His Trp Ala Phe Arg Lys Gly Ser Pro Arg Arg Cys Trp Ala
50 55 60

Cys Val Gln Ala Gln Arg Trp Cys Gly Trp
65 70

<210> 3592
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E1178fs"

<400> 3592
Arg Gly Leu Gly Arg Ser Asp Phe Gly Arg Asp Arg Gly Pro Phe Arg
1 5 10 15

Pro Glu Pro Gly Asp Gly Gly Glu Lys Cys Ile His Ile Thr Gly Met
20 25 30

Ser Leu Leu Gly Leu His Gly Thr Met Glu Lys Ser Glu Gly Met Lys
35 40 45

Ser Phe His
50

<210> 3593
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E634K"

<400> 3593
Ile Met His Leu Leu Tyr Asn Ile Cys His Ser Cys Asp Ala Gly Ala

1 5 10 15

Val Leu Ile Phe Leu Pro Gly Tyr Asp Lys Lys Ile Val Gly Leu Arg
20 25 30

Asp Arg Ile Leu Phe Asp Asp Lys Arg Phe Ala Asp Ser Thr His Arg
35 40 45

Tyr Gln Val Phe
50

<210> 3594
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E185K"

<400> 3594
Asn Arg Glu Met Ser Lys Thr Ser Gly Arg Leu Asn Asn Gly Ile Pro
1 5 10 15

Gln Ile Pro Val Lys Arg Gly Glu Ser Lys Lys Phe Asp Ser Phe Arg
20 25 30

Gln Ser Leu Pro Val Phe Glu Lys Gln Glu Glu Ile Val Lys Ile Ile
35 40 45

Lys Glu Asn Lys
50

<210> 3595
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q42H"

<400> 3595
Cys Pro Pro Cys Ser Tyr Arg Tyr Pro Tyr Pro Ala Ala Thr Lys Gly
1 5 10 15

Lys Gly Ala Ala Gly Gly Ser Trp Gln His His Arg Gly Arg Gly Cys
20 25 30

Leu Pro Ala Ser Ser Pro Cys Ser Ala Gly Ala Ala Ser Leu Ser Phe
35 40 45

Pro Gly Cys Gly
50

<210> 3596
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R596I"

<400> 3596
Thr Lys Ser Ser Leu Leu Leu Gln Glu Ile Ala Cys Arg Ser Lys Pro
1 5 10 15

Ile Thr Lys Gln Tyr Gln Gly Leu Glu Ile Ile Phe Phe Ile Phe Asp
20 25 30

Thr Asn Glu Arg Leu Asn Leu Leu Pro Ser His Arg Leu Glu Cys Asn
35 40 45

Asn Ser Ser Thr
50

<210> 3597
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E151del"

<400> 3597
Lys Pro Lys Ile Asn Gly Lys Val Cys Gly Gln Cys Glu Asn Lys Ala
1 5 10 15

Ala Leu Leu Val Cys Leu Glu Cys Gly Asp Tyr Cys Ser Gly Cys Phe
20 25 30

Ala Lys Val His Gln Lys Gly Ala Leu Lys Leu His Arg Thr Thr Leu
35 40 45

Leu Gln Ala Lys Ser
50

<210> 3598
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S385L"

<400> 3598
Pro Ser Leu Leu Pro Pro Glu Gly Glu Leu Ser Ser Val Ser Ser Ser
1 5 10 15

Pro Val Lys Pro Val Arg Glu Ser Pro Leu Leu Ala Ser Ser Ser Pro
20 25 30

Asp Arg Leu Thr Glu Asp Leu Gln Ser His Leu Asn Pro Gly Asp Gly
35 40 45

Leu Met Glu Asp
50

<210> 3599
<211> 67
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.P692fs"

<400> 3599
Cys Lys Lys Lys Phe Ser His Lys Thr Leu Leu Glu Arg His Val Ala
1 5 10 15

Leu His Ser Ala Ser Asn Gly Thr Pro Leu Gln Ala His Pro Gln Val
20 25 30

Pro Ala Leu Ala Pro Gln Ala Trp Trp Pro Ala Arg Arg Gly Pro Leu
35 40 45

Thr Ser Ala Pro Ser Ala Gln Gln Ser Leu Thr Lys Ser Ser Ser Ser
50 55 60

Thr Thr Thr
65

<210> 3600
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.L607I"

<400> 3600
Gln Asn Met Thr Ala Asp Gln Ala Ala Asn Leu Thr Leu Leu Thr Gln
1 5 10 15

Gln Pro Glu Gln Leu Gln Asn Leu Ile Ile Ile Ser Ala Gln Gln Glu
20 25 30

Gln Thr Glu His Ile Gln Ser Leu Asn Met Ile Glu Ser Gln Met Gly
35 40 45

Pro Ser Gln Thr
50

<210> 3601

<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.L262fs"

<400> 3601
Gln Leu Asn Phe Leu Leu Glu Asn Glu Gly Val Phe Ser Asp Ala Leu
1 5 10 15

Met Val Thr Gln Asp Val Leu Lys Lys Thr Arg Asn Val Phe Arg Asn
20 25 30

<210> 3602
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G342fs"

<400> 3602
Glu Leu Pro Pro Pro Pro Pro Pro Pro Phe Pro Asn Asp Phe Phe Lys
1 5 10 15

Asp Met Phe Pro Asp Leu Pro Gly Gly Ala Ser Gly Thr His Gln Gly
20 25 30

Gly Glu Arg Leu Arg Cys Leu Ser Gln Leu Pro Glu Cys His Pro Pro
35 40 45

Gly Arg Pro Leu Pro Thr Leu Ala Pro Gly Arg Arg Ala Gln Ala Glu
50 55 60

Ala Gln Gly Leu Ser Ala Val Pro His Leu Pro Gln Ser His His Gly
65 70 75 80

Gly Arg Glu Ala Ala Ala Ala His Glu Asp Pro Tyr Arg Gly Glu Ala
85 90 95

Ile His Val His His Leu Arg Gly Pro Leu His Gln Ala Gly Gln Ala
100 105 110

Glu Asn Pro His Ala Glu Ala His Arg Gly Ala Ala Leu Pro Val His
115 120 125

Pro Leu Gln Arg Gln Val Arg Ala Gln Leu Arg Pro Gln Glu Pro His
130 135 140

Ala His Pro His Gly Arg Ala Ala Leu Pro Val Arg Val Leu Leu Gln
145 150 155 160

Glu Leu His Ala Leu
165

<210> 3603
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D154fs"

<400> 3603
Ile Leu Asn Ala Ala Arg Met Leu Glu Ile Gln Cys Ile Val Asn Val
1 5 10 15

Cys Leu Glu Ile Met Glu Pro Gly Gly Thr Gly Gly Arg Arg Met Thr
20 25 30

Arg Arg Thr Met Thr Thr Thr Lys Met Met Met Met Arg Arg Thr Lys
35 40 45

Arg Arg Arg Arg Lys Arg Arg Arg Met Thr Met Met Thr Arg Arg Thr
50 55 60

Leu Leu Thr Lys Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr
65 70 75 80

Lys Ala Leu Pro Arg Gln Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr
85 90 95

Pro Pro Gly Thr Ser Leu Thr Pro Ser Arg Leu Ala Val Leu Ala Ile
100 105 110

Trp Gly

<210> 3604
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E157fs"

<400> 3604
Ala Ala Arg Met Leu Glu Ile Gln Cys Ile Val Asn Val Cys Leu Glu
1 5 10 15

Ile Met Glu Pro Gly Gly Asp Gly Gly Arg Arg Met Thr Arg Arg Thr
20 25 30

Met Thr Thr Thr Lys Met Met Met Met Arg Arg Thr Lys Arg Arg Arg
35 40 45

Arg Lys Arg Arg Arg Met Thr Met Met Thr Arg Arg Thr Leu Leu Thr
50 55 60

Lys Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu
65 70 75 80

Pro Arg Gln Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro Gly
85 90 95

Thr Ser Leu Thr Pro Ser Arg Leu Ala Val Leu Ala Ile Trp Gly
100 105 110

<210> 3605
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

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<400> 3605
Ser Ala Gly Gly Arg Val Pro Gly Pro Leu Ser Leu Pro Ser Pro Glu
1 5 10 15

Ser Gln Phe Ser Pro Gly Asp Leu Pro Ser Ser Pro Pro Gly Leu Gln
20 25 30

Leu Gln Pro Arg Gly Glu His Arg Pro Arg Asp Leu His Gly Asp Leu
35 40 45

Leu Ser Pro Arg
50

<210> 3606
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

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<223> /note="p.K1006fs"

<400> 3606
Asn Ile Glu Thr Thr Ser Glu Asp Gly Gln Val Phe Ser Pro Lys Lys
1 5 10 15

Gly Gln Lys Lys Lys Ser Ile Glu Lys Asn Val Lys Asn Pro Lys Val
20 25 30

Ile Leu Ile Phe Leu Met Lys Lys Gln Pro Ser Lys Val Arg Arg Lys
35 40 45

Glu Ala His Gly Leu Pro Leu
50 55

<210> 3607
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

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<223> /note="p.T701fs"

<400> 3607
Pro Val Pro Glu Pro Thr Lys Pro Gly Asp Pro Arg Glu Ala Arg Arg
1 5 10 15

Lys Glu Arg Pro Ala Arg Thr Pro Pro Gln Glu Ala Asp Ala Lys Arg
20 25 30

Gln Arg Gln Trp Gln Trp
35

<210> 3608
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

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<400> 3608
Pro Lys Ser Ala Lys Pro Pro Ala Gly Gly Lys Ser Ser Gln Gln Pro
1 5 10 15

Ser Thr Pro Gln Gln Ala Pro Pro Gly Ser Pro Ser Arg Ala His Leu
20 25 30

Trp Pro Thr Arg Arg Ser Ser
35

<210> 3609
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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<223> /note="p.E798K"

<400> 3609
Ile Gln Gln Lys Gln Gln Glu Glu Glu Glu Arg Ala Arg Arg Leu Ala
1 5 10 15

Glu Ser Ser Lys Gln Asp Arg Glu Asn Lys Lys Glu Gly Asp Thr Gly
20 25 30

Asn Trp Tyr Ser Ser Asp Glu Asp Glu Gly Gly Ser Ser Val Thr Ser
35 40 45

Ile Leu Lys Thr
50

<210> 3610
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.C575S"

<400> 3610
Asn Gly Lys Ile Asn Leu Thr Val Phe Lys Leu Leu Gln Glu His Leu
1 5 10 15

Gly Glu Phe Ile Phe Leu Cys Glu Lys Ser Ser Phe Asp His Lys Pro
20 25 30

Arg Met Ile Ser Lys Arg Asn Lys Asp Asn Ser Thr Ala Cys Ser His
35 40 45

Pro Val Thr Lys
50

<210> 3611
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.K937N"

<400> 3611
Gly Lys His Val Glu Arg Ala Leu Leu Val Glu Leu Asn Lys Ile Ser
1 5 10 15

Leu Lys Glu Glu Asn Val Cys Glu Glu Asn Asn Asn Ser Pro Val Asp
20 25 30

Gln Ser Asp Phe Phe Tyr Glu Phe Ser Lys Leu Ile Phe Thr Lys Gly
35 40 45

Lys Ser Pro Thr
50

<210> 3612
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3612
Lys Gly Val Ala Phe Ile Leu Phe Leu Asp Lys Asp Ser Ala Gln Asn
1 5 10 15

Cys Thr Arg Ala Ile Asn Asn Lys Gln Phe Phe Phe Gly Arg Val Ile
20 25 30

Lys Ala Ser Ile Ala Ile Asp Asn Gly Arg Ala Ala Glu Phe Ile Arg
35 40 45

Arg Arg Asn Tyr
50

<210> 3613
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D144N"

<400> 3613
Asp Arg Phe Lys Gly Lys Tyr Val Thr Tyr Asp Pro Asp Gly Asn Val
1 5 10 15

Glu Glu Tyr His Ile Glu Phe Leu Gly Asn Asn Pro His Ser Arg Ser
20 25 30

Trp Ile Lys Ala Thr Phe Val Gly His Tyr Ser Ile Thr Leu Lys Pro
35 40 45

Glu Lys Cys Lys
50

<210> 3614
<211> 52
<212> PRT
<213> Artificial Sequence

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polypeptide"

<220>
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<223> /note="p.H250Q"

<400> 3614
Pro Val Gln Val Gln Thr Leu Ile Val Val Ile Ile Gly Met Leu Val
1 5 10 15

Leu Leu Leu Asp Phe Leu Gly Leu Val Gln Gln Leu Gly Gln Leu Leu
20 25 30

Ile Phe His Ile Tyr Leu Lys Ala Lys Lys Met Thr Thr Phe Glu Tyr
35 40 45

Leu Ile Asn Asn
50

<210> 3615

<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3615
Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp
1 5 10 15

Tyr Arg Gly Asp Trp Ala Trp Cys Gln His His Cys Pro Leu Val Ala
20 25 30

Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser His
35 40 45

Gly Leu Arg Ser
50

<210> 3616
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3616
Pro Thr Ala Pro Tyr Leu Gly Arg Ser Met Ser Tyr Ser Ser Gln Lys
1 5 10 15

Ala Gln Pro Gly Val Ser Glu Thr Glu Val Ala Leu Gln Pro Leu Leu
20 25 30

Thr Pro Lys Asp Glu Val Gln Leu Lys Thr Thr Tyr Ser Lys Ser Asn
35 40 45

Gly Gln Pro Lys Ser
50

<210> 3617
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.P316fs"

<400> 3617
Leu Lys Ser Glu Lys Pro Thr Trp Glu Arg Arg Leu Arg Trp Glu Gly
1 5 10 15

Met Lys Ser Val Phe Gly Gly Pro Pro His Ser Ser Gly
20 25

<210> 3618
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<220>
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<223> /note="p.E1094K"

<400> 3618
Ser Tyr Ser Gln His Met Asn His Arg Tyr Ser Tyr Cys Lys Arg Glu
1 5 10 15

Ala Glu Glu Arg Glu Ala Ala Glu Arg Lys Lys Ala Arg Glu Lys Gly
20 25 30

His Leu Glu Pro Thr Glu Leu Leu Met Asn Arg Ala Tyr Leu Gln Ser
35 40 45

Ile Thr Pro Gln
50

<210> 3619
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3619
Asn Asn Gly Thr Val Lys Asn Ala Asn Cys Thr Ser Asp Phe Glu Glu
1 5 10 15

Tyr Phe Ala Lys Arg Lys Leu Glu Glu His His Asp Gly His Ala Val
20 25 30

Ser Ile Glu Glu Tyr Leu Gln Arg Ser Asp Thr Ala Ile Ile Tyr Pro
35 40 45

Glu Ala Pro Glu
50

<210> 3620
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.I149T"

<400> 3620
Ile Lys His Arg His Pro Leu Asp His Asp Cys Ser Gly Glu Gly His
1 5 10 15

Pro Thr Ser Arg Ala Gly Leu Ala Ala Thr Thr Ser Arg Ala Gln Ala
20 25 30

Val Ala Ser Thr Ser Thr Val Pro Ser Pro Ser Gln Thr Met Pro Ser
35 40 45

Cys Thr Ser Pro
50

<210> 3621
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<400> 3621
Lys Lys Leu Gly Glu Asp Glu Glu Glu Leu Ser Glu Leu Gln Leu Arg
1 5 10 15

Leu Leu Ala Leu Gln Ser Ala Ser Lys Asn Gly Asn Lys Lys Asn Ser
20 25 30

Arg

<210> 3622
<211> 85
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E763fs"

<400> 3622
Lys Gly Asn Leu Ser Ile His Met Gln Ser Asp Lys His Leu Asn Asn
1 5 10 15

Met Gln Asn Leu Gln Asn Gly Gly Gly Ser Arg Ser Ser Ala Thr Leu
20 25 30

Pro Gly Arg Arg Arg Arg Arg Trp Leu Arg Arg Arg Arg Gln Pro Ile
35 40 45

Ser Val Ala Pro Ala Gly Pro Pro Arg Arg Pro Asn Gln Lys Pro Asn
50 55 60

Pro Pro Gly Gly Ala Arg Cys Val Ile Met Arg Pro Thr Trp Pro Gly

65 70 75 80

Thr Ser Ala Phe Thr
85

<210> 3623
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V777del"

<400> 3623
Asn Asn Met Gln Asn Leu Gln Asn Gly Gly Gly Glu Gln Val Phe Ser
1 5 10 15

His Thr Ala Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
20 25 30

Asn Ile Ser Ser Ser Cys Gly Ala Pro Ser Pro Thr Lys Pro Lys Thr
35 40 45

Lys Pro Thr Trp Arg
50

<210> 3624
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R1893fs"

<400> 3624
Leu Gln Pro Ser Gln His Pro Glu Lys Lys Asn Lys Leu Val Ile Lys
1 5 10 15

Glu Lys Glu Lys Glu Ser Gln Arg Glu Gly Gln Arg Arg Gly Gly Arg
20 25 30

Gly Gln His Arg Ser Glu Gly Asn Thr Ala Arg Cys Leu Glu Gly Gln
35 40 45

Arg Glu Glu Arg Val Gly Thr Arg Gly Trp Phe
50 55

<210> 3625
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.L408fs"

<400> 3625
Ala Ser Thr Ser Ser Ser Ala Glu Gln Pro Leu Gly Ile Thr Gln Met
1 5 10 15

Pro Lys Ala Glu Val Asn Leu Gly Gly Ala Val
20 25

<210> 3626
<211> 52
<212> PRT
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<220>
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<400> 3626
Met Thr Ser Glu Lys His Met His Asn Met Met Leu Leu Gln Gln Asn
1 5 10 15

Met Lys Gln Ile Gln His Asn Leu His Phe Phe Gly Leu Ala Pro Ala
20 25 30

Glu Ala Glu Leu Tyr Gln Tyr Tyr Leu Ala Gln Asn Ile Gly Leu Thr
35 40 45

Gly Met Lys Leu
    50

<210> 3627
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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      polypeptide"

<220>
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<223> /note="p.T1663N"

<400> 3627
Ile Ala Ala Asn Val Asn Ser Pro Gly Gln Gly Met Leu Asp Ser Met
1   5   10   15

Ser Leu Ala Ala Val Asn Ser Lys Asp Asn Asn His Leu Asp Ala Lys
            20   25   30

Glu Leu Asn Lys Lys Gln Thr Pro Asp Leu Ile Ser Ala Gln Pro Ala
        35   40   45

His His Pro Pro
    50

<210> 3628
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.H2511Q"

<400> 3628
Leu Pro Pro Gln Leu Leu Gln Tyr Gln Cys Asp Gln Cys Thr Val Ala
1   5   10   15

Phe Pro Thr Leu Glu Leu Trp Gln Glu Gln Gln Gln His Met His Phe
            20   25   30

Leu Ala Ala Gln Asn Gln Phe Leu His Ser Pro Phe Leu Glu Arg Pro
35 40 45

Met Asp Met Pro
50

<210> 3629
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R386C"

<400> 3629
Ser Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys
1 5 10 15

Thr Phe Arg Leu Arg Gln Gln Leu Val Cys Cys His Gln Arg Ile His
20 25 30

Thr Arg Glu Lys Pro Tyr Glu Cys Met Glu Cys Trp Lys Thr Phe Ser
35 40 45

Ser Tyr Ser Gln
50

<210> 3630
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q17L"

<400> 3630
Met Ala His Gly Ser Val Thr Phe Arg Asp Val Ala Ile Asp Phe Ser
1 5 10 15

Leu Leu Glu Glu Trp Glu Phe Leu Asp Pro Ala Gln Arg Asp Leu Tyr

20 25 30

Arg Asp Val Met Trp Glu Asn Tyr Ser Asn Phe
35 40

<210> 3631
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R150I"

<400> 3631
Thr Gly Glu Lys Pro Tyr Lys Cys Asn Val Cys Gly Lys His Phe Ile
1 5 10 15

Glu Arg Ser Ser Leu Thr Val His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Ser Met
35 40 45

Asn Leu Thr Val
50

<210> 3632
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R273I"

<400> 3632
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Thr Phe Arg
1 5 10 15

Val Ser Ser Gln Leu Ile Gln His Gln Ile Ile Ile His Thr Glu Glu
20 25 30

Arg Tyr His Glu Cys Asn Glu Cys Gly Lys Ala Phe Lys His Ser Ser
35 40 45

Gly Leu Ile Arg
50

<210> 3633
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.D240N"

<400> 3633
Ile His Asn Ala Asp Glu Arg Arg Pro Ala Pro Ser Gly Gly Ala Ser
1 5 10 15

Gly Asp Leu Arg Ala Phe Gly Thr Arg Asn Asn Ala Leu His Leu Gly
20 25 30

Phe Pro Arg Glu Pro Arg Pro Lys Leu His His Ser Leu Ser Phe Ser
35 40 45

Gly Phe Pro Ser
50

<210> 3634
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V227I"

<400> 3634
Arg Ala Ala Leu Arg Lys His Leu Leu Ile His Gly Pro Arg Asp His
1 5 10 15

Val Cys Ala Glu Cys Gly Lys Ala Phe Ile Ile Glu Ser Ser Lys Leu
20 25 30

Lys Arg His Phe Leu Val His Thr Gly Glu Lys Pro Phe Arg Cys Thr
35 40 45

Phe Glu Gly Cys
50

<210> 3635
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T264M"

<400> 3635
His Thr Gly Glu Lys Pro Phe Arg Cys Thr Phe Glu Gly Cys Gly Lys
1 5 10 15

Arg Phe Ser Leu Asp Phe Asn Leu Arg Met Met His Val Arg Ile His
20 25 30

Thr Gly Glu Lys Arg Phe Val Cys Pro Phe Gln Gly Cys Asn Arg Arg
35 40 45

Phe Ile Gln Ser
50

<210> 3636
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.R591fs"

<400> 3636

Ile Gln His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn
1 5 10 15

Glu Cys Gly Arg Ala Phe Arg Lys Lys Asn Gln Pro Ala
20 25

<210> 3637
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E444fs"

<400> 3637
Gly Leu Ala Pro Thr Pro Ser Pro Gly Leu Asp Arg Lys Ala Leu Ala
1 5 10 15

Glu Ala Thr Asn Gly Glu Ala Arg Ala Ala Ser Gly Pro Glu Trp Arg
20 25 30

Gln Gln Arg Ala Pro Gly Gly Pro Gln Glu His Gln Gly Gly Gly Gly
35 40 45

Gly Gly Ala Gly Gly Gly Pro His Pro Gly Pro Arg Arg Ala Trp Ala
50 55 60

Pro Gly Pro Val Ala Asp Ala Val Ala Ala Gln Pro Arg Pro Gly Gln
65 70 75 80

Gly Gln Gly Arg Ala Val Gln Pro His Ala Gly Leu Gln Pro Gly Ala
85 90 95

Arg Arg Ala Gly Pro Gly Arg Gly Pro Val Pro Ser Ala Val Arg Val
100 105 110

Arg Ala Arg Arg Gly Ala Pro Arg Leu Gly Asp Pro Gly Gln Asp Val
115 120 125

Arg Ala Gly Ala Gln Pro Ala Ala Ala Gly Arg Gly Arg Gly Arg Arg
130 135 140

Arg Arg Ala Asp Arg Ala Leu Pro Arg Gly Pro Gln Gly Arg Tyr Val

145 150 155 160

Leu Arg Val Arg Asp His Leu Gln Gln Arg Gln Gln Leu Leu Arg Ala
165 170 175

Gln Ala Pro Leu Leu Phe Arg Pro Pro Cys Ala Arg Gly Arg Ala Cys
180 185 190

Arg Ala Gln Ala Gln Gly Ala Pro Arg Pro Gly Pro Arg Ala Pro Arg
195 200 205

Pro Ala Arg Arg Thr Arg Arg Ala Ala Leu Val Pro Gly Pro Arg Ser
210 215 220

Ala Arg Gly Gly Gly Trp Gly Arg Gly His Ala Arg Gly Arg Arg Gly
225 230 235 240

Arg Pro Gly Gln Arg Gly Gln Pro Glu Pro Gly
245 250

<210> 3638
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P445fs"

<400> 3638
Ala Pro Thr Pro Ser Pro Gly Leu Asp Arg Lys Ala Leu Ala Glu Ala
1 5 10 15

Thr Asn Gly Glu Ala Arg Ala Glu Pro Trp Pro Arg Met Glu Ala Ala
20 25 30

Ala Ser Pro Arg Arg Pro Pro Gly Ala Ser Arg Trp Arg Arg Trp Arg
35 40 45

Ser Arg Arg Arg Pro Pro Ser Trp Ala Pro Glu Ser Leu Gly Pro Arg
50 55 60

Pro Arg Arg Gly Arg Arg Arg Arg Ala Ala Pro Pro Arg Pro Gly Ser
65 70 75 80

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Arg Pro Ser Cys Pro Ala Pro Arg Arg Ala Pro Ala Arg Cys Pro Ala
                85                  90                  95

Ser Trp Ala Trp Pro Gly Pro Cys Ser Phe Arg Ser Thr Cys Ser Gly
            100                 105                 110

Pro Thr Arg Arg Pro Pro Pro Arg Arg Ser Trp Pro Arg Cys Pro Ser
        115                 120                 125

Trp Cys Thr Ala Gly Cys Ser Arg Ala Arg Ala Arg Ala Pro Ala Ala
    130                 135                 140

Arg Arg Pro Gly Ser Ser Pro Gly Pro Pro Arg Ala Leu Arg Ala Ser
145                 150                 155                 160

Ser Ala Arg Ser Pro Ser Ala Thr Ser Thr Thr Thr Thr Cys Thr Ser
                165                 170                 175

Ala Ser Thr Val Gln Ala Ala Val Arg Pro Arg Thr Arg Leu Pro Arg
            180                 185                 190

Ala Gly Pro Arg Arg Pro Pro Ala Arg Pro Ala Arg Pro Pro Ala Ser
        195                 200                 205

Pro Pro Asn Pro Thr Arg Arg Ala Arg Pro Arg Ala Pro Glu Arg Ala
    210                 215                 220

Arg Arg Gly Leu Gly Ala Arg Pro Arg Pro Arg Thr Ala Arg Ala Ala
225                 230                 235                 240

Gly Ala Ala Arg Ala Ala Arg Ala Arg Val Ala Pro Trp Thr Thr Arg
                245                 250                 255

Arg Thr Thr Pro Ala Ala Arg Cys Ala Arg Pro Ala Thr Ser Ala Ser
            260                 265                 270

Ala Ala Thr Arg Pro Thr Pro Cys Thr Ser Gly Thr Thr Ala Pro Arg
        275                 280                 285

Ala Thr Thr Arg Arg Arg Ala Asp Arg Pro Arg Pro Arg Asp Pro Leu
    290                 295                 300

Gly Arg Pro Arg Pro Arg Pro Pro Leu Pro Pro Arg Leu Cys Ala Arg
305                 310                 315                 320
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Ala Asp Ala Ala Ser Ser Thr Ser Cys Thr Arg Pro Ala Pro Arg Pro
325 330 335

Pro Arg Arg Pro Ala Thr Pro Pro Arg Pro Ser Arg Arg Gly Pro Glu
340 345 350

Ala Glu Ala Glu Ala Ala Pro Ala Ser Pro Leu Arg Ala Arg Pro Ala
355 360 365

Pro Arg Pro Thr Ala Pro Ser Thr
370 375

<210> 3639
<211> 52
<212> PRT
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<220>
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<220>
<221> source
<223> /note="p.Y107N"

<400> 3639
Thr Thr Met Ala Thr Tyr Gln Asp Ser Tyr Ser Tyr Gly Gln Ser Ala
1 5 10 15

Ala Ala Arg Ser Tyr Glu Asp Arg Pro Asn Asn Phe Gln Ser Ala Ala
20 25 30

Leu Gln Ser Gly Arg Met Thr Ala Ala Asp Ser Gly Gln Pro Gly Thr
35 40 45

Gln Glu Ala Cys
50

<210> 3640
<211> 52
<212> PRT
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.R266Q"

<400> 3640
Gly Ala Thr Val Asn Leu Ser Gln Arg Thr Arg Leu Leu Leu Lys Val
1 5 10 15

Leu Ala Ile Ser Asp Leu Val Ile Tyr Gln Gln Thr His Ala Asp Arg
20 25 30

Leu His Asn Asp Leu Phe Lys Phe Leu Gly Asp Ala Ser Glu Ala Tyr
35 40 45

Leu Lys His Phe
50

<210> 3641
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.M1147I"

<400> 3641
Val Val Gln Gly Leu Val Val Asp Met Glu Val Arg Lys Thr Ser Ile
1 5 10 15

Lys Ile Pro Ser Asn Arg Tyr Asn Glu Ile Ile Met Lys Ala Met Asn
20 25 30

Lys Ser Asn Glu His Val Leu Ala Gly Gly Ala Cys Phe Asn Glu Lys
35 40 45

Ala Asp Ser His
50

<210> 3642
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N249K"

<400> 3642
Glu Val Arg Glu Gly Asp His Ser Phe Ile Asn Gly Ala Val Pro Val
1 5 10 15

Ser Gln Ala Ser Ala Ser Ser Ala Lys Lys Lys Pro His Ala Ala Asn
20 25 30

Gly Pro Leu Ile Gly Thr Val Pro Val Leu Pro Ala Gly Ile Ala Gln
35 40 45

Phe Leu Ser Leu
50

<210> 3643
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<220>
<221> source
<223> /note="p.A112E"

<400> 3643
Gly Ser Tyr Ser Ser Ala Ala Phe Asn Ser Thr Arg Asp Phe Leu Phe
1 5 10 15

Arg Asn Arg Gly Phe Gly Asp Ala Ala Glu Glu Ala Ala Ser Ala Gln
20 25 30

His Ser Leu Phe Ala Ala Ser Ala Gly Gly Phe Gly Gly Pro His Gly
35 40 45

His Thr Asp Ala
50

<210> 3644
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.S305L"

<400> 3644
Gly Glu Lys Pro Phe Arg Cys Glu Phe Glu Gly Cys Glu Arg Arg Phe
1 5 10 15

Ala Asn Ser Ser Asp Arg Lys Lys His Leu Leu His Val His Thr Ser
20 25 30

Asp Lys Pro Tyr Thr Cys Lys Val Arg Gly Cys Asp Lys Cys Tyr Thr
35 40 45

His Pro Ser Ser
50

<210> 3645
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.D352N"

<400> 3645
Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Ile Cys Glu Lys
1 5 10 15

Ala Phe Ser Gln Lys Ser Asn Val Ile Asn Asn His Glu Lys Ile His
20 25 30

Thr Gly Lys Arg Ala Tyr Glu Cys Asp Leu Cys Gly Asn Thr Phe Ile
35 40 45

Gln Lys Lys Asn
50

<210> 3646
<211> 73
<212> PRT

<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.I384fs"

<400> 3646
Gly Lys Arg Ala Tyr Glu Cys Asp Leu Cys Gly Asn Thr Phe Ile Gln
1 5 10 15

Lys Lys Asn Leu Ile Gln His Lys Lys Ser Ile Leu Gly Lys Ser Pro
20 25 30

Met Asn Val Thr Asp Val Glu Lys Pro Ser Phe Arg Ser Gln Thr Phe
35 40 45

Ile Ala Ile Arg Lys Leu Ile Ala Glu Arg Gly Pro Ile Asp Val Val
50 55 60

Asn Val Glu Lys Pro Ser Ser Gly Asn
65 70

<210> 3647
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R541fs"

<400> 3647
Lys Cys Thr Lys Cys Gly Lys Ala Phe Thr Arg Ser Ser Thr Leu Thr
1 5 10 15

Leu His His Arg Ile His Ala Arg Glu Ser Leu
20 25

<210> 3648
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.K200A"

<400> 3648
Val Gly Ser Gln Pro Leu Gln Asp Arg Val Leu Gln Val Pro Val Leu
1 5 10 15

Ala His Gly Gly Cys Cys Arg Glu Asp Ala Ala Val Val Ala Ser Arg
20 25 30

Leu Thr Pro Glu Ser Gln Gly Leu Leu Lys Val Glu Asp Val Ala Leu
35 40 45

Thr Leu Thr Pro Glu
50

<210> 3649
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R319Q"

<400> 3649
Ile Pro Thr His Ala Glu Ala Gly Glu Gln Glu Gly Arg Leu Gln Arg
1 5 10 15

Lys Gln Lys Asn Ala Ile Gly Ser Arg Gln Gln His Tyr Cys His Glu
20 25 30

Cys Gly Lys Ser Phe Ala Gln Ser Ser Gly Leu Thr Lys His Arg Arg
35 40 45

Ile His Thr Gly
50

<210> 3650

<211> 26
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<223> /note="p.D13fs"

<400> 3650
Met Ile Met Thr Glu Ser Arg Glu Val Ile Asp Leu Asp Pro Gln Leu
1 5 10 15

Arg Leu Pro Arg Ser Arg Lys Thr Phe Ser
20 25

<210> 3651
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D1048fs"

<400> 3651
Met Pro Glu Pro Ser Leu Asp Leu Leu Pro Glu Leu Thr Asn Pro Asp
1 5 10 15

Glu Leu Leu Ser Tyr Leu Asp Pro Pro Thr Cys Arg Ala Ile Val Thr
20 25 30

Met Thr Ser Cys Leu Tyr Leu Arg Thr Thr Glu Gly His Pro Val Gly
35 40 45

Ala Ile Pro Pro His Ser Ala Ser Tyr Pro Thr Tyr Pro Thr His Phe
50 55 60

Ser Thr Trp Glu Pro Val Pro Ser Asp Arg Pro Ala Pro Glu Pro Arg
65 70 75 80

Ala Val Gly Arg Gly Ala Leu Pro Arg Cys Ser Pro Leu Arg Thr Glu
85 90 95

Gly

<210> 3652
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.VAAAAATATATATAT153del"

<400> 3652
Leu Gly Leu Pro Ser His Ala Ala Arg Pro Ser Thr Asp Phe Thr Gln
1 5 10 15

Ala Ala Ala Ala Ala Ala Val Ala Ala Leu Gln Glu Lys Gln Ser Gln
20 25 30

Glu Leu Ser Gln Tyr Gly Ala Met Gly Ala Gly Gln Ser Phe Asn Ser
35 40 45

Gln Phe Leu Gln His Gly Gly Pro Arg Gly Pro Ser Val Pro Ala Gly
50 55 60

Met Asn Pro Thr Gly Ile Gly Gly Val Met Gly Pro Ser Gly Leu Ser
65 70 75 80

Pro Leu Ala Met Asn Pro Thr Arg Ala Ala Gly Met Thr Pro Leu
85 90 95

<210> 3653
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K345fs"

<400> 3653
Ser Ser Gly Met Asn Lys Met Leu Pro Ser Val Pro Ala Thr Ala Val
1 5 10 15

Arg Val Ser Cys Ser Gly Cys Lys Lys Ser Ser Arg Arg Gly Lys Leu
20 25 30

Leu Ile Arg Gly Lys Gly Leu Leu Ser Tyr Ser Ala Pro His Cys Ala
35 40 45

Ser Leu Asp Ile Gln Phe His Leu Pro Ala His Arg Leu Leu Ser Pro
50 55 60

Arg Lys Leu Val Gln Val Ala Gln Lys Thr Phe
65 70 75

<210> 3654
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T367I"

<400> 3654
Ser Gly Cys Lys Lys Ile Leu Gln Lys Gly Gln Thr Ala Tyr Gln Arg
1 5 10 15

Lys Gly Ser Thr Gln Leu Phe Cys Ser Ile Ile Leu Cys Leu Thr Gly
20 25 30

Tyr Thr Val Pro Pro Ala Arg Pro Pro Pro Pro Leu Thr Lys Lys Thr
35 40 45

Cys Ser Ser Cys
50

<210> 3655
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R1446Q"

<400> 3655
Thr Tyr Leu Arg Phe Phe Pro Pro Leu Gln Lys Gln Glu Ser Glu Pro
1 5 10 15

Asp Lys Leu Thr Val Gly Lys Arg Lys Gln Gln Asn Glu Asp Asp Glu
20 25 30

Val Pro Val Gly Val Glu Met Ala Glu Asn Thr Asp Asn Pro Leu Arg
35 40 45

Cys Pro Val Arg
50

<210> 3656
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R185I"

<400> 3656
Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn
1 5 10 15

Gln Thr Ser His Leu Ile Arg His Lys Ile Ile Ile His Thr Glu Glu
20 25 30

Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser
35 40 45

Thr Leu Thr Thr
50

<210> 3657
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T339fs"

<400> 3657
Gly Glu Lys Pro Tyr Glu Cys Gln Lys Cys Gly Lys Ala Phe Ser Arg
1 5 10 15

Ala Ser Thr Leu Trp Lys His Lys Lys Leu Ile Leu Glu Lys Ser Pro
20 25 30

Ile Asn Val Lys Lys Cys Lys Gly Phe Asn His Tyr Ser Phe Cys Gln
35 40 45

Lys His Glu Gln Ser His Thr
50 55

<210> 3658
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.T408N"

<400> 3658
Arg Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Thr Gln Asn Ser
1 5 10 15

Gly Leu Ile Lys His Arg Arg Val His Asn Asn Gly Glu Lys Pro Tyr
20 25 30

Glu Cys Thr Glu Cys Gly Lys Ser Phe Ser His Asn Ser Ser Leu Ile
35 40 45

Lys His Gln Arg
50

<210> 3659
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R452W"

<400> 3659
His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Asp Cys Gly Lys Ala Phe
1 5 10 15

Ser Gln Ser Ser Ser Leu Ile Gln His Trp Trp Arg Ile His Thr Gly
20 25 30

Glu Lys Pro His Val Cys Asn Val Cys Gly Lys Ala Phe Ser Tyr Ser
35 40 45

Ser Val Leu Arg
50

<210> 3660
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R683I"

<400> 3660
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Val Phe Ser
1 5 10 15

Tyr Ser Ser Ser Leu Met Val His Gln Ile Ile Thr His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Asn Asp Cys Gly Lys Ala Phe Ser Asp Ser Ser
35 40 45

Gln Leu Ile Val
50

<210> 3661
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P353T"

<400> 3661
Cys Asp Asp Cys Gly Lys Ser Phe Thr Trp Asn Ser Glu Leu Lys Arg
1 5 10 15

His Lys Arg Val His Thr Gly Glu Arg Thr Thr Tyr Thr Cys Gly Glu
20 25 30

Cys Gly Asn Cys Phe Gly Arg Gln Ser Thr Leu Lys Leu His Gln Arg
35 40 45

Ile His Thr Gly
50

<210> 3662
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R401I"

<400> 3662
Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Ser
1 5 10 15

Arg Ser Ser His Leu Val Ser His Gln Ile Ile Thr His Thr Gly Glu
20 25 30

Lys Pro Tyr Arg Cys Asn Gln Cys Gly Lys Ser Phe Ser Gln Ser Tyr
35 40 45

Val Leu Val Val
50

<210> 3663
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R569I"

<400> 3663
Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Asn
1 5 10 15

Arg Ser Ser His Leu Val Met His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ser Phe Ser Gln Ser Tyr
35 40 45

Val Leu Val Val
50

<210> 3664
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R625I"

<400> 3664
Thr Gly Glu Lys Pro Tyr Glu Cys Ser Gln Cys Gly Lys Ser Phe Arg
1 5 10 15

Gln Ser Ser Cys Leu Thr Gln His Gln Ile Ile Thr His Thr Gly Glu
20 25 30

Lys Pro Phe Glu Cys Asn Gln Cys Gly Lys Thr Phe Ser Leu Ser Ala

35 40 45

Arg Leu Ile Val
50

<210> 3665
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R349I"

<400> 3665
Thr Gly Glu Lys Pro Tyr Ser Cys Lys Val Cys Gly Gln Ala Phe Asn
1 5 10 15

Phe His Thr Lys Leu Thr Arg His Gln Ile Ile Ile His Ser Glu Glu
20 25 30

Lys Pro Phe Asp Cys Val Asp Cys Gly Lys Ala Phe Ser Ala Gln Glu
35 40 45

Gln Leu Lys Arg
50

<210> 3666
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R59Q"

<400> 3666
Leu Glu Asn Tyr Arg Asn Leu Phe Ser Val Gly Leu Thr Val Cys Lys
1 5 10 15

Pro Gly Leu Ile Thr Cys Leu Glu Gln Gln Gln Lys Glu Pro Trp Asn
20 25 30

Val Lys Arg Gln Glu Ala Ala Asp Gly His Pro Glu Met Gly Phe His
35 40 45

His Ala Thr Gln
50

<210> 3667
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R384C"

<400> 3667
Thr Gly Glu Lys Pro Tyr Thr Cys Pro Ala Cys Arg Lys Ser Phe Ser
1 5 10 15

His His Ser Thr Leu Ile Gln His Gln Cys Cys Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Val Cys Asp Arg Cys Ala Lys Arg Phe Thr Arg Arg Ser
35 40 45

Asp Leu Val Thr
50

<210> 3668
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G23W"

<400> 3668
Met Thr Met Ser Lys Glu Ala Val Thr Phe Lys Asp Val Ala Val Val
1 5 10 15

Phe Thr Glu Glu Glu Leu Trp Trp Leu Leu Asp Leu Ala Gln Arg Lys
20 25 30

Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Arg Asn Leu Leu Ser Val
35 40 45

Gly

<210> 3669
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F122fs"

<400> 3669
Asn Ile Lys Lys Glu Lys Ser Asn Thr Ile Asp Gly Thr Val Lys Asp
1 5 10 15

Glu Thr Ser Pro Val Glu Glu Cys Phe Leu Val Lys Val Gln Thr His
20 25 30

Ile Ser Val Ile Pro Ser Leu Glu Ser Ser Pro Leu Gly Val Gln Asp
35 40 45

Trp Gly Asn Pro Ser Ala Leu Ile Gln Asn Ser
50 55

<210> 3670
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.T1410M"

<400> 3670

Asn Ile Thr Leu Gln Ile Asp Pro Ser Ile Leu Gln Gln Thr Leu Gln
1 5 10 15

Gln Gly Asn Leu Leu Ala Gln Gln Leu Met Met Gly Glu Pro Gly Leu
20 25 30

Ala Pro Gln Asn Ser Ser Leu Gln Thr Ser Asp Ser Thr Val Pro Ala
35 40 45

Ser Val Val Ile
50

<210> 3671
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S1480L"

<400> 3671
Gly Pro Leu Ser Glu Gln Asp Ser Val Leu Thr Thr Asn Ser Ser Gly
1 5 10 15

Thr Gln Asp Leu Thr Gln Val Met Thr Leu Leu Gln Gly Leu Val Ser
20 25 30

Pro Ser Gly Gly Pro His Glu Ile Thr Leu Thr Ile Asn Asn Ser Ser
35 40 45

Leu Ser Gln Val
50

<210> 3672
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="p.R568I"

<400> 3672
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Ala Cys Gly Lys Thr Phe Ser
1 5 10 15

Gln Arg Ser Val Leu Thr Lys His Gln Ile Ile Ile His Thr Arg Val
20 25 30

Lys Ala Leu Ser Thr Ser
35

<210> 3673
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K179N"

<400> 3673
Phe Gln Cys Asp Lys Tyr Leu Lys Val Phe Tyr Lys Phe Leu Asn Ser
1 5 10 15

Asn Arg Pro Lys Ile Arg His Thr Glu Asn Asn Lys Ser Phe Lys Cys
20 25 30

Lys Lys Arg Val Lys Leu Phe Cys Met Leu Ser His Lys Thr Gln His
35 40 45

Lys Ser Ile Tyr
50

<210> 3674
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R392I"

<400> 3674
Thr Lys Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn
1 5 10 15

Arg Ser Ser His Leu Thr Lys His Lys Ile Ile Ile His Thr Arg Glu
20 25 30

Lys Ala Tyr Lys Cys Asp Glu Tyr Cys Lys Ala Phe Asn Trp Ser Ser
35 40 45

Ala Leu Thr Thr
50

<210> 3675
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R174I"

<400> 3675
Leu Ile Thr Arg Ala Ile Ser Gly Leu Glu Gln Asp Gln Pro Ala Arg
1 5 10 15

Arg Ala Asn Lys Asp Ala Thr Ala Glu Ile Ile Ile Asp Glu Phe Ile
20 25 30

Val Lys Leu Lys Glu Leu Lys Gln Val Ala Ser Pro Phe Thr Leu Ile
35 40 45

Ile Asp Asp Pro
50

<210> 3676
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R510I"

<400> 3676
Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Glu Ile Phe Ala
1 5 10 15

His Ser Ser Asn Leu Leu Arg His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Arg Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Arg Ser Ser
35 40 45

His Leu Val Ile
50

<210> 3677
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R344Q"

<400> 3677
Thr Ala Lys Asp Pro Phe Glu Cys Lys Ile Cys Gly Lys Ser Phe Arg
1 5 10 15

Asn Ser Ser Cys Leu Ser Asp His Phe Gln Gln Ile His Thr Gly Ile
20 25 30

Lys Pro Tyr Lys Cys Lys Asp Cys Gly Lys Ala Phe Thr Gln Asn Ser
35 40 45

Asp Leu Thr Lys
50

<210> 3678
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="p.R512Q"

<400> 3678
Thr Gly Glu Lys Pro Tyr Lys Cys Lys Gln Cys Gly Lys Ser Phe Ser
1 5 10 15

Tyr Ser Asn Ser Phe Gln Leu His Glu Gln Gln Thr His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Ser Ser Ser
35 40 45

Ser Phe Arg Asn
50

<210> 3679
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F901del"

<400> 3679
Asn Ser Gln Leu Ile Val His Gln Arg Thr His Ser Gly Glu Lys Pro
1 5 10 15

Tyr Gly Cys Asn Glu Cys Gly Lys Thr Ser Gln Lys Ser Ile Leu Ser
20 25 30

Ala His Gln Arg Thr His Thr Gly Glu Lys Pro Cys Lys Cys Thr Glu
35 40 45

Cys Gly Lys Ala Phe
50

<210> 3680
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.N319K"

<400> 3680
Asp Cys Gly Lys Val Phe Ser Val Phe Ser Val Leu Thr Lys His Lys
1 5 10 15

Ile Ile His Thr Gly Thr Lys Pro Tyr Lys Lys Cys Glu Glu Cys Gly
20 25 30

Lys Gly Phe Ser Ile Phe Ser Thr Leu Thr Lys His Lys Ile Ile His
35 40 45

Thr Gly Glu Lys
50

<210> 3681
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.E363K"

<400> 3681
Ser Trp Glu Asn His Thr Thr Cys Gln His Cys His Arg Gln Phe Pro
1 5 10 15

Thr Pro Phe Gln Leu Gln Cys His Ile Lys Lys Asn Val His Thr Ala
20 25 30

Gln Glu Pro Ser Thr Val Cys Lys Ile Cys Glu Leu Ser Phe Glu Thr
35 40 45

Asp Gln Val Leu
50

<210> 3682
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E400K"

<400> 3682
Cys Lys Ile Cys Glu Leu Ser Phe Glu Thr Asp Gln Val Leu Leu Gln
1 5 10 15

His Met Lys Asp His His Lys Pro Gly Lys Lys Met Pro Tyr Val Cys
20 25 30

Gln Val Cys His Tyr Arg Ser Ser Val Phe Ala Asp Val Glu Thr His
35 40 45

Phe Arg Thr Cys
50

<210> 3683
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R392Q"

<400> 3683
Lys Ile His Thr Gly Lys Lys Pro Tyr Glu Cys Lys Ile Cys Gly Lys
1 5 10 15

Ala Phe Cys Trp Gly Tyr Gln Leu Thr Gln Gln His Gln Ile Phe His
20 25 30

Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Asn
35 40 45

Cys Gly Ser Ser
50

<210> 3684
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S62L"

<400> 3684
Glu Ala Thr Gly Ser Ser Ser Trp Asp Ile Gln Asn Ser Phe Arg Arg
1 5 10 15

Glu Lys Leu Glu Gln Lys Ser Pro Asp Leu Leu Lys Thr Leu Gln Glu
20 25 30

Asp Ser Pro Gly Val Arg Gln Arg Val Tyr Glu Cys Gln Glu Cys Gly
35 40 45

Lys Ser Phe Arg
50

<210> 3685
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K106N"

<400> 3685
Val Gln Ser Ser Asp Leu Thr Ser His Gln Arg Ile His Asn Tyr Glu
1 5 10 15

Lys Pro Tyr Lys Cys Ser Lys Cys Glu Asn Asn Ser Phe Trp His His
20 25 30

Leu Val Leu Ser Gly His Gln Arg Thr His Ala Gly Lys Lys Phe Tyr
35 40 45

Thr Cys Asp Ile
50

<210> 3686
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R554Q"

<400> 3686
Thr Gly Glu Lys Leu Tyr Glu Cys Ala Thr Cys Gly Gln Val Leu Ser
1 5 10 15

Arg Leu Ser Thr Leu Lys Ser His Met Gln Gln Thr His Thr Gly Glu
20 25 30

Lys Pro Tyr Val Cys Gln Glu Cys Gly Arg Ala Phe Ser Glu Pro Ser
35 40 45

Ser Leu Arg Lys
50

<210> 3687
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K426fs"

<400> 3687
Glu Cys Lys Glu Cys Gly Lys Thr Phe Phe Cys Gln Ser Ala Leu Thr
1 5 10 15

Ala His Gln Arg Ile His Thr Gly Glu Asn Pro Met Asn Val Val Asn
20 25 30

Val Arg Lys Pro Ser Phe Val Asn Leu Pro Ser Met Cys Ile Glu Glu

35 40 45

Val Ile Gln Glu Arg Ser Pro Met Asn Ala Val Asn Val Glu Asn Phe
50 55 60

Tyr Val Arg Asn Gln Pro Ser Leu His Ile Arg
65 70 75

<210> 3688
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R402I"

<400> 3688
Thr Gly Glu Lys Pro Phe Lys Cys Ser Glu Cys Gly Arg Ala Phe Ser
1 5 10 15

Gln Ser Ala Ser Leu Ile Gln His Glu Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Arg Cys Asn Glu Cys Gly Lys Gly Phe Thr Ser Ile Ser
35 40 45

Arg Leu Asn Arg
50

<210> 3689
<211> 30
<212> PRT
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<400> 3689
Gly Lys Leu Phe Ser Gln Arg Ser Ser Leu Thr Asn His Tyr Lys Ile
1 5 10 15

His Ile Glu Glu Asp Ser Leu Lys Ala Asn Asn Leu His Val
20 25 30

<210> 3690
<211> 59
<212> PRT
<213> Artificial Sequence

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<223> /note="p.T130fs"

<400> 3690
Asp Pro Asn Ser Asp Thr Leu Ser Pro Gly Asp Pro Lys Val Asp Pro
1 5 10 15

Ile Ser Ser Gly Leu Thr Ala Thr Pro Arg Ser Trp Pro Pro Ala Pro
20 25 30

Arg Cys Ser Pro Pro Pro Pro Ala Arg Pro Gly Pro Ser Pro Ala Arg
35 40 45

Ile Ala Gly Glu Pro Ser Ala Ala Ala Pro Gly
50 55

<210> 3691
<211> 52
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<400> 3691
Phe Gly Asp Ser Thr Gly Trp Glu Lys Ser Leu Leu Asn Thr Lys His
1 5 10 15

Glu Lys Ile His Pro Ala Val Asn Leu Gln Gln Lys Gln Thr Glu Arg
20 25 30

Val Leu Ser Gly Lys Gln Glu Leu Ile Gln His Gln Lys Val Gln Ala
35 40 45

Pro Glu Gln Pro
50

<210> 3692
<211> 52
<212> PRT
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<223> /note="p.T226S"

<400> 3692
Lys Arg Leu Leu Tyr Cys Ser Leu Cys Lys Val Ala Val Asn Ser Ala
1 5 10 15

Ser Gln Leu Glu Ala His Asn Ser Gly Ser Ser Lys His Lys Thr Met
20 25 30

Leu Glu Ala Arg Asn Gly Ser Gly Thr Ile Lys Ala Phe Pro Arg Ala
35 40 45

Gly Val Lys Gly
50

<210> 3693
<211> 52
<212> PRT
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<400> 3693
Gly Glu Lys Pro Tyr Thr Cys Glu Glu Cys Gly Lys Val Phe Asn Trp
1 5 10 15

Ser Ser Arg Leu Thr Thr His Lys Lys Ile Ile Leu Asp Thr Asn Ser
20 25 30

Thr Asn Val Lys Asn Val Ala Lys Leu Leu Thr Ser Pro Gln Ser Leu
35 40 45

Leu Pro Ile Arg
50

<210> 3694
<211> 52
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<220>
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<223> /note="p.R280C"

<400> 3694
Tyr Lys Leu Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Lys Ser
1 5 10 15

Ser Ile Leu Thr Thr His Lys Ile Ile Cys Cys Thr Gly Glu Lys Phe
20 25 30

Tyr Lys Cys Lys Glu Cys Ala Lys Ala Phe Asn Gln Ser Ser Asn Leu
35 40 45

Thr Glu His Lys
50

<210> 3695
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R306C"

<400> 3695
Gln Asn Ser Gln Ile Tyr Arg Ala Met Ala Glu Gly Leu Trp Glu Gln

1900

1 5 10 15

Gly Phe Leu Arg Thr Pro Glu Gln Cys Cys Thr Lys Phe Lys Ser
20 25 30

Leu Gln Leu Ser Tyr Arg Lys Val Arg Arg Gly Arg Val Pro Glu Pro
35 40 45

Cys Ile Phe Tyr
50

<210> 3696
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R262I"

<400> 3696
Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ser Phe Ser
1 5 10 15

Tyr Ser Ala Thr His Arg Ile His Glu Ile Ile Thr His Ile Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Gln Glu Cys Gly Lys Ala Phe His Ser Pro Arg
35 40 45

Ser Cys His Arg
50

<210> 3697
<211> 52
<212> PRT
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<400> 3697
Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Arg Cys Gly
1 5 10 15

Arg Ala Phe Ser Val Ser Ser Ser Leu Gln Gln Ile His Glu Arg Thr
20 25 30

His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe
35 40 45

His His Leu Gly
50

<210> 3698
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R301I"

<400> 3698
Thr Gly Glu Lys Pro Tyr Lys Cys Lys Gln Cys Ser Lys Ala Phe Pro
1 5 10 15

Asp Ser Ser Ser Cys Leu Ile His Glu Ile Ile Thr His Thr Gly Glu
20 25 30

Lys Pro Tyr Thr Cys Lys Gln Cys Gly Lys Ala Phe Ser Val Ser Gly
35 40 45

Ser Leu Gln Arg
50

<210> 3699
<211> 52
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<400> 3699
Glu Cys Arg Glu Gly Phe Arg Gln Ser Pro Asp Cys Ser Gln Pro Gln
1 5 10 15

Gly Ala Pro Ala Val Glu Lys Thr Phe Met Met Cys Gln Gln Cys Gly
20 25 30

Lys Thr Phe Thr Arg Lys Lys Thr Leu Val Asp His Gln Arg Ile His
35 40 45

Thr Gly Glu Lys
50

<210> 3700
<211> 52
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R376I"

<400> 3700
Thr Gly Glu Lys Pro Phe Glu Cys Asn Glu Cys Gly Lys Ala Phe Arg
1 5 10 15

Val Asn Ser Ser Leu Thr Glu His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Arg Asp Asn Ser
35 40 45

Ser Phe Ala Arg
50

<210> 3701
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
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<223> /note="p.S190I"

<400> 3701
Ser Asp Gln Ser Gln Gly Phe Gln Pro Ser Lys Asn Ala Phe Glu Cys
1 5 10 15

Ser Glu Cys Gly Lys Val Phe Ser Lys Ile Ile Ser Thr Leu Asn Lys
20 25 30

His Gln Lys Ile His Asn Glu Lys Asn Ala Asn Gln Lys Ile His Ile
35 40 45

Lys Glu Lys Arg
50

<210> 3702
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.S650T"

<400> 3702
Phe Cys Asp Asn Leu Pro Lys Phe Glu Gly Gln Pro Ser Ser Leu Pro
1 5 10 15

Leu Glu Asn Glu Thr Asp Ser His Pro Thr Thr Ser Ser Asn Thr Val
20 25 30

Lys Lys Ser Gln Thr Ser Ile Leu Gly Leu Ser Ser Lys Asn Asn Phe
35 40 45

Val Ala Lys Ala
50

<210> 3703
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R641I"

<400> 3703
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Val Cys Gly Lys Ala Phe Ser
1 5 10 15

His Arg Lys Ser Leu Thr Leu His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Lys Glu Cys Ser Lys Ala Phe Ser Gln Val Ala
35 40 45

His Leu Thr Leu
50

<210> 3704
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R282I"

<400> 3704
Thr Gly Glu Lys Leu Phe Glu Cys Lys Glu Cys Arg Lys Ala Phe Lys
1 5 10 15

Gln Ser Glu His Leu Ile Gln His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Lys Glu Cys Arg Lys Ala Phe Arg Gln Pro Ala
35 40 45

His Leu Ala Gln
50

<210> 3705
<211> 52

<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R235H"

<400> 3705
His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Gly Ile Cys
1 5 10 15

Gly Lys Gly Phe Gly Asp Ser Ser Ala His His Ile Lys His Gln Arg
20 25 30

Thr His Arg Gly Glu Gln Pro Pro Arg Pro Val Val Pro Arg Arg Gln
35 40 45

Pro Ser Arg Ala
50

<210> 3706
<211> 67
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 3706
Ile Cys Gly Lys Gly Phe Gly Asp Ser Ser Ala Arg Ile Lys His Gln
1 5 10 15

Arg Thr His Arg Gly Glu Gln Pro Pro Asp Gln Trp Cys Pro Asp Gly
20 25 30

Ser His Leu Gly Gln Pro Arg Gln Leu Pro Arg Asp Arg Arg Pro Arg
35 40 45

Thr Ser His Ile Ser Ala Leu Ile Ala Ala Arg Gly Leu Cys Ser Ala
50 55 60

Ala Ala Ser
65

<210> 3707
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R138C"

<400> 3707
Ser Ile Leu Glu Glu Leu Trp Lys Asp Asp Glu His Thr Arg Lys Cys
1 5 10 15

Gly Glu Asn Gln Asn Lys Pro Leu Ser Cys Cys Val Val Phe Ile Asn
20 25 30

Lys Lys Thr Leu Ala Asn Asp Ser Ile Phe Glu Tyr Lys Asp Ile Gly
35 40 45

Glu Ile Val His
50

<210> 3708
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R374I"

<400> 3708
Ser Gly Asn Lys Pro Tyr Gln Cys Arg Asp Cys Gly Lys Ala Phe Thr
1 5 10 15

Lys Ser Ser Thr Leu Thr Gly His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr His Cys Lys Lys Cys Gly Lys Ala Phe Arg His Ser Ser
35 40 45

Gly Leu Val Glu
50

<210> 3709
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R206Q"

<400> 3709
Pro Ala Gly Glu Ser Ala Asp Ala Leu Gly Glu Leu Ser Gly Leu Leu
1 5 10 15

Asn Thr Thr Asp Leu Ala Cys Trp Gly Gln Gln Leu Ser Thr Pro Lys
20 25 30

Leu Leu Val Gly Asp Leu Trp Asn Leu Gln Ala Leu Pro Gln Asn Ala
35 40 45

Pro Leu Cys Ser
50

<210> 3710
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R343Q"

<400> 3710
Glu Arg Thr His Thr Gly Glu Lys Pro Asp Gly Cys Lys Gln Cys Gly
1 5 10 15

Lys Ala Phe Arg Ser Ala Lys Tyr Ile Gln Gln Ile His Gly Arg Thr

20 25 30

His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe
35 40 45

His Cys Val Ser
50

<210> 3711
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P392H"

<400> 3711
Cys Glu Val Cys Ser Lys Ala Phe Ser Arg Phe Ser His Leu Thr Thr
1 5 10 15

His Lys Arg Ile His Thr Gly Glu Lys His His Tyr Lys Cys Glu Glu
20 25 30

Cys Gly Lys Ala Phe Asn Leu Ser Ser Gln Leu Thr Thr His Lys Ile
35 40 45

Ile His Thr Gly
50

<210> 3712
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V81G"

<400> 3712
Pro Gly Glu Glu Gly Thr Thr Asn Ser Phe Leu Lys Ala Arg Pro Arg
1 5 10 15

Asp Leu Met Thr Phe Glu Asp Val Ala Gly Gly Glu Phe Ser Gln Trp
20 25 30

Glu Trp Gly Gln Leu Asn Pro Ala Gln Lys Asp Leu Tyr Arg Glu Val
35 40 45

Met Leu Glu Asn
50

<210> 3713
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.H431Y"

<400> 3713
Cys Lys Glu Cys Gly Lys Ala Phe Asn Arg Ala Ser His Leu Thr Gln
1 5 10 15

His Gln Arg Ile His Thr Gly Glu Lys Tyr Tyr Phe Lys Cys Lys Glu
20 25 30

Cys Gly Lys Ala Phe Asn Arg Gly Ser His Leu Thr Arg His Gln Arg
35 40 45

Ile His Thr Gly
50

<210> 3714
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G640C"

<400> 3714
Thr Ser Leu Lys Met Met Gln Ala Val Gly Gly Ala Pro Ala Arg Pro
1 5 10 15

Thr Gly Glu Tyr Ile Cys Asn Gln Cys Cys Cys Ala Lys Tyr Thr Ser
20 25 30

Leu Asp Ser Phe Gln Thr His Leu Lys Thr His Leu Asp Thr Val Leu
35 40 45

Pro Lys Leu Thr
50

<210> 3715
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.P270H"

<400> 3715
Thr Gln Lys Cys Ser Gln Cys Glu Glu Gly Phe Asp Phe Pro Glu Asp
1 5 10 15

Leu Gln Lys His Ile Ala Glu Cys His His His Glu Cys Ser Pro Asn
20 25 30

Glu Asp Arg Ala Ala Leu Gln Cys Val Tyr Cys His Glu Leu Phe Val
35 40 45

Glu Glu Thr Ser
50

<210> 3716
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<221> source
<223> /note="p.R279Q"

<400> 3716
Ser Asn Leu Ser Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
1 5 10 15

Lys Cys His Glu Cys Asp Lys Val Phe Gln Gln Ser Ser Ser Lys Leu
20 25 30

Ala Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys His
35 40 45

Glu Cys Asp Lys
50

<210> 3717
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N583K"

<400> 3717
Thr Gly Glu Lys Pro Tyr Ser Cys Asn Glu Cys Gly Lys Val Phe Ser
1 5 10 15

Arg Asn Ser His Leu Ala Arg His Arg Lys Lys Ile His Thr Gly Glu
20 25 30

Lys Pro His Ser Cys Asn Glu Cys Gly Lys Val Phe Ser Arg Asn Ser
35 40 45

His Leu Ala Arg
50

<210> 3718
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G663W"

<400> 3718
Arg Val Phe Arg Thr Tyr His Gln Val Val Val His Ser Arg Val His
1 5 10 15

Lys Arg Asp Arg Lys Gly Glu Glu Asp Trp Trp Leu His Val Gly Leu
20 25 30

Asp Glu Arg Arg Gly Ser Gly Ser Asp Gln Glu Ser Gln Ser Val Ser
35 40 45

Arg Ser Thr Thr
50

<210> 3719
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G186C"

<400> 3719
Pro Tyr Cys Asp His Arg Ala Ala Gln Lys Gly Asn Leu Lys Ile His
1 5 10 15

Leu Arg Thr His Lys Leu Gly Asn Leu Cys Cys Lys Gly Arg Gly Arg
20 25 30

Val Arg Glu Glu Asn Arg Leu Leu His Glu Leu Glu Glu Arg Ala Ile
35 40 45

Leu Arg Asp Lys
50

<210> 3720
<211> 52
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E284K"

<400> 3720
Pro Ser Ser Ser His Leu Arg Glu Cys Val Arg Ile Tyr Gly Gly Glu
1 5 10 15

Arg Pro Tyr Thr His Lys Glu Tyr Val Lys Lys Thr Phe Ser His Ser
20 25 30

Thr Ala Leu Phe Val His Met Gln Thr Gln Asp Gly Glu Lys Phe Tyr
35 40 45

Glu Cys Lys Ala
50

<210> 3721
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W208fs"

<400> 3721
Asn Leu Arg Arg His Met Val Val Gln Gly Gly Asn Arg Pro Tyr Lys
1 5 10 15

Cys Lys Leu Cys Gly Lys Ala Phe Phe Gly Pro Val Tyr Tyr Val Cys
20 25 30

Met Lys Glu Leu Thr Leu Glu Arg Asn Arg Met Asn Val Ser Ser Val
35 40 45

Leu Lys Pro Phe Leu Phe Thr Val Pro Ile Glu Asp Met Arg Glu Cys
50 55 60

Thr Leu Gly Arg Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Cys
65 70 75 80

Leu Ile Pro Val Pro Ile
85

<210> 3722
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K26N"

<400> 3722
Met Asp Ala Val Ala Phe Glu Asp Val Ala Val Asn Phe Thr Gln Glu
1 5 10 15

Glu Trp Ala Leu Leu Gly Pro Ser Gln Asn Asn Asn Leu Tyr Arg Tyr
20 25 30

Val Met Gln Glu Thr Ile Arg Asn Leu Asp Cys Ile Arg Met Ile Trp
35 40 45

Glu Glu Gln Asn
50

<210> 3723
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R350I"

<400> 3723
Thr Gly Lys Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Gly Tyr Thr
1 5 10 15

Thr Ala Ser Tyr Phe Leu Leu His Gln Ile Ile Ile His Lys Gly Gly
20 25 30

Lys Pro Tyr Glu Cys Lys Glu Cys Lys Lys Thr Phe Thr Leu Tyr Arg
35 40 45

Asn Leu Thr Arg
50

<210> 3724
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G311S"

<400> 3724
Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ser Phe Ser Tyr Lys Ser Ser
1 5 10 15

Leu Thr Cys His Arg Arg Cys His Thr Ser Ser Glu Lys Pro Tyr Lys
20 25 30

Cys Asn Glu Cys Gly Lys Ser Phe Ser Tyr Lys Ser Ser Leu Thr Cys
35 40 45

His His Arg Cys
50

<210> 3725
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R344I"

<400> 3725
Thr Gly Glu Arg Pro Phe Glu Cys Ile Glu Cys Gly Lys Ala Phe Ser
1 5 10 15

Asn Gly Ser Phe Leu Ala Gln His Gln Ile Ile Ile His Thr Gly Glu

20 25 30

Lys Pro Tyr Val Cys Asn Val Cys Gly Lys Ala Phe Ser His Arg Gly
35 40 45

Tyr Leu Ile Val
50

<210> 3726
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E491D"

<400> 3726
Tyr Met Cys Asn Lys Cys Gly Lys Ala Phe Thr Asn Arg Ser Asn Leu
1 5 10 15

Ile Thr His Gln Lys Thr His Thr Gly Asp Asp Lys Ser Tyr Ile Cys
20 25 30

Ser Lys Cys Gly Lys Ala Phe Thr Gln Arg Ser Asp Leu Ile Thr His
35 40 45

Gln Arg Ile His
50

<210> 3727
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.E638K"

<400> 3727
Lys Ser Phe Thr Ser Lys Ser Gln Leu Leu Val His Gln Pro Val His
1 5 10 15

Thr Gly Glu Lys Pro Tyr Val Cys Ala Lys Lys Cys Gly Lys Ala Phe
20 25 30

Ser Gly Arg Ser Asn Leu Ser Lys His Gln Lys Thr His Thr Gly Glu
35 40 45

Lys Pro Tyr Ile
50

<210> 3728
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P500T"

<400> 3728
Pro Gly Ser Gln Thr Gly Lys Lys Gln Gln Ser Thr Ala Leu Gln Ala
1 5 10 15

Ser Thr Leu Ala Pro Ala Asn Leu Leu Thr Thr Lys Ala Val His Leu
20 25 30

Ala Asn Leu Asn Leu Val Pro His Ser Val Ala Ala Ser Val Thr Ala
35 40 45

Lys Ser Ser Val
50

<210> 3729
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K324Q"

<400> 3729
Val Thr Lys Glu Asp Gln Pro Gly His Thr Lys Asp Leu Ser Gly Pro
1 5 10 15

Thr Lys Glu Ser Ser Lys Gly Ser Pro Gln Gln Met Pro Lys Ser Pro
20 25 30

Lys Ser Pro Arg Ser Pro Leu Glu Ala Thr Arg Lys Ser Ile Lys Pro
35 40 45

Ser Asp Ser Pro
50

<210> 3730
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R287I"

<400> 3730
Thr Gly Glu Lys Pro Tyr Glu Cys Tyr Asp Cys Gly Gln Met Phe Ser
1 5 10 15

Gln Ser Ser His Leu Val Pro His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Leu Lys Cys Asn Glu Cys Glu Lys Ala Phe Arg Gln His Ser
35 40 45

His Leu Thr Glu
50

<210> 3731
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.E25G"

<400> 3731
Met Ala Ala Ala Gly Gly Ala Glu Gly Arg Arg Ala Asp Met Glu Ala
1 5 10 15

Glu Ala Ala Ala Ala Pro Glu Arg Gly Gly Gly Gly Ser Cys Val Leu
20 25 30

Cys Cys Gly Asp Leu Glu Ala Thr Ala Leu Gly Arg Cys Asp His Pro
35 40 45

Val Cys Tyr
50

<210> 3732
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.A465fs"

<400> 3732
Ser Ala Ala Ala Ala Pro Gly Ser Glu Ala Ser Phe Thr Glu Ser Arg
1 5 10 15

Gly Leu Gln Asn Lys Asn Arg Gly Gly Pro Met Gly Lys Gly Gly Gly
20 25 30

Ala Ala Ser Met Pro Ala Asp Glu Gly His Pro Gln Ile Val Leu Leu
35 40 45

Arg Ile Ser Lys Pro Ala Leu Pro Pro Pro Thr Lys Gly Lys Thr Ser
50 55 60

Leu Gln Trp Ser Trp Thr
65 70

<210> 3733
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="p.R390I"

<400> 3733
Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Asp Lys Val Phe Ser
1 5 10 15

Arg Lys Ser Thr Ile Glu Thr His Lys Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Arg Cys Lys Val Cys Asp Thr Ala Phe Thr Trp His Ser
35 40 45

Gln Leu Ala Arg
50

<210> 3734
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.R235Q"

<400> 3734
Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe His
1 5 10 15

Ser Ser Thr Cys Leu His Ala His Lys Gln Lys Thr His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Val Ser Phe Asn
35 40 45

Ser Val Arg Tyr
50

<210> 3735
<211> 52

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K473R"

<400> 3735
Thr Gly Glu Lys Phe Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Lys
1 5 10 15

Cys Ser Ser Asn Leu Thr Thr His Lys Arg Arg Ile His Thr Gly Glu
20 25 30

Arg Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser
35 40 45

Ile Leu Thr Thr
50

<210> 3736
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.D400N"

<400> 3736
Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro Phe Gly Ile Val Lys Ala
1 5 10 15

Ser Trp Leu Pro Lys Phe Ser His Ala Asn Asn Ala Gln Lys Met Lys
20 25 30

Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr Tyr Ala Ala Ser Pro
35 40 45

Arg Ile Phe Pro
50

<210> 3737
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.G21W"

<400> 3737
Met Arg Ser Phe Leu Gln Gln Asp Val Asn Lys Thr Lys Ser Arg Leu
1 5 10 15

Asn Val Leu Asn Trp Trp Leu Ala Asn Asn Met Asp Asp Leu Lys Ile
20 25 30

Asn Thr Asp Ile Thr Gly Ala Lys Glu Glu Leu Leu Asp Asp Asn
35 40 45

<210> 3738
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R154C"

<400> 3738
Ser Leu Gln Ala His Ile Lys Arg Arg His Lys Arg Ala Arg Lys Gln
1 5 10 15

Val Thr Ser Ala Ser Leu Glu Lys Val Cys Cys Pro His Ile Ala Pro
20 25 30

Pro Gln Thr Glu Ile Ser Asp Ile Pro Lys Arg Leu Gln Asp Arg Asp
35 40 45

His Leu Ser Tyr
50

<210> 3739
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R198I"

<400> 3739
Asn Ile Glu Lys Ala His Glu Cys Thr Asp Cys Gly Lys Ala Phe Leu
1 5 10 15

Lys Lys Ser Gln Leu Thr Glu His Lys Ile Ile Ile His Thr Gly Lys
20 25 30

Lys Pro His Val Cys Ser Leu Cys Gly Lys Ala Phe Tyr Lys Lys Tyr
35 40 45

Arg Leu Thr Glu
50

<210> 3740
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.K327N"

<400> 3740
Val Ser Cys Asn Lys Ser Phe Lys Lys Leu Trp Ser Leu His Glu His
1 5 10 15

Ile Lys Ile Val His Gly Tyr Ala Glu Asn Asn Lys Phe Ser Cys Glu
20 25 30

Ile Cys Glu Lys Lys Phe Tyr Thr Met Ala His Val Arg Lys His Met
35 40 45

Val Ala His Thr

50

<210> 3741
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R405I"

<400> 3741
Thr Lys Glu Asn Ile Tyr Glu Cys Ser Lys Cys Gly Lys Ser Phe Arg
1 5 10 15

Gly Lys Ser His Leu Ser Val His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Ser Ile Cys Gly Lys Thr Phe Ser Gly Lys Ser
35 40 45

His Leu Ser Val
50

<210> 3742
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R220I"

<400> 3742
Thr Lys Val Asn Phe Cys Lys Cys Glu Glu Cys Glu Lys Ala Val Asn
1 5 10 15

Gln Ser Ser Lys Leu Thr Lys His Lys Ile Ile Ile Tyr Thr Cys Glu
20 25 30

Lys Leu Tyr Lys Cys Gln Glu Cys Asp Arg Thr Phe Asn Gln Phe Ser
35 40 45

Asn Leu Thr Glu
50

<210> 3743
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P43T"

<400> 3743
Pro Asp Leu Ile Ile Phe Leu Glu Gln Gly Lys Glu Pro Trp Asn Met
1 5 10 15

Lys Arg His Glu Met Val Glu Glu Pro Thr Thr Val Ile Cys Ser His
20 25 30

Phe Ser Gln Glu Phe Trp Pro Glu Gln Gly Ile Glu Asp Ser Phe Gln
35 40 45

Lys Met Ile Leu
50

<210> 3744
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R451I"

<400> 3744
Pro Gly Glu Lys Pro His Lys Cys Asn Val Cys Gly Arg Ala Phe Ile
1 5 10 15

Gln Ser Ser Ser Leu Val Glu His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Asn Lys Cys Asp Lys Ala Phe Ile Lys Arg Ser
35 40 45

His Leu Trp Gly
50

<210> 3745
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R131T"

<400> 3745
Phe Asp Ser Leu Trp Asp Tyr Asp Val Lys Asn Tyr Lys Gly Met Pro
1 5 10 15

Leu Thr Cys Asn Lys Asn Leu Thr His Thr Thr Lys Asp Gln Gln His
20 25 30

Asn Lys Ser Ser Ile His Phe Ser Leu Lys Gln Ser Val Ser Ile Arg
35 40 45

Asp Ser Ala His
50

<210> 3746
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R501W"

<400> 3746
Thr Leu Ala Asn His Lys Arg Ile His Ala Arg Glu Lys Pro Tyr Lys
1 5 10 15

Cys Glu Glu Cys Gly Lys Ala Phe Asn Trp Trp Ser Ser His Leu Thr
20 25 30

Arg His Lys Lys Ile His Thr Gly Glu Lys Leu Tyr Lys Pro Glu Lys
35 40 45

Cys Asp Asn Asn
50

<210> 3747
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.F858C"

<400> 3747
Asp Thr Val Phe Thr His Lys Pro Leu Leu Ser Ser His Phe Asp Gln
1 5 10 15

His Leu Leu Pro Gln Arg Val Ser Val Cys Cys Lys Cys Pro Ser Cys
20 25 30

Pro Leu Leu Phe Ala Gln Lys Arg Thr Met Leu Glu His Leu Lys Asn
35 40 45

Thr His Gln Ser
50

<210> 3748
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R41I"

<400> 3748
Gln Asp Ser Val Val Phe Glu Asp Val Ala Val Asp Phe Thr Gln Glu

1 5 10 15

Glu Trp Ala Leu Leu Asp Leu Ala Gln Ile Ile Asn Leu Tyr Arg Asp
20 25 30

Val Met Leu Glu Asn Phe Gln Asn Leu Ala Ser Leu Gly Tyr Pro Leu
35 40 45

His Thr Pro His
50

<210> 3749
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R337I"

<400> 3749
Thr Gly Glu Lys Pro Tyr Arg Cys Glu Glu Cys Gly Lys Ala Phe Gly
1 5 10 15

Gln Ser Ser Ser Leu Ile His His Gln Ile Ile Ile His Thr Gly Glu
20 25 30

Arg Pro Tyr Gly Cys Arg Glu Cys Gly Lys Ala Phe Ser Gln Gln Ser
35 40 45

Gln Leu Val Arg
50

<210> 3750
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R244I"

<400> 3750
Thr Gly Lys Arg Pro Tyr Glu Cys Arg Glu Cys Gly Lys Asp Phe Ser
1 5 10 15

Arg Ser Ser Ser Leu Arg Lys His Glu Ile Ile Ile His Thr Gly Glu
20 25 30

Arg Pro Tyr Gln Cys Lys Glu Cys Gly Lys Ser Phe Asn Gln Ser Ser
35 40 45

Gly Leu Ser Gln
50

<210> 3751
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S649C"

<400> 3751
Asn Leu Arg Lys His Gly Arg Thr His Thr Gly Glu Lys Pro Tyr Glu
1 5 10 15

Cys Lys Gln Cys Gly Lys Ala Phe Arg Cys Cys Ala Ser Asn Leu Gln
20 25 30

Met His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu
35 40 45

Cys Glu Lys Ala
50

<210> 3752
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N652H"

<400> 3752
Lys His Gly Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln
1 5 10 15

Cys Gly Lys Ala Phe Arg Ser Ala Ser His His Leu Gln Met His Glu
20 25 30

Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Glu Lys
35 40 45

Ala Phe Cys Lys
50

<210> 3753
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Q654R"

<400> 3753
Gly Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly
1 5 10 15

Lys Ala Phe Arg Ser Ala Ser Asn Leu Arg Arg Met His Glu Arg Thr
20 25 30

His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Glu Lys Ala Phe
35 40 45

Cys Lys Phe Ser
50

<210> 3754
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<220>
<221> source
<223> /note="p.D298N"

<400> 3754
Gly Asn Lys Ile Ile His Thr Gly Glu Lys Pro His Ala Cys Leu Leu
1 5 10 15

Cys Gly Lys Ala Phe Ser Leu Ser Ser Asn Asn Leu Arg
20 25

<210> 3755
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.I8N"

<400> 3755
Met Ala Arg Gly Gln Gln Lys Asn Asn Gln Ser Gln Gln Lys Asn Ala
1 5 10 15

Lys Lys Gln Ala Gly Gln Lys Lys Lys Gln Gly His Asp Gln Lys Ala
20 25 30

Ala Ala

<210> 3756
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R468I"

<400> 3756
Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Ser

1 5 10 15

Cys Ser Ser Ser Phe Arg Met His Glu Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Ser Phe Ser Ser
35 40 45

Ser Phe Arg Met
50

<210> 3757
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.V411L"

<400> 3757
Ile Cys Lys Lys His Phe Thr Gly Arg Ser Ser Leu Ile Val His Gln
1 5 10 15

Ile Val His Thr Gly Glu Lys Pro Tyr Leu Leu Cys Gly Glu Cys Gly
20 25 30

Lys Ala Phe Ser Gln Ser Ala Tyr Leu Ile Glu His Gln Arg Ile His
35 40 45

Thr Gly Glu Lys
50

<210> 3758
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="p.L737fs"

<400> 3758
Ser Val His Thr Lys Asp Gln Pro Leu Lys Cys Lys Arg Cys Lys Arg
1 5 10 15

Gly Phe Arg Gln Gln Asn Glu Leu Lys Asn Ile
20 25

<210> 3759
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.H263L"

<400> 3759
Glu Lys Pro Tyr Arg Cys Glu Glu Cys Gly Lys Ala Phe Ser Trp Ser
1 5 10 15

Ala Ser Leu Thr Lys His Lys Arg Ile Leu Leu Thr Gly Glu Lys Pro
20 25 30

Tyr Thr Cys Glu Glu Arg Gly Lys Val Phe Ser Arg Ser Thr Leu Thr
35 40 45

Asn Tyr Lys Arg
50

<210> 3760
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.N594I"

<400> 3760
Gly Lys Ser Phe His Cys Lys Ser Phe Leu Thr Ile His Gln Arg Thr
1 5 10 15

His Ala Gly Lys Lys Pro Tyr Glu Cys Ile Ile Glu Cys Glu Lys Thr
20 25 30

Phe Ile Asn Lys Leu Asn Leu Gly Ile His Lys Arg Thr His Thr Gly
35 40 45

Glu Arg Pro Tyr
50

<210> 3761
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C844S"

<400> 3761
Cys Arg Lys Thr Phe Ser Gln Lys Ser Lys Leu Phe Val His His Arg
1 5 10 15

Thr His Thr Gly Glu Lys Pro Phe Arg Ser Ser Asn Glu Cys Arg Lys
20 25 30

Thr Phe Ser Gln Lys Ser Gly Leu Ser Ile His Gln Arg Thr His Thr
35 40 45

Gly Glu Lys Pro
50

<210> 3762
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W315C"

<400> 3762

Lys Pro Ser Ile Ser Lys Ser Asp Leu Met Leu Gln Cys Lys Met Pro
1 5 10 15

Thr Glu Glu Lys Pro Tyr Ala Cys Asn Cys Cys Cys Glu Lys Leu Phe
20 25 30

Ser Tyr Lys Ser Ser Leu Ile Ile His Gln Arg Ile His Thr Gly Glu
35 40 45

Lys Pro Tyr Gly
50

<210> 3763
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S96fs"

<400> 3763
Leu Asp Pro Lys Gln Thr Asn Gln Pro Asp Ala Thr Ala Lys Pro Ala
1 5 10 15

Ser Ser Lys Ser Val Ala Asn Gly Leu Cys Leu Arg Leu Glu Ala Ser
20 25 30

Ala Gln Leu Cys Gln Gly Arg His Gln Gly Lys Pro Gly Ala Ala Ser
35 40 45

Pro Gly Asn Pro Gln Val Pro Gly Thr Glu Ala Ser Pro Pro Gln Gly
50 55 60

Ile Thr Leu Gln Glu Pro Ser Ser Gly Ser Arg Pro Arg Cys Pro Ala
65 70 75 80

Cys Ser Gly Arg Arg Ser Ser Ala Phe Cys Ile Cys Ser Ser Arg Arg
85 90 95

Ala Gln Thr Gln Gly Ala Arg Gln Arg Arg Gly Ala Arg Asp Thr Gly
100 105 110

Phe Thr Gln Pro His Cys Gln Gly Arg Val Phe Pro His Gln Val Gly

115 120 125

Leu Pro His Ser Trp Leu Pro Leu Glu Ser Arg Leu Thr Phe Pro Ser
130 135 140

Thr Arg Val Ser Thr
145

<210> 3764
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.S254L"

<400> 3764
Leu Leu Arg Lys His Gln Leu Ile His Leu Gly Glu Lys Gln Tyr Lys
1 5 10 15

Cys Asp Ile Cys Gly Lys Val Phe Asn Leu Leu Lys Arg Tyr Val Ala
20 25 30

Arg His Arg Arg Cys His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu
35 40 45

Cys Gly Lys Thr
50

<210> 3765
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R423Q"

<400> 3765
Thr Gly Glu Arg Pro Tyr Lys Cys Gly Glu Cys Gly Lys Ser Phe Asn
1 5 10 15

Gln Ser Ser His Phe Ile Thr His Gln Gln Ile His Leu Gly Asp
20 25 30

Arg Pro Tyr Arg Cys Pro Glu Cys Gly Lys Thr Phe Asn Gln Arg Ser
35 40 45

His Phe Leu Thr
50

<210> 3766
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R466Q"

<400> 3766
Ser Asn Glu Lys Pro Phe Val Cys Arg Glu Cys Glu Met Ala Phe Arg
1 5 10 15

Tyr His Cys Gln Leu Ile Glu His Ser Gln Gln Ile His Thr Gly Asp
20 25 30

Lys Pro Phe Glu Cys Gln Asp Cys Gly Lys Ala Phe Asn Arg Gly Ser
35 40 45

Ser Leu Val Gln
50

<210> 3767
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G484W"

<400> 3767
Phe Asn Tyr Lys Ser Ile Leu Ile Val His Gln Arg Thr His Thr Gly
1 5 10 15

Glu Lys Pro Phe Glu Cys Asn Glu Cys Trp Trp Lys Ser Phe Ser His
20 25 30

Met Ser Gly Leu Arg Asn His Arg Arg Thr His Thr Gly Glu Arg Pro
35 40 45

Tyr Lys Cys Asp
50

<210> 3768
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.C145F"

<400> 3768
Lys Pro His Asn Arg Asp Ile Asn Ile Phe Arg Ala Arg Met Met Pro
1 5 10 15

Cys Lys Cys Asp Ile Ala Gly Ser Ala Phe Phe Gln Gly Leu Ser Leu
20 25 30

Met Ala Pro His Cys Gln Tyr Ser Lys Glu Lys Ala His Glu Arg Asn
35 40 45

Val Cys Asp Lys
50

<210> 3769
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> source
<223> /note="p.K247T"

<400> 3769
Lys Ala Phe Leu Glu Lys Ala Ala Leu Val Thr Ser Asn Ser Thr His
1 5 10 15

Pro Lys Gly Lys Ser Tyr Asn Phe Asn Thr Thr Phe Gly Glu Asn Lys
20 25 30

Tyr Asp Lys Ser Thr Phe Ile Ile Pro Gln Asn Met Asn Pro Glu Lys
35 40 45

Ser His Tyr Glu
50

<210> 3770
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.W41G"

<400> 3770
Ile Arg Val Asp Ala Gly His Lys Pro His Glu Tyr Gln Glu Tyr Gly
1 5 10 15

Glu Lys Arg Asn Thr Arg Lys Gln Phe Gly Gly Lys Thr Phe Ser Tyr
20 25 30

Cys His Ser Phe Gln Thr His Lys Ile Ser His Thr Gly His Lys Pro
35 40 45

Tyr Asp Cys Lys
50

<210> 3771
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.T43A"

<400> 3771
Val Asp Ala Gly His Lys Pro His Glu Tyr Gln Glu Tyr Gly Glu Lys
1 5 10 15

Arg Asn Thr Arg Lys Gln Phe Trp Lys Ala Ala Phe Ser Tyr Cys His
            20 25 30

Ser Phe Gln Thr His Lys Ile Ser His Thr Gly His Lys Pro Tyr Asp
        35 40 45

Cys Lys Glu Cys
    50

<210> 3772
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.C453R"

<400> 3772
Lys Ala Tyr Arg Ile Ser Ser Ser Leu Arg Arg His Glu Thr Thr His
1 5 10 15

Thr Gly Glu Lys Pro Tyr Lys Cys Lys Arg Arg Gly Lys Ala Phe Ile
            20 25 30

Asp Phe Tyr Ser Phe Gln Asn His Lys Thr Thr His Ala Gly Glu Lys
        35 40 45

Pro Tyr Glu Cys
    50

<210> 3773
<211> 53
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P644S"

<400> 3773
Asn Asp Ile Asp Glu Asp Leu Ser Phe Pro Ser Tyr Ile Ser Arg Phe
1 5 10 15

Lys Lys His Lys Leu Ile Pro Cys Ser Ser Ser His Leu Glu Phe Glu
20 25 30

Asp Glu Arg Gln Phe Asn Cys Lys Ser Ser Pro Cys Thr Val Gly Gly
35 40 45

His Ser Asp His Gly
50

<210> 3774
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.G320E"

<400> 3774
Lys His Glu Cys Gly Glu Cys Gly Lys Ser Phe Ser Lys Tyr Val Ser
1 5 10 15

Phe Ser Asn His Gln Arg Val His Thr Glu Glu Lys Arg Pro Tyr Glu
20 25 30

Cys Gly Glu Cys Gly Lys Ser Phe Ser Lys Tyr Ala Ser Phe Ser Asn
35 40 45

His Gln Arg Val His
50

<210> 3775
<211> 52
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.P323H"

<400> 3775
Cys Gly Glu Cys Gly Lys Ser Phe Ser Lys Tyr Val Ser Phe Ser Asn
1 5 10 15

His Gln Arg Val His Thr Gly Lys Arg His His Tyr Glu Cys Gly Glu
20 25 30

Cys Gly Lys Ser Phe Ser Lys Tyr Ala Ser Phe Ser Asn His Gln Arg
35 40 45

Val His Thr Glu
50

<210> 3776
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.Y324H"

<400> 3776
Gly Glu Cys Gly Lys Ser Phe Ser Lys Tyr Val Ser Phe Ser Asn His
1 5 10 15

Gln Arg Val His Thr Gly Lys Arg Pro His His Glu Cys Gly Glu Cys
20 25 30

Gly Lys Ser Phe Ser Lys Tyr Ala Ser Phe Ser Asn His Gln Arg Val
35 40 45

His Thr Glu Lys
50

<210> 3777
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R547I"

<400> 3777
Ser Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser
1 5 10 15

Trp Leu Thr Cys Leu Leu Arg His Glu Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Glu Cys Leu Gln Cys Gly Lys Ala Phe Thr Arg Ser Arg
35 40 45

Phe Leu Arg Gly
50

<210> 3778
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 3778
Pro Gly Gly Gln Ala Ser Pro His Leu Thr Leu Gly Pro Val Leu Leu
1 5 10 15

Pro Pro Glu Gln Gly Leu Ala Pro Pro His Cys Val Pro Glu Gly Pro
20 25 30

Ala His Pro Thr Val Pro His Gly Ala Ser Arg Gly Pro Pro Ala Pro
35 40 45

Arg Pro Ala Ser Asp Gly Gln Pro Arg Trp Gly Gln Arg Ala Leu His

50 55 60

Thr Gln Pro Cys Ala Ala Ala
65 70

<210> 3779
<211> 52
<212> PRT
<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.Q617K"

<400> 3779
Ala Arg Glu Ala Met Ala Gly Lys Gly Arg Ala Gly Gly Arg Lys Cys
1 5 10 15

Gly Gln Arg Arg Leu Lys Met Phe Ser Lys Lys Glu Lys Trp Gln Val
20 25 30

Tyr Gly Asp Glu Thr Phe Lys Arg Ile Tyr Gln Lys Met Lys Ala Ser
35 40 45

Pro His Gly Gly
50

<210> 3780
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.E949D"

<400> 3780
Gln Ala Pro Arg Val Leu Ser Ala Leu Ala Asp Asn Ala Phe Ser Pro
1 5 10 15

Lys Tyr Leu Leu Arg Leu Pro Gln Ala Asp Asp Thr Pro Leu Pro Leu
20 25 30

Pro Ile Pro Trp Gly Pro Arg His Ser Gln Asp Ser Leu Cys Ser Ser
35 40 45

Gly Trp Pro Glu
50

<210> 3781
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R1393Q"

<400> 3781
Glu Gly Asp Cys Arg Gln Thr Leu Gly Thr Leu Ser Leu Gly Thr Ser
1 5 10 15

Ser Arg Ile Val Arg Glu Met Asp Lys Gln Gln Thr Val Lys Asp Ile
20 25 30

Ser Pro Ser Ala Gly Glu His Gly Asp Cys Thr Thr His Ser Thr Ala
35 40 45

Ala Thr Ser Gly
50

<210> 3782
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="p.I571N"

<400> 3782
Arg Ile His Thr Gly Glu Gln Pro Tyr Lys Cys Asn Val Cys Gly Lys
1 5 10 15

Val Phe Asn Tyr Ser Gly Asn Leu Ser Asn Asn His Lys Arg Ile His
20 25 30

Thr Gly Glu Lys Pro Phe Gln Cys Asn Glu Cys Gly Thr Val Phe Arg
35 40 45

Asn Tyr Ser Cys
50

<210> 3783
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.K608Q"

<400> 3783
Gln Cys Asn Glu Cys Gly Thr Val Phe Arg Asn Tyr Ser Cys Leu Ala
1 5 10 15

Arg His Leu Arg Ile His Thr Gly Gln Gln Gln Pro Tyr Lys Cys Asn
20 25 30

Val Cys Gly Lys Val Phe Asn Asp Ser Gly Asn Leu Ser Asn His Lys
35 40 45

Arg Ile His Thr
50

<210> 3784
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R630I"

<400> 3784

Thr Gly Gln Lys Pro Tyr Lys Cys Asn Val Cys Gly Lys Val Phe Asn
1 5 10 15

Asp Ser Gly Asn Leu Ser Asn His Lys Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Phe Gln Cys Asn Glu Cys Gly Lys Val Phe Ser Tyr Tyr Ser
35 40 45

Cys Leu Ala Arg
50

<210> 3785
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> /note="p.R854I"

<400> 3785
Thr Gly Asp Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Ile
1 5 10 15

Glu Arg Ser Lys Leu Val Tyr His Gln Ile Ile Asn His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Ile Glu Cys Gly Lys Ala Phe Gly Arg Phe Ser
35 40 45

Cys Leu Asn Lys
50

<210> 3786
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R757I"

<400> 3786
Thr Gly Glu Met Pro Tyr Lys Cys Ile Glu Cys Gly Lys Val Phe Asn
1 5 10 15

Ser Thr Thr Thr Leu Ala Arg His Arg Ile Ile Ile His Thr Gly Glu
20 25 30

Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe Arg Tyr Arg Ser
35 40 45

Gly Leu Ala Arg
50

<210> 3787
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.M423I"

<400> 3787
Leu Thr Arg His Arg Arg Leu His Thr Gly Glu Lys Pro Tyr Lys Cys
1 5 10 15

Asn Asp Cys Gly Lys Thr Phe Ser Gln Ile Ile Ser Ser Leu Val Tyr
20 25 30

His Arg Arg Leu His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys
35 40 45

Asp Glu Ala Phe
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<210> 3788
<211> 52
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R925H"

<400> 3788
Ala His Leu Ala Cys His His Arg Ile His Thr Gly Glu Lys Pro Tyr
1 5 10 15

Lys Cys Asn Glu Cys Gly Lys Thr Phe His His His Asn Ser Val Leu
20 25 30

Val Ile His Lys Thr Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn
35 40 45

Glu Cys Gly Lys
50

<210> 3789
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.Q406R"

<400> 3789
Glu Cys Lys Glu Cys Gly Lys Val Phe Arg His Lys Phe Cys Leu Thr
1 5 10 15

Asn His His Arg Met His Thr Gly Glu Arg Arg Pro Tyr Lys Cys Asn
20 25 30

Glu Cys Gly Lys Ala Phe Arg Asp Cys Ser Gly Leu Thr Ala His Leu
35 40 45

Leu Ile His Thr
50

<210> 3790
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.V362fs"

<400> 3790
Val Met Ser Gln Trp Ser Arg Ser Ala Ser Arg Asn Arg Arg His Val
1 5 10 15

Thr Glu Glu Ala Asp Val Thr Val Gly Ala Thr Asp Leu Pro Gly Gln
20 25 30

Glu Gly

<210> 3791
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="p.R154C"

<400> 3791
Asn Phe Glu Glu Ser Met Ser Gly Ile Tyr Thr Cys Phe Leu Glu Tyr
1 5 10 15

Lys Pro Thr Val Glu Glu Ile Val Lys Cys Cys Leu Gln Leu Lys Tyr
20 25 30

Ala Ile Tyr Ala Tyr Arg Glu Pro His Tyr Tyr Tyr Gln Phe Thr Ala
35 40 45

Arg Tyr His Ala
50

<210> 3792
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="p.P225fs"

<400> 3792
Ser Ser Ile Leu Ser Asp Gly Val Tyr Glu Arg His Met Asp Pro Leu
1 5 10 15

Leu Leu Pro Gly Glu Leu Ala Ser Pro Gln Pro Gly Pro Trp Ser Trp
20 25 30

Gly Asp Pro Gly Thr Phe
35

<210> 3793
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.S214Y"

<400> 3793
Thr Ser Met Leu Lys Cys Pro Leu Cys Arg Lys Glu Phe Ala Pro Leu
1 5 10 15

Lys Leu Ile Leu Glu Glu Phe Lys Asn Tyr Tyr Ser Lys Leu Val Ala
20 25 30

Ala Ala Glu Lys Glu Arg Leu Asp Lys His Leu Gly Ile Pro Cys Asn
35 40 45

Asn Cys Lys Gln
50

<210> 3794
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="p.E407K"

<400> 3794
Gly Pro Ser Leu Gln Pro Thr Met Ala Pro Ala Pro Glu Leu Leu Gln
1 5 10 15

Lys Gly Ser Thr Cys Ile Thr Asn Thr Lys Lys Gly Trp Val Gly His
            20 25 30

Pro Leu Asp Pro Ile Gly Cys Leu Cys Arg Ala Leu Leu Glu Ala Cys
        35 40 45

Arg Leu Glu Glu
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<210> 3795
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<220>
<221> source
<223> /note="p.Q610fs"

<400> 3795
Leu Ala Ile Ala Ile Val Asn Thr Leu Arg Arg Gln Gln Gln Lys Gln
1 5 10 15

Leu Glu Met Phe Arg Thr Gln Lys Lys Ser Tyr Pro Ile Lys Thr
            20 25 30

<210> 3796
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="p.V30A"

<400> 3796
Pro Ser His Ser Ser Glu Asp Glu Ala Ala Ala Ala Gly Gly Glu Gly
1 5 10 15

Trp Gly Pro His Gln Asp Trp Ala Ala Ala Ala Ser Gly Thr Thr Pro
20 25 30

Gly Pro Gly Val Ala Ala Pro Ala Leu Pro Pro Ala Ala Ala Leu Leu
35 40 45

Glu Pro Ala Arg
50

<210> 3797
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R5Q"

<400> 3797
Met Ala Ala Ser Gln Gln Ser Thr Arg Val Thr Arg Ser Thr Val Gly
1 5 10 15

Leu Asn Gly Leu Asp Glu Ser Phe Cys Gly Arg Thr Leu Arg Asn
20 25 30

<210> 3798
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="p.R162Q"

<400> 3798
Ile Lys Ser Asp Lys Glu Ser Val Glu Gln Arg Ser Thr Val Val Asp
1 5 10 15

Asn Asp Ala Asp Phe Gln Gly Thr Lys Gln Gln Ala Cys Arg Cys Leu
20 25 30

Ile Leu Asp Asp Cys Glu Lys Arg Glu Ile Lys Lys Val Asn Val Ser
35 40 45

Glu Glu Gly Pro
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<210> 3799
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3799
Val Gln Lys Tyr Phe Pro Glu Thr Trp
1 5

<210> 3800
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3800
Gln Lys Tyr Phe Pro Glu Thr Trp Ile
1 5

<210> 3801
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3801
Glu Thr Val Gln Lys Tyr Phe Pro Glu Thr
1 5 10

<210> 3802
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3802
Val Gln Lys Tyr Phe Pro Glu Thr Trp Ile
1 5 10

<210> 3803
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3803
Gln Lys Tyr Phe Pro Glu Thr Trp Ile Trp
1 5 10

<210> 3804
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3804
Glu Pro His Thr Glu Thr Val Gln Lys Tyr
1 5 10

<210> 3805
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3805
His Ser Glu Pro Ala Phe His Tyr Leu
1 5

<210> 3806
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3806
Met Pro Gln Gly His Ser Glu Pro Ala
1 5

<210> 3807
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3807
Pro Gln Gly His Ser Glu Pro Ala Phe
1 5

<210> 3808
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3808
Gly His Ser Glu Pro Ala Phe His Tyr
1 5

<210> 3809
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3809
Phe His Tyr Leu Glu Ala Leu Val Leu
1 5

<210> 3810
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3810
Glu Pro Ala Phe His Tyr Leu Glu Ala
1 5

<210> 3811
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3811
Gln Gly His Ser Glu Pro Ala Phe His Tyr
1 5 10

<210> 3812
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3812
Glu Pro Ala Phe His Tyr Leu Glu Ala Leu
1 5 10

<210> 3813
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3813
Met Pro Gln Gly His Ser Glu Pro Ala Phe
1 5 10

<210> 3814
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3814
Ser Glu Pro Ala Phe His Tyr Leu Glu Ala
1 5 10

<210> 3815
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3815
Ile Asp Leu Ser Trp Arg Asp Thr Ile
1 5

<210> 3816
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3816
Ser Trp Arg Asp Thr Ile Leu Asn Gly
1 5

<210> 3817
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3817
Asp Thr Ile Leu Asn Gly Thr Cys Val
1 5

<210> 3818
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3818
Ile Asp Leu Ser Trp Arg Asp Thr Ile Leu
1 5 10

<210> 3819
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3819
Met Ala Lys Thr Val Gly Leu Pro Thr Arg
1 5 10

<210> 3820
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3820
Leu Pro Thr Arg His Gly Ser Gln Asn Val
1 5 10

<210> 3821
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3821
Val His Arg Ile Ile His Thr Gly Glu Lys
1 5 10

<210> 3822
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 3822
Gln Ser Ala Asn Leu Tyr Val His Arg Ile
1 5 10

<210> 3823
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3823
Lys Thr Val Thr Asp Thr Val Arg Arg
1 5

<210> 3824
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3824
Val Thr Asp Thr Val Arg Arg Ala Leu Val
1 5 10

<210> 3825
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3825
Ala Ala Lys Thr Val Thr Asp Thr Val Arg
1 5 10

<210> 3826
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3826
Asp Ala Ala Lys Thr Val Thr Asp Thr Val
1 5 10

<210> 3827
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3827
Thr Val Thr Asp Thr Val Arg Arg Ala Leu
1 5 10

<210> 3828
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3828
His Met Trp Arg Ala Ile Gln Thr Ala
1 5

<210> 3829
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3829
Ile Gln Thr Ala Phe Lys Asn Arg Lys
1 5

<210> 3830
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3830
Met Trp Arg Ala Ile Gln Thr Ala Phe
1 5

<210> 3831
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3831
Ala Ile Gln Thr Ala Phe Lys Asn Arg
1 5

<210> 3832
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3832
Gln Thr Ala Phe Lys Asn Arg Lys Arg
1 5

<210> 3833
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3833
Met Trp Arg Ala Ile Gln Thr Ala Phe Lys
1 5 10

<210> 3834
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3834

Ala Ile Gln Thr Ala Phe Lys Asn Arg Lys
1 5 10

<210> 3835
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3835
His Met Trp Arg Ala Ile Gln Thr Ala Phe
1 5 10

<210> 3836
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3836
Lys Gln His Met Trp Arg Ala Ile Gln Thr
1 5 10

<210> 3837
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3837
Arg Ala Ile Gln Thr Ala Phe Lys Asn Arg
1 5 10

<210> 3838
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3838
Gln His Met Trp Arg Ala Ile Gln Thr Ala

1 5 10

<210> 3839
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3839
Met Val Ile Phe Ile Leu Phe Phe Tyr
1 5

<210> 3840
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3840
Val Ile Phe Ile Leu Phe Phe Tyr Met
1 5

<210> 3841
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3841
Ile Leu Phe Phe Tyr Met Ala Tyr Leu
1 5

<210> 3842
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3842
Leu Phe Phe Tyr Met Ala Tyr Leu Trp
1 5

<210> 3843
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3843
Phe Ile Leu Phe Phe Tyr Met Ala Tyr
1 5

<210> 3844
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3844
Met Val Ile Phe Ile Leu Phe Phe Tyr Met
1 5 10

<210> 3845
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3845
Val Ile Phe Ile Leu Phe Phe Tyr Met Ala
1 5 10

<210> 3846
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3846
Phe Ile Leu Phe Phe Tyr Met Ala Tyr Leu
1 5 10

<210> 3847
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3847
Ile Leu Phe Phe Tyr Met Ala Tyr Leu Trp
1 5 10

<210> 3848
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3848
Phe Met Val Ile Phe Ile Leu Phe Phe Tyr
1 5 10

<210> 3849
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3849
Ile Phe Ile Leu Phe Phe Tyr Met Ala Tyr
1 5 10

<210> 3850
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3850
Lys Leu Lys Cys Thr Gly Ser Ser Leu
1 5

<210> 3851
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 3851
Cys Thr Gly Ser Ser Leu Phe Leu Lys
1 5

<210> 3852
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<210> 3861
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<210> 3872
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<210> 3873
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<210> 3878
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<210> 3879
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 3881
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<210> 3882
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<210> 3883
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<210> 3893
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<400> 3893
Asn Val Arg Thr Val His Ala Phe Ala
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<210> 3894
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<210> 3914
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<210> 3916

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<210> 3923
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Arg Val Arg Cys Gly Gly Trp Leu Cys Gly
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Cys Leu Arg Val Arg Cys Gly Gly Trp Leu
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1 5

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1 5 10

<210> 3932
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<400> 3932
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1 5 10

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1 5 10

<210> 3941
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<400> 3941
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Arg Leu Val Ala Gln Ala Tyr Arg Leu
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<400> 3945
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1 5

<210> 3946
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<400> 3946
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1 5

<210> 3947
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<400> 3947
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1 5

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<400> 3949
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Gln Thr Arg Gly Ile Arg Gly Ser Ser Ala
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1 5 10

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<210> 3992
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Arg Leu Leu Thr Trp His Ala Ala Met
1 5

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Leu Leu Thr Trp His Ala Ala Met Leu
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1 5

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1 5

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1 5 10

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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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His Ala Ala Met Leu Lys Asp Asn Lys Lys
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<210> 4005
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<400> 4005
Arg Glu Glu Glu Glu Arg Leu Arg Leu
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<210> 4006
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<400> 4008
His Val Asn His Val Gln Asp Lys Leu Arg
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<210> 4009
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<210> 4010
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<400> 4010
Leu Leu Lys Ile Pro Ile Met Gly Met
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<210> 4011
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<400> 4011
Thr Leu Arg Arg Cys Thr Ser Ser Val
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<210> 4012
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<210> 4013
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1 5

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Arg Ser Trp Arg Arg Pro Thr Glu Ala
1 5

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Leu Thr Arg Pro His Pro Glu Val Leu
1 5

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<400> 4017

Gly Ala Ala Glu Arg Ser Trp Arg Arg
1 5

<210> 4018
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<400> 4018
Cys Thr Ser Ser Val Ser Gly Ala Ala
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<400> 4020
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1 5

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<400> 4021
His Pro Glu Val Leu His Phe Ser Val

1 5

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Asn Leu Leu Leu Lys Ile Pro Ile Met
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Gly Ser Tyr Asp Pro Gln Asn Asn Leu
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<400> 4024
Thr Glu Ala Gly Ser Cys Pro Ala Ala
1 5

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Gly Ser Cys Pro Ala Ala Ala Ser Leu
1 5

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<400> 4026
Ala Ala Ala Ser Leu Thr Arg Pro His
1 5

<210> 4027
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Ala Glu Arg Ser Trp Arg Arg Pro Thr
1 5

<210> 4028
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Leu Leu Leu Lys Ile Pro Ile Met Gly Met
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Ser Leu Thr Arg Pro His Pro Glu Val Leu
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<210> 4031
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<400> 4031
Ile Met Gly Met Thr Leu Thr Leu Arg Arg
1 5 10

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<400> 4032
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1 5 10

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<400> 4033
Ala Ser Leu Thr Arg Pro His Pro Glu Val
1 5 10

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<400> 4034
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Pro Ile Met Gly Met Thr Leu Thr Leu Arg
1 5 10

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Ser Gly Ala Ala Glu Arg Ser Trp Arg Arg
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<210> 4038

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<400> 4038
Arg Pro Thr Glu Ala Gly Ser Cys Pro Ala
1 5 10

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Gly Ser Tyr Asp Pro Gln Asn Asn Leu Leu
1 5 10

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Leu Lys Ile Pro Ile Met Gly Met Thr Leu
1 5 10

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1 5 10

<210> 4042
<211> 10

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<210> 4043
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Asp Pro Gln Asn Asn Leu Leu Leu Lys Ile
1 5 10

<210> 4044
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<400> 4044
Cys Leu His Gln Arg Arg Gly Ala Leu
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<210> 4045
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<400> 4046
Gln Arg Arg Gly Ala Leu Ala Glu Leu
1 5

<210> 4047
<211> 10
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<400> 4047
Cys Leu His Gln Arg Arg Gly Ala Leu Ala
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<210> 4048
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Arg Ile Met Gln His Ala Asp Ala Val His
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<400> 4247
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1 5 10

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<210> 4501
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<210> 4507
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1 5 10

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Cys Phe Gln Lys Gly Leu Leu His Val Arg
1 5 10

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Leu Leu Cys Gly Pro Ala Trp Thr Cys Phe
1 5 10

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1 5 10

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<210> 4541
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Val Glu Val Phe Cys Ser Ala Leu Thr
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Cys Ser Ala Leu Thr Gln His Met Glu Arg
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Val Phe Cys Ser Ala Leu Thr Gln His Met
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<210> 4550
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Lys Pro Lys Pro Lys Lys Asn Lys Lys
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<210> 4551
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Lys Met Lys Gly Asp Val Asp Val Phe
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Lys Met Lys Gly Asp Val Asp Val Phe Leu
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<210> 4553
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<400> 4554
Pro Lys Met Lys Gly Asp Val Asp Val Phe
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<210> 4555
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<400> 4555
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<400> 4557
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<210> 4562
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<210> 4564
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1 5 10

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<210> 4578
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Arg Arg Leu His Gly Ala Gly Val Gln Ile
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<210> 4590
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Glu Phe Lys His Tyr Met Pro Lys Lys
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1 5

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1 5 10

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Phe Phe Glu Phe Lys His Tyr Met Pro Lys
1 5 10

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Glu Phe Lys His Tyr Met Pro Lys Lys Arg
1 5 10

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Ala Ile Phe Phe Glu Phe Lys His Tyr Met
1 5 10

<210> 4612
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<210> 4613
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Ala Val Leu Gln Trp Arg Leu Gln Arg
1 5

<210> 4614
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1 5

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<400> 4615
Arg Thr Ile Lys Glu Gln Ala Leu Leu
1 5

<210> 4616
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Leu Gln Trp Arg Leu Gln Arg Thr Ile
1 5

<210> 4617
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<400> 4617
Val Leu Gln Trp Arg Leu Gln Arg Thr Ile
1 5 10

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1 5 10

<210> 4619
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Leu Gln Arg Thr Ile Lys Glu Gln Ala Leu
1 5 10

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1 5

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Thr Val Met Thr Trp Val Arg Ser Lys
1 5

<210> 4623
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1 5

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<400> 4624
Leu Ser Thr Val Met Thr Trp Val Arg
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<210> 4625
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1 5 10

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<400> 4626
Thr Val Met Thr Trp Val Arg Ser Lys Ala
1 5 10

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<400> 4627

Val Met Thr Trp Val Arg Ser Lys Ala Leu
1 5 10

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<210> 4631
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1 5

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1 5 10

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Arg Gly His Gly Arg Ile Asn Cys Gly Arg
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Arg Gly Lys Tyr Ile Lys Thr Trp Arg
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1 5

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<210> 4735
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Cys Glu Asn Gln Asp Leu Ile Ser Ser
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<400> 4736
Lys Tyr Ile Cys Glu Asn Gln Asp Leu Ile
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<400> 4737
Ala Lys Tyr Ile Cys Glu Asn Gln Asp Leu
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<210> 4738
<211> 9
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Cys Leu Ala Phe Ser Leu Gly Ser Val
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<210> 4739
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Gln Ala Ala Cys Leu Ala Phe Ser Leu
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<210> 4740
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Ala Val Gln Ala Ala Cys Leu Ala Phe
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<210> 4741
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<210> 4742
<211> 10
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1 5

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Asp Val Ala Thr Pro Phe Gly Gly Phe
1 5

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Asn Lys Thr Asp Val Ala Thr Pro Phe
1 5

<210> 4747
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<400> 4747
Asp Val Ala Thr Pro Phe Gly Gly Phe Lys
1 5 10

<210> 4748
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Tyr Asn Lys Thr Asp Val Ala Thr Pro Phe
1 5 10

<210> 4749
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<400> 4749

Thr Asp Val Ala Thr Pro Phe Gly Gly Phe
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Ser Met Met Ser Leu Trp Ser Gly Ala
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<210> 4751
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<210> 4752
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<210> 4753
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1 5

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Lys Leu Ser Leu Arg Arg Ser Ser Ala
1 5

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<210> 4757
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<210> 4758
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1 5

<210> 4760
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1 5

<210> 4761
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1 5

<210> 4762
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1 5

<210> 4763
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1 5

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1 5

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1 5

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1 5

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1 5

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1 5

<210> 4769
<211> 9
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1 5

<210> 4770

<211> 9
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1 5

<210> 4771
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1 5

<210> 4772
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<400> 4772
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1 5

<210> 4773
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<400> 4773
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1 5

<210> 4774
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1 5

<210> 4775
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<400> 4775
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1 5

<210> 4776
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<400> 4776
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1 5

<210> 4777
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<400> 4777
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1 5

<210> 4778
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Ser Leu Trp Ser Gly Ala Leu Pro Gly
1 5

<210> 4779
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1 5

<210> 4780
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Leu Gly Trp Ser Gly Thr Pro Leu Ile
1 5

<210> 4781
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<400> 4781
Gly Arg Arg Trp Met Lys Leu Ser Leu
1 5

<210> 4782
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<400> 4782
Arg Ser Cys Cys Val Val Gly Ala Leu
1 5

<210> 4783
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<400> 4783
Met Pro Ile Trp Ile Gly Pro Trp Asn
1 5

<210> 4784
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<400> 4784
Ser Met Met Ser Leu Trp Ser Gly Ala Leu
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<400> 4785
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1 5 10

<210> 4786
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<400> 4786
Cys Val Val Gly Ala Leu Leu Leu Thr Val
1 5 10

<210> 4787
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<400> 4787
Val Val Gly Ala Leu Leu Leu Thr Val Val
1 5 10

<210> 4788
<211> 10
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<400> 4788
Ser Ser Ala Thr Ser Thr Arg Gly Ser Lys
1 5 10

<210> 4789
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<400> 4789
Cys Gln Met Pro Ile Trp Ile Gly Pro Trp
1 5 10

<210> 4790
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<220>

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<400> 4790
Ser Thr Arg Ala Ser Ala Ala Val Pro Ala
1 5 10

<210> 4791
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<212> PRT
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<220>
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<400> 4791
Arg Ala Ser Ala Ala Val Pro Ala Pro Gly
1 5 10

<210> 4792
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<400> 4792
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<210> 4793
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<400> 4793
Arg Thr Ser Met Met Ser Leu Trp Ser Gly
1 5 10

<210> 4794
<211> 10
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 4794
Thr Ser Met Met Ser Leu Trp Ser Gly Ala
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<210> 4795
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<400> 4795
Arg Pro Ser Arg Gly Arg Arg Trp Met Lys
1 5 10

<210> 4796
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<400> 4796
Arg Gly Arg Arg Trp Met Lys Leu Ser Leu
1 5 10

<210> 4797
<211> 10
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<400> 4797
Gly Ser Lys Arg Gly Arg Ser Cys Cys Val
1 5 10

<210> 4798
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peptide"

<400> 4798
Arg Gly Arg Ser Cys Cys Val Val Gly Ala
1 5 10

<210> 4799
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Arg Ser Cys Cys Val Val Gly Ala Leu Leu
1 5 10

<210> 4800
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Met Pro Ile Trp Ile Gly Pro Trp Asn Arg
1 5 10

<210> 4801
<211> 10
<212> PRT
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<400> 4801
Leu Ile Ala Arg Pro Ser Arg Gly Arg Arg
1 5 10

<210> 4802
<211> 10
<212> PRT
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<400> 4802
Ser Ala Thr Ser Thr Arg Gly Ser Lys Arg
1 5 10

<210> 4803
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<400> 4803
Cys Ser Ser Thr Arg Ala Ser Ala Ala Val
1 5 10

<210> 4804
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Leu Thr Val Val Thr Ser Ser Ser Pro Leu
1 5 10

<210> 4805
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Ala Pro Thr Ser Ser Cys Gln Met Pro Ile
1 5 10

<210> 4806
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<400> 4806
Gly Pro Trp Asn Arg Pro Thr Ser Pro Cys
1 5 10

<210> 4807
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<400> 4807
Ser Pro Cys Ser Ser Thr Arg Ala Ser Ala
1 5 10

<210> 4808
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<400> 4808
Gly Pro Ser Cys Arg Arg Thr Ser Met Met
1 5 10

<210> 4809
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<400> 4809
Gly Arg Ala Pro Thr Ser Ser Cys Gln Met
1 5 10

<210> 4810
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 4810

Cys Arg Arg Thr Ser Met Met Ser Leu Trp
1 5 10

<210> 4811
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<400> 4811
Met Ser Leu Trp Ser Gly Ala Leu Pro Gly
1 5 10

<210> 4812
<211> 10
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<400> 4812
Trp Ser Gly Ala Leu Pro Gly Pro Ser Leu
1 5 10

<210> 4813
<211> 10
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<400> 4813
Gly Ala Leu Pro Gly Pro Ser Leu Gly Trp
1 5 10

<210> 4814
<211> 10
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<400> 4814
Ile Ala Arg Pro Ser Arg Gly Arg Arg Trp

1 5 10

<210> 4815
<211> 10
<212> PRT
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<400> 4815
Met Lys Leu Ser Leu Arg Arg Ser Ser Ala
1 5 10

<210> 4816
<211> 10
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<400> 4816
Gly Arg Ser Cys Cys Val Val Gly Ala Leu
1 5 10

<210> 4817
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<400> 4817
Thr Ser Ser Ser Pro Leu Cys Leu Glu Met
1 5 10

<210> 4818
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<400> 4818
Leu Glu Leu Gly Gly Arg Ala Pro Thr Ser
1 5 10

<210> 4819
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<400> 4819
Ser Pro Leu Cys Leu Glu Met Cys Arg Met
1 5 10

<210> 4820
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<400> 4820
Gly Leu Lys Val Arg Tyr Pro Arg Ala
1 5

<210> 4821
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<400> 4821
Lys Val Arg Tyr Pro Arg Ala Arg Pro
1 5

<210> 4822
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<400> 4822
Glu Gly Leu Lys Val Arg Tyr Pro Arg
1 5

<210> 4823
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<400> 4823
Gly Leu Lys Val Arg Tyr Pro Arg Ala Arg
1 5 10

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<400> 4824
Lys Val Arg Tyr Pro Arg Ala Arg Pro Arg
1 5 10

<210> 4825
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<400> 4825
Thr Phe Leu Arg Tyr Phe Ser Asp Lys
1 5

<210> 4826
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<400> 4826
Gln Tyr Val Thr Phe Leu Arg Tyr Phe
1 5

<210> 4827
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<400> 4827
Arg Tyr Phe Ser Asp Lys Gln Lys Ile
1 5

<210> 4828
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Gly Gln Tyr Val Thr Phe Leu Arg Tyr
1 5

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<400> 4829
Tyr Val Thr Phe Leu Arg Tyr Phe Ser
1 5

<210> 4830
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<400> 4830
Leu Gly Gln Tyr Val Thr Phe Leu Arg Tyr
1 5 10

<210> 4831

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<400> 4831
Val Thr Phe Leu Arg Tyr Phe Ser Asp Lys
1 5 10

<210> 4832
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<400> 4832
Phe Leu Arg Tyr Phe Ser Asp Lys Gln Lys
1 5 10

<210> 4833
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<400> 4834
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Leu Leu Gly Thr Glu His Val Phe Tyr
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<400> 4838
Asn Leu Leu Gly Thr Glu His Val Phe Tyr
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Leu Ile Val Thr Ser Ser Thr Ser Leu
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Ile Val Thr Ser Ser Thr Ser Leu Thr Val
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Met Pro Thr Asn Val Cys Leu Ile Val Thr
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<210> 4893
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<210> 4894
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<400> 4896
Cys Val Cys Val Cys Val Cys Val Cys Arg
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Arg Glu His Pro Gly Arg Ser Pro Pro Gly
1 5 10

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Arg Trp Tyr Cys Trp Arg Gly Ser Lys
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Cys Tyr Arg Trp Tyr Cys Trp Arg Gly
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Gln Ala Glu Arg Gly Leu Cys Tyr Arg
1 5

<210> 4901
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<400> 4901
Leu Cys Tyr Arg Trp Tyr Cys Trp Arg
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<210> 4902
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<400> 4902
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1 5

<210> 4903
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<400> 4903
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1 5

<210> 4904
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Arg Gly Leu Cys Tyr Arg Trp Tyr Cys Trp
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<210> 4905
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Gly Leu Cys Tyr Arg Trp Tyr Cys Trp Arg
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<210> 4906
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Phe Ile Ile Ile Glu Thr Pro Leu Leu
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Ile Ile Ile Glu Thr Pro Leu Leu Val
1 5

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<400> 4910
Ile Ile Glu Thr Pro Leu Leu Val Lys
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Ile Glu Thr Pro Leu Leu Val Lys Ile
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1 5 10

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Ile Ile Ile Glu Thr Pro Leu Leu Val Lys
1 5 10

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1 5 10

<210> 4915
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<400> 4915
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1 5 10

<210> 4916
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<400> 4916
His Leu Leu Lys Arg Asp Tyr Arg Lys
1 5

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<400> 4917
Lys His Leu Leu Lys Arg Asp Tyr Arg
1 5

<210> 4918
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<400> 4918
Lys His Leu Leu Lys Arg Asp Tyr Arg Lys
1 5 10

<210> 4919
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<400> 4919
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<400> 4922
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<400> 4925
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1 5

<210> 4926
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<400> 4926
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1 5

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<400> 4927
Ile Lys Asp Lys Asp His Ser Pro Thr Phe
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<400> 4928
Leu Gln Lys Lys Ser Lys Leu Glu Lys
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Thr Leu Gln Lys Lys Ser Lys Leu Glu Lys
1 5 10

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<400> 4930
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1 5

<210> 4931
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 5553
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1 5 10

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1 5 10

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Arg Ala Gly Ser Gly Arg Ala Ala Ala
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Trp Thr Ala Pro Ser Ser Pro Pro Ser
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Thr Pro Arg Ala Gly Ser Gly Arg Ala
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<400> 5725

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Gln Pro Gly Gly Gly Arg Gly Gly Glu Leu
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1 5

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<210> 5741
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<210> 5742
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<210> 5748
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<210> 5750
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Gly Leu Ile Ala Leu Leu Leu Leu Leu Val
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1 5 10

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<400> 6109
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<400> 6110
Leu Leu Thr Ser Ser Ser Arg Glu Trp
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<210> 6111
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<400> 6111
Ser Ser Arg Glu Trp Lys Val Lys Phe
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<210> 6112

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<400> 6112
Trp Lys Val Lys Phe Pro Glu Leu Leu
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Val Lys Phe Pro Glu Leu Leu Cys Val
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Thr Ser Ser Ser Arg Glu Trp Lys Val Lys
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Tyr Pro Ala Tyr Ser Lys Asp Ser Gly Leu
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Leu Ala Val Leu Ala Leu Leu Ser Phe Trp
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<210> 6130
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<210> 6131
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<400> 6131
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5

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1 5 10

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Ala Gln Arg Ile Ile Ser Leu Ser Gln
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Tyr His Asp Ile Cys Phe Asn Leu Met
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1 5 10

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1 5 10

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Thr Gly Ser Pro Ser Leu Pro Ala Tyr
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Leu Pro Ala Tyr Pro Leu Leu Ser Val
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Cys Thr Gly Ser Pro Ser Leu Pro Ala Tyr
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Ser Leu Pro Ala Tyr Pro Leu Leu Ser Val
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1 5 10

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1 5 10

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1 5 10

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<400> 6201
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Tyr Leu Thr Val Tyr Gly His Thr Trp
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Met Gly Phe Leu Tyr Leu Thr Val Tyr
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Phe Leu Tyr Leu Thr Val Tyr Gly His Thr
1 5 10

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1 5 10

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<400> 6511
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Val Pro Pro Phe Tyr Arg Arg Leu Leu
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1 5

<210> 6543
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Arg Thr Lys Gly Phe Thr Ser Glu Arg
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<210> 6701
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Phe Leu Arg Thr Lys Gly Phe Thr Ser
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Lys Leu Glu Asp Arg Lys Thr Ser Trp
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<400> 6710
Val Lys Leu Glu Asp Arg Lys Thr Ser Trp
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<210> 6711
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Phe Ser Leu Pro Ala Ser Phe Leu Leu
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<210> 6712
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Gly Ser Asn Leu His Val Lys Val Lys
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1 5

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Glu Thr Leu Ala Tyr Gln His Leu Pro Ile
1 5 10

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1 5 10

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<400> 6781
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<210> 6783

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<210> 6785
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<400> 6786
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<400> 6787
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Ala Glu Trp Asn Asp Gln Thr Gly Ala
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1 5 10

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<400> 6796
Ser Ala Leu Pro Gly Pro Trp Phe Leu Ala
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<210> 6797
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<400> 6797
Leu Ala Pro Ala Arg Cys Pro Leu Pro Arg
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<400> 6798
Ala Pro His Ser Ser Pro Ile Ala Thr Leu
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Thr Ala Leu Ala Pro Ala Arg Cys Pro Leu
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<210> 6800
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Arg Lys His Ser Glu Ser Pro Pro Gln His
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<210> 6801
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<400> 6801
Ala Glu Trp Asn Asp Gln Thr Gly Ala Trp
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Ser Pro Ile Ala Thr Leu Ala Ser Pro Gly
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<400> 6804
Ser Pro Gly Ser Ala Leu Pro Gly Pro Trp
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<210> 6805
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<400> 6805
Thr Ile Thr Ser Trp Val Ser Pro Val
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<400> 6806
Trp Val Ser Pro Val Phe Asp Thr Ala
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Ile Thr Ser Trp Val Ser Pro Val Phe
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<210> 6808
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Ser Thr Ile Thr Ser Trp Val Ser Pro Val
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<400> 6810
Trp Val Ser Pro Val Phe Asp Thr Ala Ala
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<210> 6811
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<400> 6811
Val Phe Asp Thr Ala Ala Gly Ser Leu Phe
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<210> 6812
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Thr Ile Thr Ser Trp Val Ser Pro Val Phe
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<210> 6813
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<400> 6813
Leu Val Asp Asn Gln Ile Asn Ser Tyr
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<210> 6814
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Asn Gln Ile Asn Ser Tyr Ser Gly Ile
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<210> 6815
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<400> 6815
Gln Ile Asn Ser Tyr Ser Gly Ile Lys
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Gln Ile Asn Ser Tyr Ser Gly Ile Lys Arg
1 5 10

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<210> 6820
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Gln Ala Ala Met Pro Ala Trp Gly Leu
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1 5

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Arg Gln Ala Ala Met Pro Ala Trp Gly
1 5

<210> 6824
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Glu Glu Leu Glu Arg Cys Arg Gln Ala
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Glu Leu Glu Arg Cys Arg Gln Ala Ala Met
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Arg Cys Arg Gln Ala Ala Met Pro Ala Trp

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1 5

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1 5

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1 5

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1 5

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1 5

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1 5 10

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Lys Leu Ser Phe Asn Ile Gln Ala Leu
1 5

<210> 6848
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Arg Thr Lys Leu Ser Phe Asn Ile Gln
1 5

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Met Leu Gln Leu Ile Leu Asp Ile Ala
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Ala Leu Phe Gly Leu Arg Thr Phe Arg
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Leu Phe Gly Leu Arg Thr Phe Arg Leu
1 5

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Lys Gln Arg Gly Ser Met Gly Arg Arg
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Gly Ser Met Gly Arg Arg Val Ala Ala
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1 5

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1 5

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1 5

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Ser Ile Ser Ile Ile Arg Lys Gln Arg
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Thr Pro Ile Leu Lys Arg Thr Asn Leu
1 5

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Lys Glu Ile Met Leu Gln Leu Ile Leu
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<400> 6886
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1 5 10

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Glu Ala Val Lys Arg Asn Leu Arg Asn Arg
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<210> 6903
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<210> 6905

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<210> 6907
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<210> 6908
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<210> 6910
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<400> 6910
Leu Lys Arg Thr Asn Leu Pro Glu Ala Leu
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<210> 6911
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<400> 6911
Ile Lys Glu Ile Met Leu Gln Leu Ile Leu
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<210> 6912
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Arg Ser Glu Thr Asp Thr Asn Ser Glu Lys
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<210> 6913
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<210> 6917
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<210> 6918
<211> 9
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Glu Ile Met Asp Ser Gly Leu Asp Lys
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<210> 6919
<211> 9
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1 5

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Gln Leu Ser Asp Val Gly Gly Glu His Leu
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1 5

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Cys Gln Arg His Glu Glu Thr Ser Pro Val
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Lys Gly Gly Ser Tyr Asn Ser Val Ile
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1 5

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Gln Ser Phe Arg Ala Pro Ala Thr Ala
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Ser Thr Ser Leu Pro Ala Gln Ser Phe
1 5

<210> 6946
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1 5

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Gln Glu His Ile Ser Thr Ser Ile Asn Phe
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Ile Ser Thr Ser Ile Asn Phe Asn Ile Ile
1 5 10

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Arg Gln Ala Glu Gln Gly Gly Trp Leu
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<400> 6974
Pro Val Ala Cys Pro Val Ser Cys Pro Val
1 5 10

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<400> 6975
Cys Pro Val Ser Cys Pro Val Gly Ser Met
1 5 10

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1 5

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<400> 6977
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1 5

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<400> 6987
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1 5 10

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<400> 6988
Asp Thr Phe Gly Lys Ile Val Tyr Glu Arg
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<210> 6989
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Phe Gly Lys Ile Val Tyr Glu Arg Ile Phe
1 5 10

<210> 6990
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<210> 6991
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<400> 6991
Gln Met Cys Val Ser Ser Ser Ser Ser His
1 5 10

<210> 6992
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<400> 6992
Lys Ile Ile Asn Gln Ile Leu Ile Leu
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<210> 6993
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<400> 6993
Asn Arg Lys Ile Ile Asn Gln Ile Leu
1 5

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<400> 6994
Arg Lys Ile Ile Asn Gln Ile Leu Ile
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<400> 6995
Glu Ile Asn Arg Lys Ile Ile Asn Gln Ile
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<400> 6996
Arg Lys Ile Ile Asn Gln Ile Leu Ile Leu
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Ser Leu Gly Pro Gly Pro Gly Glu Val
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<400> 6998
Val Ala Ala Arg Ser Pro Val Leu Arg
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<400> 7002
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<400> 7006

Gly Val Arg Ala Ser Leu Trp Ala Ala Leu
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<210> 7007
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<210> 7008
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<400> 7008
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Gly Gly Trp Asn Gly Val Arg Ala Ser Leu
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<210> 7010
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<400> 7010
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<210> 7011
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<400> 7012
Arg Glu Glu Asn Lys Val Cys Ala Val
1 5

<210> 7013
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Asn Lys Val Cys Ala Val Pro Thr Trp
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<210> 7014
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<400> 7014
Glu Glu Asn Lys Val Cys Ala Val Pro Thr
1 5 10

<210> 7015
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<400> 7015
Cys Val Ser Arg Gln Ala Cys Arg Tyr
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<210> 7016
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<400> 7016
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<210> 7017
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<400> 7018
Ser Gln Pro Leu Gln Arg Phe Thr Phe
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<210> 7019
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Thr Phe Pro Ser Val Thr Pro Gly Met
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<210> 7021
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Cys Thr Ser Ser Ala Ser Thr Cys Val
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<210> 7022
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Phe Thr Phe Pro Ser Val Thr Pro Gly
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<210> 7024
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<210> 7025
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<210> 7026
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Pro Leu Gln Arg Phe Thr Phe Pro Ser Val
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<210> 7027

<211> 10
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Phe Thr Phe Pro Ser Val Thr Pro Gly Met
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<210> 7028
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Thr Ser Ser Ala Ser Thr Cys Val Ser Arg
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<210> 7031
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<210> 7034
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1 5 10

<210> 7035
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Asn Tyr Ile Leu Asn Thr Asp Ser Leu
1 5

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1 5 10

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<400> 7040
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Leu Ser Ile Glu Ser Val Gly Leu Leu
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Glu Ala Leu Ser Ile Glu Ser Val Gly Leu
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1 5 10

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Gln Ser His Pro Pro Pro Arg Leu Leu Ala
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<400> 7048
Val Glu Gln Ser His Pro Pro Pro Arg Leu
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Thr Ser Ser Ser Trp Ser Leu Leu Ile
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Ile Leu Met Thr Thr Ser Lys Tyr Thr
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Leu Leu Ile Leu Met Thr Thr Ser Lys
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Tyr Thr Ala Pro Met Thr Ser Tyr Arg
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1 5

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Thr Thr Ser Lys Tyr Thr Ala Pro Met
1 5

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Met Thr Ser Tyr Arg Ser Met Pro Thr
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Arg Thr Leu Ala Ser Ser Val Gly Ser
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Ala Gly Ser Cys Ala Thr Pro Pro Arg
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<400> 7066
Leu Ile Leu Met Thr Thr Ser Lys Tyr
1 5

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<400> 7067

Lys Tyr Thr Ala Pro Met Thr Ser Tyr
1 5

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<400> 7068
Thr Thr Ala Ser Gly Trp Ser Gly Ala
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Cys Thr Ser Ser Ser Trp Ser Leu Leu
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<400> 7070
Ser Thr Pro Ala Ala Met Leu Trp Ile
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<210> 7071
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<400> 7071
Tyr Pro Arg Ser Tyr Pro Leu Thr Cys

1 5

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<400> 7073
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1 5

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<400> 7074
Leu Glu Tyr Pro Arg Ser Tyr Pro Leu
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<400> 7075
Cys Ala Ala Thr Thr Ala Ser Gly Trp
1 5

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<400> 7076
Ser Ser Ser Trp Ser Leu Leu Ile Leu
1 5

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1 5

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<400> 7078
Leu Met Thr Thr Ser Lys Tyr Thr Ala
1 5

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<400> 7079
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1 5

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<400> 7083
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1 5

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Thr Ser Thr Pro Ala Ala Met Leu Trp
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<400> 7085
Thr Pro Ala Ala Met Leu Trp Ile Cys
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<210> 7086
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<400> 7086
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<400> 7087
Ser Leu Glu Tyr Pro Arg Ser Tyr Pro Leu
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<210> 7088

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Ile Leu Met Thr Thr Ser Lys Tyr Thr Ala
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<210> 7089
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Met Leu Trp Ile Cys Cys Ser Ser Gln Met
1 5 10

<210> 7090
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1 5 10

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<400> 7091
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<400> 7110
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<210> 7112
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 7114
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<210> 7115
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<400> 7116
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Thr Ala Ala Ala Cys Trp Ala Thr Ser Val
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<400> 7147
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<400> 7148
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1 5 10

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1 5 10

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His Ser Met Pro Leu Tyr Pro Pro Thr Thr
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Thr Tyr Phe Gln Ile His Ile Asn Lys
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Tyr Phe Gln Ile His Ile Asn Lys Tyr
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1 5 10

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<210> 7303
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<400> 7310
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<210> 7311
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<400> 7311

His Gln Gln Leu Gly Arg Gly Ser Pro Cys
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<210> 7312
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<210> 7313
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<210> 7314
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<210> 7315
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1 5

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<210> 7403
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<210> 7404
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1 5 10

<210> 7409
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<210> 7410
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<210> 7411
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<210> 7412
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<210> 7413
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<210> 7414
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<210> 7415
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<210> 7416
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<210> 7417
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<210> 7418
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Tyr Tyr His Val Pro Val Lys Arg Ser Lys
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1 5 10

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1 5 10

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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

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<400> 7482
Leu Met Leu Met Glu Thr Ala Gln Leu
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Phe Gln Ile Leu Met Gly Glu Asp Trp
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<210> 7596
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 7601
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<210> 7602
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<400> 7611
Ala Gln Lys Thr Ala Cys Asn Thr Ala Thr
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<400> 7616

Gln Asn Arg Gln Thr Cys Ile Arg Lys
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Ala Ser Ala Trp Pro Ala Pro Ser Ala Lys
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1 5 10

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Leu Arg Val Val Lys Trp Ile Pro Ala Leu
1 5 10

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Glu Asn Thr Trp Phe Ser Tyr Leu Lys Arg
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Lys Leu Thr Ser Val Glu Lys Ser Leu Arg
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<210> 7714
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His Ser Ser Ser Ser Ser His Gln Ser Lys
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<400> 7778
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Asn Gln Asn Ile Arg Phe Gln Lys Phe
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Phe Val Asp Ser Ser Ser Tyr His Pro Phe
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Ala Ala Phe Phe Val Asp Ser Ser Ser Tyr
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His Pro Phe Lys Ile Asn Gln Asn Ile Arg
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Asp Ser Ser Ser Tyr His Pro Phe Lys Ile
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<400> 7787
Asn Pro Trp Ser Leu Glu Glu Glu Lys Tyr
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<400> 7799

Ile Leu Lys Leu Cys Ser Lys Val Ser Phe
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Ser Lys Val Ser Phe Arg Val Asp Trp Ile
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<210> 7802
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<400> 7810
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Asp Gly Ala Ile Leu Phe Val Leu Phe
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<400> 7813
Ala Ile Leu Phe Val Leu Phe Cys Phe
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1 5

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Val Ile Ser Ala His Arg Lys Leu Arg
1 5

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Lys Leu Arg Leu Pro Gly Ser Gly His
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<210> 7820

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1 5

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1 5

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Arg Lys Asn Leu Ser Ser Leu Leu Ile
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Ala Arg His His Thr Trp Leu Ile Phe
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Ala Ile Leu Phe Val Leu Phe Cys Phe Val
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1 5 10

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Thr Leu Arg Lys Asn Leu Ser Ser Leu Leu
1 5 10

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Arg Leu Glu Cys Ser Gly Val Ile Ser Ala
1 5 10

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Arg Leu Pro Gly Ser Gly His Ser Pro Ala
1 5 10

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Cys Ser Gly Val Ile Ser Ala His Arg Lys
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Ile Asp Gly Ala Ile Leu Phe Val Leu Phe
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Gly Ala Ile Leu Phe Val Leu Phe Cys Phe
1 5 10

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Ile Leu Phe Val Leu Phe Cys Phe Val Phe
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<400> 7840
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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Gly Ala Arg His His Thr Trp Leu Ile Phe
1 5 10

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<400> 7845
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1 5 10

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<220>
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<400> 7846
Glu Cys Ser Gly Val Ile Ser Ala His Arg
1 5 10

<210> 7847
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Gly Val Ile Ser Ala His Arg Lys Leu Arg
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Gln Pro Thr Phe Thr Leu Arg Lys Asn Leu
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<210> 7849
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<210> 7850
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1 5

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<210> 7852
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Glu Val Leu Asn Arg Arg Ser Ser Met
1 5

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1 5 10

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1 5

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1 5 10

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1 5 10

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<400> 7860

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<400> 7861
Val Leu Ser Ser Cys Val Ala Leu Phe
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<210> 7862
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<400> 7863
Leu Ser Ser Cys Val Ala Leu Phe Lys
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Cys Val Ala Leu Phe Lys Gly Ala Arg

1 5

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His Ile Cys Leu Arg Glu Thr Tyr Arg
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Gly Ala Arg Glu His Ile Cys Leu Arg
1 5

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Thr Tyr Arg Leu Ile Ser Thr Ile Ala
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Ile Leu His Glu Lys Arg Glu Ile Arg
1 5

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Arg Cys Val Gln Ala Val Val Ile Leu
1 5

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<400> 7875
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1 5

<210> 7876
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5

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1 5

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<400> 8045
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<210> 8303
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1 5 10

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1 5 10

<210> 8308

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1 5 10

<210> 8309
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Val Met Thr Met Leu Arg Asn Ile Trp
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Phe Met Val Met Thr Met Leu Arg Asn Ile
1 5 10

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1 5 10

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1 5 10

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Pro Ser Phe Met Val Met Thr Met Leu Arg

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Ser Phe Ile Trp Pro Ser Phe Met Val Met
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1 5 10

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<210> 8362
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<400> 8362
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1 5 10

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<400> 8363
Gln Glu Ser Ser Phe Ile Trp Pro Ser Phe
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<210> 8365
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1 5 10

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<400> 8437
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<210> 8438
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<400> 8470

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<210> 8478
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<210> 8479
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<400> 8480
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<210> 8481
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<400> 8481
Gly Leu His Gly Ala Asp Val Val Phe
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<210> 8482
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<400> 8482
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<210> 8491

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1 5 10

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1 5 10

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1 5 10

<210> 8498
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1 5 10

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1 5

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1 5

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1 5 10

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1 5

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1 5 10

<210> 8514
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1 5

<210> 8517
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1 5

<210> 8518
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<400> 8518
Arg Ala Gly Ala Arg Leu Asp Val Arg Tyr
1 5 10

<210> 8519
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<400> 8519
Arg Leu Asp Val Arg Tyr Ala Trp Gly Arg
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Tyr Ala Trp Gly Arg Leu Pro Val Asp Leu
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Pro Leu Leu Glu Asp Ala Pro Leu Leu
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<210> 8524
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Leu Glu Asp Val Pro Leu Leu Glu Asp Ala
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1 5 10

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1 5

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1 5

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1 5

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His Thr Gln Val Ile Phe Ile Ala Lys Ile

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<400> 8537
Gln Gln His Thr Gln Val Ile Phe Ile Ala
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Leu Asn Met Asn Gly Leu Ala Pro Ala
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<400> 8540
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Ala Leu Asn Met Asn Gly Leu Ala Pro Ala
1 5 10

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<400> 8542
Gly Leu Ala Pro Ala Pro Met Thr Pro Thr
1 5 10

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Phe Leu Gly Ala Ala Ala Leu Gly Leu
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<400> 8545
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1 5

<210> 8547
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<400> 8559
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<400> 8560
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1 5

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<400> 8561
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1 5

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<400> 8562
Val Pro Ser Trp Thr Ala Arg Arg Trp
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

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1 5

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1 5

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<210> 8613

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<210> 8614
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<210> 8615
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<210> 8616
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<210> 8617
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<210> 8618
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<210> 8619
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<210> 8620
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<210> 8621
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1 5 10

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<400> 8625
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1 5 10

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1 5

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1 5

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1 5 10

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1 5 10

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1 5 10

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<400> 8636
Val Leu Asn Asp Asn Ser Met Asp Met
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<400> 8641
Met Asp Met Thr Glu Val Ile Ser Ser Leu
1 5 10

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1 5

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1 5

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Gly Arg Trp Gln Ser Leu Pro His Cys Val
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His Gln Gly Arg Arg Asp Ala Gly Leu Leu
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Asp Leu Lys His Val Lys Asn Val Tyr
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Val Lys Asn Val Tyr Ser Cys Asp Leu
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<400> 8775

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<210> 8777
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<210> 8779
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<210> 8782
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<210> 8783
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<400> 8783
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<210> 8784
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 8785
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<210> 8786
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1 5

<210> 8787
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<210> 8793
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<210> 8794
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<210> 8796

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1 5

<210> 8797
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<400> 8797
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1 5

<210> 8798
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1 5

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<210> 8800
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<210> 8802
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<210> 8804
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1 5

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1 5

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<400> 8809
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<210> 8810
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<400> 8810
Gln Pro Arg Leu Ala Leu Ser Pro Ala
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<400> 8811
Ala Gln Pro His Leu Gln Pro Pro Phe
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Ser Gln Ala Pro Gln Ala Trp Ser Thr
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<210> 8813
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<400> 8813
Thr Leu Trp Pro Pro Ala Gln Pro His
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<210> 8814
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Gln Pro Ser Gln Ala Pro Gln Ala Trp
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<210> 8815
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Ala Pro Gln Ala Trp Ser Thr Leu Trp
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<210> 8816
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Thr Leu Trp Pro Pro Ala Gln Pro His Leu
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His Leu Gln Pro Pro Phe Cys Pro Arg Ala
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<210> 8819
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Arg Ala Arg Gln Pro Leu Pro Leu Pro Pro
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<210> 8820
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 8821
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1 5 10

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<400> 8824
Leu Ala Leu Ser Pro Ala Pro Gln Gln Val
1 5 10

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<400> 8825
Ala Leu Trp Leu Ala Leu Ser Gly Lys
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<210> 8826
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Leu Trp Leu Ala Leu Ser Gly Lys Ile
1 5

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Ala Leu Trp Leu Ala Leu Ser Gly Lys Ile
1 5 10

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Gly Ala Leu Trp Leu Ala Leu Ser Gly Lys
1 5 10

<210> 8829
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Leu Trp Leu Ala Leu Ser Gly Lys Ile Lys
1 5 10

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Lys Ile Lys Asp Lys Glu Leu Pro Gln Tyr
1 5 10

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Gly Met Tyr His Glu Val Lys Ala Met
1 5

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<400> 8832
Met Tyr His Glu Val Lys Ala Met Arg
1 5

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<400> 8833
Arg Gly Ala Gly Met Tyr His Glu Val Lys
1 5 10

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<400> 8834
Met Tyr His Glu Val Lys Ala Met Arg Lys
1 5 10

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Gly Met Tyr His Glu Val Lys Ala Met Arg
1 5 10

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Leu Pro Phe Asp Pro Arg Gly Ala Gly Met
1 5 10

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1 5 10

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Ala Val Ala Asp Gln Glu Asp Ile Phe Val
1 5 10

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1 5 10

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Gln Glu Asp Ile Phe Val Val Gly Thr Ala

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Leu Leu Ser Leu Leu Pro Ala Pro Arg
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<400> 8847
Arg Val Tyr Tyr Glu Ala Asp Thr Thr Lys
1 5 10

<210> 8848
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Lys Asn Lys Lys Ala Leu Glu Thr Lys
1 5

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Lys Lys Ala Leu Glu Thr Lys Glu Ile
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Gln Leu Ser Pro Ala Arg Arg Arg Arg
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Ser Pro Ala Arg Arg Arg Arg Gln His
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Arg Arg Arg Arg Gln His Met Gln Glu Arg
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1 5

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1 5

<210> 8898
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1 5

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<400> 8910
Gln Phe Pro Met Pro Gly Ile Arg Arg
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<210> 8912
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<210> 8913
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<400> 8913
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<210> 8914
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Ser Tyr Leu Asn Ser Arg Gln Phe Pro Met
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<210> 8915
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1 5 10

<210> 8916
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<210> 8918

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1 5 10

<210> 8922
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1 5 10

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1 5 10

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<400> 8927
Arg Asn Trp Arg Leu Ala Ser Leu Glu Ala
1 5 10

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Arg Ile His Glu Arg Asn Ile Ser Lys
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<400> 8932
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Gln Phe Gly Ala Gln Val His Gln Arg
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1 5

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<400> 8940
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1 5

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1 5

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1 5

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peptide"

<400> 8946
Phe Ser Thr Thr Ser Ser Ser Phe Ala
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<400> 8947
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1 5 10

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Val Val Leu Ser Phe Asp Ser Thr Lys
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1 5

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1 5

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1 5 10

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<400> 10020
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1 5

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<210> 10077

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1 5

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1 5 10

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Leu Glu Ala Leu Gly Thr Thr Gly Phe
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Val Asn Tyr Arg Ala Leu Leu Glu Ala Leu
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Cys Leu Ala Pro Gly Leu Thr Lys Thr
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Gly Leu Thr Lys Thr Ser Phe Ser Arg
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<400> 10132
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Leu Glu Ile Phe Gln His Cys Asp Cys Ala
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Arg Val Arg Leu Asp Ser Met Val Leu
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Val Arg Leu Asp Ser Met Val Leu Leu
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<400> 10222
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<400> 10230
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1 5

<210> 10231
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<400> 10623
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<400> 10679
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Leu Val Val Pro His His Gln Pro His
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<400> 10711
Leu Pro Pro Ser Pro Asp Thr Leu Val
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Gln Leu Pro Pro Ser Pro Asp Thr Leu Val
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<400> 10713
Ala Gln Leu Pro Pro Ser Pro Asp Thr Leu
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Leu Pro Pro Ser Pro Asp Thr Leu Val Val
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<400> 10715
Thr Gln Ile Pro Arg Thr Ser Arg Trp
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<400> 10716
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1 5

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Arg Gly Lys Lys Asp Thr Gln Ile Pro Arg
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<400> 10718
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Cys Leu Lys Glu Gly Cys Thr Gly Asp Leu
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<400> 10721
Leu Lys Met Leu Ser Ser Ala Ala Ser
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<400> 11020
Leu Ser Leu Pro Thr Arg Pro Arg Leu Leu
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Arg Ile Cys Met His Asn Phe Ser Arg
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Arg Asn Phe Ser Arg Ser Asp Asn Leu
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His Tyr Arg Phe His Lys Phe His Ser
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Leu Trp Asn Leu Leu Met Pro Met Lys
1 5

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1 5 10

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<400> 11113
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1 5

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Ile Ser Lys Lys Lys His Tyr Asn Arg
1 5

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Ser Lys Lys Lys His Tyr Asn Arg Lys
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Lys His Tyr Asn Arg Lys Ile Ser Ile
1 5

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1 5 10

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1 5 10

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Leu Gln Arg Leu Phe Lys Pro Thr Thr
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1 5 10

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Gly Glu Val Thr Ser Thr Ser Lys Tyr
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1 5 10

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Phe Thr Lys Met Ile Pro Leu Leu Arg
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Glu Ser Phe Thr Lys Met Ile Pro Leu
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<210> 11806
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Lys His Phe Ser Gln Lys Tyr Ser Arg
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1 5

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1 5

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1 5

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1 5

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<210> 11850
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1 5

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1 5

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Gln Leu Phe Val Val Met Met Lys Met
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Met Lys Met Leu His His Cys Gln Pro
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Lys Met Leu His His Cys Gln Pro Asn
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<210> 11862
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<210> 11863
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1 5 10

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<210> 11867
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His Leu Gln Ala Arg Gly Pro Ala Pro Ala
1 5 10

<210> 11869
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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Gln Leu Phe Val Val Met Met Lys Met Leu
1 5 10

<210> 11871
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Thr Ser Thr Phe Thr Ser Ser His Phe Lys
1 5 10

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1 5 10

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<400> 11874
Lys Trp Ile Leu Leu Leu Thr Ile Leu Leu
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1 5 10

<210> 11876
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Ser Ser His Phe Lys Trp Ile Leu Leu Leu
1 5 10

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Gly Ala Arg Pro Val Cys His Leu Gln Ala
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<210> 11878
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Val Ala Arg His Gln Leu Phe Val Val Met
1 5 10

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Arg His Gln Leu Phe Val Val Met Met Lys
1 5 10

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1 5 10

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Trp Ile Leu Leu Leu Thr Ile Leu Leu Arg
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Leu Leu Thr Ile Leu Leu Arg Gly Ala Arg
1 5 10

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Phe Thr Ser Ser His Phe Lys Trp Ile Leu
1 5 10

<210> 11884
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1 5 10

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Gln Thr Val Ala Arg His Gln Leu Phe Val
1 5 10

<210> 11886
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<400> 11886

Gly Pro Ala Pro Ala Leu Pro Ser Gln Phe
1 5 10

<210> 11887
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<400> 11887
Leu Met Thr Ser Thr Phe Thr Ser Ser His
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His Gln Leu Phe Val Val Met Met Lys Met
1 5 10

<210> 11889
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Cys Gly Ile Met Asp Pro Pro Ser Leu Met
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Ser Thr Phe Thr Ser Ser His Phe Lys Trp

1 5 10

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Phe Lys Trp Ile Leu Leu Leu Thr Ile Leu
1 5 10

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Ala Arg His Gln Leu Phe Val Val Met Met
1 5 10

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Met Lys Met Leu His His Cys Gln Pro Asn
1 5 10

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1 5 10

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Leu Pro Ser Gln Phe Ser Ser Thr Pro Gly
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<400> 11898
Glu Glu His Leu Gly Lys Glu Gly Tyr
1 5

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<400> 11899
His Leu Gly Lys Glu Gly Tyr Leu Glu Lys
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1 5 10

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<400> 11901
Glu Glu His Leu Gly Lys Glu Gly Tyr Leu
1 5 10

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<400> 11902
Glu Glu His Leu Gly Lys Glu Gly Tyr
1 5

<210> 11903
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<400> 11997
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<210> 11998
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<400> 12002
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<400> 12003
Arg Val Ser Pro Leu Arg Pro Glu Thr
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<400> 12004
Pro Pro Lys Thr Arg Val Ser Pro Leu
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<400> 12005
Lys Thr Arg Val Ser Pro Leu Arg Pro Glu
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<400> 12006
Glu Pro Pro Lys Thr Arg Val Ser Pro Leu
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<400> 12007
Phe Ser Ala Ala Ala Ala Val Ala Ala
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<400> 12008

Ser Ala Ala Ala Ala Val Ala Ala Ala
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Ser Ala Ala Ala Ala Val Ala Ala Ala Ala
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Ala Pro Ala Pro Ala Pro Ala Leu Ala Ala
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<210> 12016
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<210> 12017
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Ser Trp Tyr Glu Lys Asn Lys Arg Ile Phe
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<210> 12018
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<400> 12018
Lys Asn Lys Arg Ile Phe Pro Ala Ser Arg
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<400> 12021
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<400> 12022
Thr Ile Leu Asp Thr Phe Asp Pro Tyr
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Asp Thr Phe Asp Pro Tyr Leu Ile Ala
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Thr Ile Leu Asp Thr Phe Asp Pro Tyr Leu
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Asp Thr Phe Asp Pro Tyr Leu Ile Ala Met
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<210> 12029

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<210> 12030
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<400> 12035
Gly Ser Phe Ser Glu Glu Thr His Trp
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<400> 12036
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<400> 12037
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<400> 12038
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<400> 12039
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1 5 10

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Gly Leu Leu Arg Arg Lys Lys Thr Ser Leu
1 5 10

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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Ser Arg Phe Thr Val Ala Pro Ser Ser Ala
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<400> 12055
Arg Phe Thr Val Ala Pro Ser Ser Ala Leu
1 5 10

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<400> 12056
Pro Ser Arg Lys Ser Ser Asp His Arg Lys
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<400> 12057
Glu Lys Ala Gln Gly Gly Gln Glu Met
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<210> 12058
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<400> 12058
Ala Gln Gly Gly Gln Glu Met Glu Met
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<210> 12059
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<400> 12059
Gln Glu Met Glu Met Ile Ser Gly Thr
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<210> 12060
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<400> 12060
Glu Met Glu Met Ile Ser Gly Thr Met
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<210> 12061
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<400> 12061
Met Glu Met Ile Ser Gly Thr Met Thr
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<210> 12062
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<400> 12062
Gln Glu Met Glu Met Ile Ser Gly Thr Met
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<400> 12063
Val Glu Lys Ala Gln Gly Gly Gln Glu Met
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<400> 12064
Lys Ala Gln Gly Gly Gln Glu Met Glu Met
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<400> 12065
Met Glu Met Ile Ser Gly Thr Met Thr Ser
1 5 10

<210> 12066
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<400> 12066
Arg Pro Ala Val Pro Val Leu Glu Leu
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<210> 12067
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<400> 12067
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<210> 12068
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<400> 12068
Leu Ser Tyr Phe His Cys Asp Asp Leu
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<210> 12069
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<400> 12069

Tyr Leu Ser Tyr Phe His Cys Asp Asp Leu
1 5 10

<210> 12070
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<400> 12070
Val Gln Gln Asp Pro Leu Ser Ser His
1 5

<210> 12071
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<400> 12071
Ser Ser His Pro Pro Glu Thr Cys Gln Met
1 5 10

<210> 12072
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His Leu Glu Asp Ser Gly Ile Ser Val
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<210> 12073
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<400> 12073
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1 5

<210> 12074
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<400> 12074
Leu Glu Asp Ser Gly Ile Ser Val Ala
1 5

<210> 12075
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<400> 12075
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1 5 10

<210> 12076
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Ser Val Ala Gln Lys Gln Glu Pro Arg Val
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<210> 12077
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<400> 12077
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<210> 12078
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1 5 10

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1 5 10

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1 5

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<400> 12082
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1 5

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<400> 12083
Arg Asp Gln Ser Phe Thr Thr Leu Leu
1 5

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<400> 12084
Gln Ser Phe Thr Thr Leu Leu Val Ala
1 5

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1 5 10

<210> 12086
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<400> 12086
Tyr Arg Asp Gln Ser Phe Thr Thr Leu Leu
1 5 10

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<400> 12087
Asp Gln Ser Phe Thr Thr Leu Leu Val Ala
1 5 10

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Val Gln Arg Leu Arg Asn Ile Gln Val
1 5

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<400> 12089
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<210> 12090

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<400> 12090
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1 5

<210> 12091
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1 5 10

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<400> 12093
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Gly Leu Val Thr Trp Asp Thr Ala Leu
1 5

<210> 12096
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<400> 12096
Val Thr Trp Asp Thr Ala Leu Tyr Leu
1 5

<210> 12097
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1 5 10

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<400> 12098
Gly Leu Val Thr Trp Asp Thr Ala Leu Tyr
1 5 10

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1 5 10

<210> 12100
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<400> 12100
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1 5 10

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Arg Met Ala Met Ala Gly Leu Val Leu
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<400> 12396
Ser Leu Leu Gly Arg His Lys Arg Lys Arg
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<400> 12397
Leu Gly Arg His Lys Arg Lys Arg Val Ile
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Arg His Lys Arg Lys Arg Val Ile Thr Tyr
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<210> 12399
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Ala Leu Ala Cys Ser Leu Glu Glu Lys
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Ala Leu Ala Cys Ser Leu Glu Glu Lys Leu
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<400> 12403
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<400> 12406
Leu Gly Tyr Lys Val Pro Ser Lys Thr Leu
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<400> 12410
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Thr Arg Met Gly Pro Thr Gln Leu Leu
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Gln Leu Thr Arg Met Gly Pro Thr Gln Leu
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Leu Thr Arg Met Gly Pro Thr Gln Leu Leu
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Val Met Pro Ser Lys Ser Thr Ser Ala
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<210> 12417
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<400> 12417
Gly Val Met Pro Ser Lys Ser Thr Ser Ala
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<400> 12418
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<210> 12419
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Met Pro Ser Lys Ser Thr Ser Ala Ser Ala
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<210> 12420
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<400> 12420
Gly Glu Thr Val Pro Lys Pro Gly Val Met
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<210> 12421
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1 5

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1 5

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<400> 12423
Lys Ser Thr Ser Val Ser Ala Ile Met
1 5

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1 5

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Gly Val Thr Pro Ser Lys Ser Thr Ser Val
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Ser Val Ser Ala Ile Met Asn Gly Gly Lys
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Thr Pro Ser Lys Ser Thr Ser Val Ser Ala
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1 5 10

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1 5

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1 5

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1 5

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Leu Gln Glu Asp Asp Gln Arg Pro Ala
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<400> 12459
Leu Pro Gly Gly Pro Gly His Gly Val
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<400> 12460
Cys Leu Pro Gly Gly Pro Gly His Gly Val
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Arg Ala Arg Arg Ala Pro Gly Pro Gly Leu
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Leu Leu Leu Arg His Leu Gln Ala Ala Arg
1 5 10

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Leu Pro Gly Gly Pro Gly His Gly Val Leu
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Arg Glu Phe Leu Arg Ala Arg Arg Ala Pro
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Arg Arg Ala Pro Gly Pro Gly Leu Leu Leu
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Arg His Leu Gln Ala Ala Arg Gly Ala Ala
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His Leu Gln Ala Ala Arg Gly Ala Ala His
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Ala Ala His Leu Gln Gly Pro Gly Val Leu
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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Arg Ile Leu Pro Pro Gly Ala Glu Val
1 5

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Arg Leu Ser Ala Asp Gly Glu Thr Ala
1 5

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Cys Val Cys Val Cys Ala His Pro Arg
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<400> 12487
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1 5

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1 5

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1 5

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<400> 12494
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<400> 12496

Gln Gln Cys Glu Gly Ser Leu Ala Ala
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<400> 12497
Ala Gly Ala Gln Pro Leu Pro Gly Met
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<400> 12498
Ala Gln Pro Leu Pro Gly Met Arg Leu
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<400> 12499
Ala Glu Val Pro Trp Val Ser Pro Leu
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<400> 12501
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<400> 12502
Ser Leu Ala Ala His Pro Ala Ala Gly Ala
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Gly Leu Cys Val Cys Val Cys Val Cys Val
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Leu Leu Cys Asn Gly Leu Leu Thr Gly Ala
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<210> 12508
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<400> 12508
Glu Thr Ala Thr Gln Ser Phe Gly Leu Cys
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<210> 12509
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<400> 12509
Cys Val Cys Ala His Pro Arg Val Pro Val
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Gln Pro Leu Pro Gly Met Arg Leu Ser Ala
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<210> 12513
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<210> 12514
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<400> 12515
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<210> 12516
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<400> 12516
Cys Glu Gly Ser Leu Ala Ala His Pro Ala
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<210> 12517

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<400> 12517
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<210> 12518
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1 5

<210> 12519
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Leu Glu Cys Ser Pro His Arg Pro Ile
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<210> 12520
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1 5

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1 5

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His Thr His Thr His Thr Leu Ser His
1 5

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His Thr Leu Ser His Thr Leu Thr Arg
1 5

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1 5

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1 5

<210> 12531
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Asp Ile His Thr His Thr His Thr Leu
1 5

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1 5

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Gly Gln Gly Pro Pro Ala His Pro Leu
1 5

<210> 12536
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Glu Glu Trp Pro Ala Pro Gln Ala Val
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1 5

<210> 12538
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<400> 12538
Ser Val Leu Asp Gly Thr Val Ser Ala Val
1 5 10

<210> 12539
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1 5 10

<210> 12540
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1 5 10

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<210> 12542
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1 5 10

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<400> 12543
Gly Pro Pro Ala His Pro Leu Ser Val Leu
1 5 10

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Thr Asp Ile His Thr His Thr His Thr Leu
1 5 10

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<400> 12546
Ile His Thr His Thr His Thr Leu Ser His
1 5 10

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Arg Gln Gly Thr His Gly Glu Glu Glu Trp
1 5 10

<210> 12548
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<400> 12548
Glu Glu Trp Pro Ala Pro Gln Ala Val Cys
1 5 10

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<400> 12549
Glu Glu Glu Trp Pro Ala Pro Gln Ala Val
1 5 10

<210> 12550
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<400> 12550
Gly Glu Glu Glu Trp Pro Ala Pro Gln Ala
1 5 10

<210> 12551
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<400> 12551
Arg Thr Leu Ser Lys Pro Val Leu Thr
1 5

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Val Ile Gln Arg Thr Leu Ser Lys Pro Val
1 5 10

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Thr Leu Ser Lys Pro Val Leu Thr Gly Thr
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Arg Thr Leu Ser Lys Pro Val Leu Thr Gly
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Ile Gln Arg Thr Leu Ser Lys Pro Val Leu
1 5 10

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<400> 12557

Tyr Lys Val Asp Val Ile Gln Arg Thr Leu
1 5 10

<210> 12558
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Lys Val Arg Ser Asp Leu Lys Pro Val
1 5

<210> 12559
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Gln Cys Lys Val Arg Ser Asp Leu Lys
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<400> 12560
Phe Gln Cys Lys Val Arg Ser Asp Leu
1 5

<210> 12561
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Lys Val Arg Ser Asp Leu Lys Pro Val Ile

1 5 10

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Asp Leu Lys Pro Val Ile Gln Trp Leu Lys
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<400> 12563
Cys Lys Val Arg Ser Asp Leu Lys Pro Val
1 5 10

<210> 12564
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<400> 12564
Ser Val Ala Glu Arg Glu Leu Glu Arg
1 5

<210> 12565
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<400> 12565
Leu Gln Tyr Val Gly Gly Gly Asp Val
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<210> 12566
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<400> 12566
Ala Glu Arg Glu Leu Glu Arg Asp Leu
1 5

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Val Leu Gln Tyr Val Gly Gly Gly Asp Val
1 5 10

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<400> 12568
Leu Gln Tyr Val Gly Gly Gly Asp Val Cys
1 5 10

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<400> 12569
Ala Glu Arg Glu Leu Glu Arg Asp Leu Leu
1 5 10

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<400> 12570
Arg Met Arg Ser Phe Phe Gly Lys Leu
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<210> 12571
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<400> 12571
Arg Ser Phe Phe Gly Lys Leu Phe Arg
1 5

<210> 12572
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<400> 12572
Lys Arg Met Arg Ser Phe Phe Gly Lys
1 5

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<400> 12573
Ser Phe Phe Gly Lys Leu Phe Arg Arg
1 5

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<400> 12574
Lys Thr Pro Pro Ser Leu Pro Phe Leu
1 5

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<400> 12575
Lys Lys Arg Met Arg Ser Phe Phe Gly
1 5

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<400> 12576
Phe Gly Lys Leu Phe Arg Arg Ser Lys
1 5

<210> 12577
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<400> 12577
Leu Phe Arg Arg Ser Lys Phe Glu Ala
1 5

<210> 12578

<211> 9
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<400> 12578
Arg Ser Lys Phe Glu Ala Lys Pro Thr
1 5

<210> 12579
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<400> 12579
Thr Thr Lys Leu Ile Gln Arg Pro Leu
1 5

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<400> 12580
Ile Gln Arg Pro Leu Arg Ser Ser Leu
1 5

<210> 12581
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<400> 12581
Pro Leu Arg Ser Ser Leu Gly Ser Arg
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<210> 12582
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<400> 12582
Gly Ser Arg Lys Thr Pro Pro Ser Leu
1 5

<210> 12583
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<400> 12583
Thr Ser Gly Pro Trp Gln Pro Gly Arg
1 5

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<400> 12584
Asn Ile Thr Thr Lys Leu Ile Gln Arg
1 5

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<400> 12585
Gly Pro Trp Gln Pro Gly Arg Asn Ile
1 5

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<400> 12586
Leu Pro Phe Leu Gly Glu Glu Glu Leu
1 5

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<400> 12587
Met Arg Ser Phe Phe Gly Lys Leu Phe
1 5

<210> 12588
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1 5

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<400> 12589
Arg Lys Thr Pro Pro Ser Leu Pro Phe
1 5

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<400> 12590
Lys Leu Phe Arg Arg Ser Lys Phe Glu Ala
1 5 10

<210> 12591
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<400> 12591
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1 5 10

<210> 12592
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Arg Ser Phe Phe Gly Lys Leu Phe Arg Arg
1 5 10

<210> 12593
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1 5

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<400> 12691
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<400> 12790
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<210> 12811
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<210> 12812
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<210> 12813
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<210> 12814
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<210> 12822

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<210> 12830
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Lys Asn Phe Thr Glu Ile Ser Ser Lys
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1 5 10

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<400> 12844
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<400> 12845
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5

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Trp Gln Asn Ser Ile Trp His Asn Leu
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Ala Ala Ser Tyr Leu Trp Pro Ser Arg
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<400> 12862

Ser Ala Ala Ser Tyr Leu Trp Pro Ser
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Thr Leu Thr Cys Pro Thr Met Pro Gly Arg
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<400> 12874
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<400> 12875
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Ser Leu Phe Ser Ala Ser Phe Leu Leu
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Phe Leu Leu Asn Ile Asn Glu Tyr Leu
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Leu Asn Ile Asn Glu Tyr Leu Ala Val
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1 5 10

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1 5 10

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<400> 12911
Trp Val Ala Gly Phe Gln Met Thr Arg
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<210> 12916
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1 5

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Ser Ala Ser Asn Ser Cys Phe Ile Arg
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1 5 10

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1 5 10

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Val Lys Leu Ser Asp Ser Arg Thr Ala Leu
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<400> 13045

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1 5

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<400> 13315
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1 5 10

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Lys Leu Asn Ala Arg Ser Ala Ser Ser
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Leu Asn Ala Arg Ser Ala Ser Ser Arg Leu
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Tyr Thr Phe Pro Gly Gly Thr Cys His
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1 5

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<400> 13348
Tyr Thr Phe Pro Gly Gly Thr Cys His Val
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Thr Phe Pro Gly Gly Thr Cys His Val Ile
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<400> 13350

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1 5

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Glu Ile Ile Asn Leu Asp Thr Phe Thr Tyr
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Met Asp Ile Trp Gly Gly Arg Glu Phe
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1 5 10

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Gln Met Asp Ile Trp Gly Gly Arg Glu Phe
1 5 10

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Gly Gly Glu Asn Leu Lys Leu Ser Phe
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1 5

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1 5

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1 5 10

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Gly Glu Asn Leu Lys Leu Ser Phe Lys Ala
1 5 10

<210> 13368
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Leu Ser Thr Trp Ser Pro Gly Lys Lys
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Val Ile Asp Asp Ile Thr Leu Glu Tyr
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Pro Leu Ile Asp Val Ile Asp Asp Ile
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<210> 13376
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1 5 10

<210> 13377
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<400> 13377
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1 5

<210> 13378
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1 5 10

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<400> 13411

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Glu Ser Lys Ile Met Phe Ala Thr Leu
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1 5

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peptide"

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1 5

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Tyr Met Phe Leu Lys Ala Glu Ser Lys Ile
1 5 10

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1 5 10

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Phe Cys Arg Ser Ser Ile Met Lys Pro Lys

1 5 10

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1 5 10

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1 5 10

<210> 13479
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<210> 13619
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<210> 13676

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1 5

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1 5

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<210> 13859

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1 5

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Arg Ala Glu Trp Ala Leu Ala Glu Asp Met
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<210> 13899
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<210> 13904
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<210> 14013
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1 5 10

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1 5

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Leu Trp His Gly Phe Asn Met Pro His Leu
1 5 10

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Leu Ser Ser Ile Trp Leu Ser Val Val
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Lys Tyr Ser Thr Val Leu Ser Ser Ile
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1 5 10

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1 5

<210> 14069
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<400> 14069
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<400> 14375
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<400> 14387

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1 5 10

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<210> 14461
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<210> 14516
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<210> 14517
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<210> 14578
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1 5

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<210> 14613
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1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<400> 14738
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<400> 14741
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1 5 10

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1 5

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1 5

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1 5

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Tyr Leu Arg Met His Arg Leu Cys Ala Thr
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<210> 15064
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<210> 15079

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1 5 10

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Tyr Lys Leu Val Val Val Gly Ala Ser Gly
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1 5 10

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1 5

<210> 15330
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<210> 15331
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1 5 10

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<400> 15345
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<210> 15347
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Phe Pro Val Pro Ser Ser Ser Ala Ser Ser
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<400> 15737
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Trp Thr Met Ala Trp Ala Gln His Gly Ser
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<210> 15761
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<210> 15762
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<210> 15763
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 15801
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<210> 15809
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<210> 15810
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<210> 15811

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<210> 15812
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<210> 15813
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<210> 15814
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<210> 15815
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1 5

<210> 15816
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<210> 15817
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<400> 15817
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1 5

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<400> 15820
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1 5

<210> 15822
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<400> 15822
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1 5

<210> 15823
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<400> 15823
Leu Leu His Ser Leu Gly Thr Thr Gly
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<210> 15824
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1 5

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<210> 15838
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1 5

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<400> 16510
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<400> 16625
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<400> 16627
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Lys Asn Ser Leu Ile Thr Gln Met Met Lys
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<400> 16632
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<400> 16633
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<210> 16638
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<400> 16638
Lys Arg Phe Ser Thr Gln Asp Ala Ala
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<400> 16639
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<210> 16641
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<400> 16644

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<400> 16648
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<400> 16649
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<400> 16650
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<400> 16665
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<400> 16666
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<400> 16668
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<400> 16670
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<400> 16671
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1 5 10

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1 5 10

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<400> 16678
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<400> 16679
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<400> 16683
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<400> 16687
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<400> 16693
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Thr Trp Arg Thr Gly Gly Gly Ser Ser Val
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Asp Gly Lys Ser Trp Asn Ser Arg Arg Arg
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<400> 16699
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<400> 16700
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<400> 16701
Arg Pro Lys Arg Arg Arg Gly Gly Gly Trp
1 5 10

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<400> 16702
Glu Arg Arg Glu Arg Arg Ser Ala Ser Ala
1 5 10

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1 5 10

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<400> 16704
Arg Arg Arg Leu Arg Asp Gly Lys Ser Trp
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<210> 16705
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<400> 16705

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1 5

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<400> 16706
Lys Met Arg Gly Gly Ala Gln Lys Ala
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<400> 16707
Arg Glu Arg Glu Gly Ala Arg Ala Pro
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<400> 16709
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1 5

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<400> 16710
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1 5 10

<210> 16711
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<400> 16711
Lys Met Arg Gly Gly Ala Gln Lys Ala Gly
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<210> 16712
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<400> 16712
Arg Glu Arg Glu Gly Ala Arg Ala Pro Gly
1 5 10

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<400> 16713
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1 5 10

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<400> 16714
Arg Lys Met Arg Gly Gly Ala Gln Lys Ala
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<400> 16716
Val Met Asp Asn Gln Leu Lys Ser Met
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Met Asp Asn Gln Leu Lys Ser Met Trp
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<210> 16719
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<210> 16721
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<400> 16721
Met Asp Asn Gln Leu Lys Ser Met Trp Phe
1 5 10

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<400> 16722
Arg Ala Ala Ile Ile Phe Gly Tyr Arg
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<210> 16723
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<400> 16723
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Ala Ala Ile Ile Phe Gly Tyr Arg Ile
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<210> 16748
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<210> 16751
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<400> 16776
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1 5 10

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1 5 10

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1 5 10

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<400> 16812
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<400> 16813
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<400> 16815
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1 5

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<400> 16817
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1 5 10

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1 5 10

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<400> 16819
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<400> 16820
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Gln Leu Ala Ile Met Asp Cys Ser Asp Phe
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<210> 17512
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 17601
Ile Phe Ala Gly Leu Leu His Ile Phe Phe
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<210> 17602
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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

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1 5

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1 5

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<400> 18006
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<210> 18007

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Leu Phe Asp Lys Phe Tyr Lys Tyr Val Tyr
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<210> 18059
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Phe Leu Leu Asn Phe Ile Leu Ile Leu
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1 5 10

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<210> 18512
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1 5

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1 5

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<210> 18710
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<210> 18714
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<210> 18739

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<210> 18812
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

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1 5 10

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<210> 19008
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Asn Leu Phe Ser Leu Asn Lys Thr Leu
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Ser Ile Asn Leu Phe Ser Leu Asn Lys
1 5

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1 5

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Ala Lys Ser Ile His Leu Ser Ile Asn Leu
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1 5 10

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1 5 10

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Ala Leu Ala Lys Pro Leu Asn Asp Lys
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<210> 19082
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Arg Cys Ala Leu Trp Asn Gly Ser Met
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<400> 19086
Gly Met Tyr Leu Met His Ala Pro Leu
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Tyr Leu Met His Ala Pro Leu Asp Leu
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<210> 19096
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<210> 19097
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<210> 19099
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<210> 19101
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<210> 19103
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<210> 19112
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1 5

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1 5 10

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1 5 10

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1 5 10

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Phe Thr Asn Glu Ala Pro Gln Leu Leu
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Gln Leu Leu Ser Gln Thr Pro Arg Leu
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Ser Gln Thr Pro Arg Leu Pro Pro Cys
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Arg Asp Phe Thr Asn Glu Ala Pro Gln Leu
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Cys Leu His Thr Glu Glu Pro Ser His Trp
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1 5

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1 5

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1 5 10

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Ser Met Tyr Ile Gly Tyr Thr Ile Trp
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Tyr Gly Ser Asn Pro Ile Ser Met Tyr
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<210> 19303
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<210> 19304
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<400> 19377
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<210> 19447
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<400> 19450

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<400> 19476
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<210> 19478
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<400> 19478
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<210> 19479
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<210> 19482
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<210> 19483
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<400> 19483
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<210> 19484
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<210> 19485
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<210> 19486
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<210> 19487
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<210> 19489
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Trp Ala Pro Ala Pro Pro Thr Arg Cys Val
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<210> 19490
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<210> 19491
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<210> 19492
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<210> 19493
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<210> 19494
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<210> 19495
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 19496
<211> 9
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<400> 19496
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<210> 19497
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<210> 19498
<211> 10
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<210> 19499
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<210> 19500
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<210> 19501
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<210> 19502
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<400> 19502
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<210> 19503
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<210> 19504
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<210> 19506
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<210> 19507
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<400> 19510
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<210> 19511
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<400> 19511

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1 5 10

<210> 19512
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<210> 19513
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<210> 19514
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1 5 10

<210> 19515
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<210> 19516
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<400> 19516
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1 5

<210> 19517
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Gln Lys Arg Pro Ile Pro Ile Lys Tyr
1 5

<210> 19518
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Gly Glu Thr Pro Gln Leu Pro Arg Gly Leu
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Ala Leu Gly Gly Gly Ala Trp Glu Leu
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Ser Leu Val Glu Asp Val Leu Cys Ala
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Gly Leu Ala Arg Trp Gly Pro Leu Cys
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Leu Val Glu Asp Val Leu Cys Ala Lys
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<210> 19532

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<400> 19532
Cys Ala Lys Trp Phe Ile Cys Pro Ala
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Val Glu Ala Leu Gly Gly Gly Ala Trp
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Trp Glu Leu Gly Gly Leu Ala Arg Trp
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Cys Gln Val Leu Leu Leu Ser Ser Ser
1 5

<210> 19538
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Ser Phe Asn Pro Gln Asn Asp Ser Met
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Ser Ser Ser Ser Ser Ser Ser Ser Leu Val
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1 5 10

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Val Thr Val Glu Ala Leu Gly Gly Gly Ala
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Glu Ala Leu Gly Gly Gly Ala Trp Glu Leu
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Cys Gln Val Leu Leu Leu Ser Ser Ser Thr
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Ala Lys Trp Phe Ile Cys Pro Ala Ser Phe
1 5 10

<210> 19547
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Ala Ser Phe Asn Pro Gln Asn Asp Ser Met
1 5 10

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Trp Glu Leu Gly Gly Leu Ala Arg Trp Gly
1 5 10

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1 5 10

<210> 19556
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 19557
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1 5 10

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<210> 19559
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<400> 19560
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1 5 10

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1 5

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1 5

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1 5 10

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1 5 10

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Ile Ser Thr Asn Pro Phe Asn Phe Pro Phe
1 5 10

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<400> 19574
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<400> 19575
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<210> 19576
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<400> 19576
Ala Gln Leu Ile Met Arg Thr Gln Ala

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<210> 19577
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<400> 19577
Asp Glu Lys Leu Ala Gln Leu Ile Met
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<210> 19578
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Leu Ile Met Arg Thr Gln Ala Ile Cys Arg
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<210> 19579
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<400> 19579
Ile Met Arg Thr Gln Ala Ile Cys Arg Gly
1 5 10

<210> 19580
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<210> 19581
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Met Arg Thr Gln Ala Ile Cys Arg Gly Phe
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<400> 19583
Leu Leu Lys Ser Ala Glu Met Glu Lys
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<210> 19584
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<400> 19584
Lys Pro Leu Leu Lys Ser Ala Glu Met
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<210> 19585
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<400> 19585
Lys Ser Ala Glu Met Glu Lys Glu Met
1 5

<210> 19586
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<400> 19586
Ala Glu Met Glu Lys Glu Met Ala Thr
1 5

<210> 19587
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<400> 19587
Glu Met Glu Lys Glu Met Ala Thr Met
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<210> 19588
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<400> 19588
Ile Lys Pro Leu Leu Lys Ser Ala Glu Met
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<210> 19589
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<400> 19589
Leu Lys Ser Ala Glu Met Glu Lys Glu Met
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<210> 19590
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<210> 19591
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<210> 19592
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<400> 19592
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<210> 19593

<211> 9
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<400> 19593
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<210> 19594
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1 5 10

<210> 19595
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<212> PRT
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<210> 19596
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<400> 19596
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1 5 10

<210> 19597
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<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 19597
Ala Glu Leu Glu Glu Leu Cys Ala Val
1 5

<210> 19598
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<400> 19598
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<210> 19599
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 19599
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1 5 10

<210> 19600
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<400> 19600
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1 5 10

<210> 19601
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<400> 19601
Lys Leu Val Gln Ile Ile Thr Arg Thr
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<210> 19602
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<400> 19602
Val Gln Ile Ile Thr Arg Thr Gln Ala
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<210> 19603
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<400> 19603
Asp Glu Lys Leu Val Gln Ile Ile Thr
1 5

<210> 19604
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1 5 10

<210> 19605
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<400> 19605
Glu Met Arg Asp Glu Lys Leu Val Gln Ile
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<400> 19606
Leu Gln Glu Thr Asn Gln Gln Thr Leu
1 5

<210> 19607
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<400> 19607
Ala Leu Gln Glu Thr Asn Gln Gln Thr Leu
1 5 10

<210> 19608
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<400> 19608
Lys Leu Gln Met Asp Leu Glu Arg Ala
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<210> 19609
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<400> 19609
Leu Glu Gln Glu Lys Lys Leu Gln Met
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<210> 19610
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<400> 19610
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1 5

<210> 19611
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<400> 19611
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 19612
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1 5 10

<210> 19613
<211> 9
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 19613
Lys Ile Lys Glu Leu Gln Ala Cys Ile
1 5

<210> 19614
<211> 9
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Lys Lys Ile Lys Glu Leu Gln Ala Cys
1 5

<210> 19615
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 19615
Lys Lys Ile Lys Glu Leu Gln Ala Cys Ile
1 5 10

<210> 19616
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<400> 19616
Lys Glu Leu Gln Ala Cys Ile Glu Glu Leu
1 5 10

<210> 19617
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 19617
Gly Val Trp Ser Thr Leu Leu Ser Leu
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<210> 19618
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<400> 19618
Arg Leu Met Gly Thr Met Trp Arg Ala
1 5

<210> 19619
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Thr Met Trp Arg Ala Ser Pro Gly Met
1 5

<210> 19620
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Val Trp Ser Thr Leu Leu Ser Leu Val
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<400> 19621
Val Gln Ala Pro Arg Thr Trp Pro Trp
1 5

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<400> 19622
Trp Trp Arg Leu Met Gly Thr Met Trp
1 5

<210> 19623
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Arg Ala Arg Pro Val Gly Val Trp Ser
1 5

<210> 19624
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<400> 19624
Gly Thr Met Trp Arg Ala Ser Pro Gly
1 5

<210> 19625
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<400> 19625
Met Trp Arg Ala Ser Pro Gly Met Arg
1 5

<210> 19626
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<400> 19626
Gln Pro Cys Trp Ile Gly Ala Pro Arg
1 5

<210> 19627
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<400> 19627
Cys Trp Ile Gly Ala Pro Arg Ala Arg
1 5

<210> 19628
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Leu Leu Ser Leu Val Gln Ala Pro Arg
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<400> 19629
Glu Thr Leu Ala Ser Pro Cys Gly Ala
1 5

<210> 19630
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<400> 19630
Cys Pro His Leu Pro Ser Gly Ser Trp
1 5

<210> 19631
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<400> 19631
Ala Pro Arg Ala Arg Pro Val Gly Val
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<210> 19632
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<400> 19632
Arg Pro Val Gly Val Trp Ser Thr Leu
1 5

<210> 19633
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<400> 19633

Ser Leu Val Gln Ala Pro Arg Thr Trp
1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Gln Glu Ile Asp Trp Trp Arg Leu Met
1 5

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<400> 19635
Trp Arg Ala Ser Pro Gly Met Arg Leu
1 5

<210> 19636
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<400> 19636
Arg Ala Ser Pro Gly Met Arg Leu Trp
1 5

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<400> 19637
Leu Pro Pro Trp Cys Pro Cys Pro His

1 5

<210> 19638
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<400> 19638
Ser Pro Cys Gly Ala Gln Pro Cys Trp
1 5

<210> 19639
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Trp Pro Trp Gly Trp Cys Gln Glu Ile
1 5

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<400> 19640
Gly Val Trp Ser Thr Leu Leu Ser Leu Val
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<210> 19641
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Trp Ile Gly Ala Pro Arg Ala Arg Pro Val
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<210> 19642
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<400> 19642
Thr Met Trp Arg Ala Ser Pro Gly Met Arg
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<210> 19643
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<400> 19643
Thr Leu Leu Ser Leu Val Gln Ala Pro Arg
1 5 10

<210> 19644
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Arg Ala Ser Pro Gly Met Arg Leu Trp Arg
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<400> 19645
Thr Trp Pro Trp Gly Trp Cys Gln Glu Ile
1 5 10

<210> 19646
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Asp Trp Trp Arg Leu Met Gly Thr Met Trp
1 5 10

<210> 19647
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<400> 19647
Met Trp Arg Ala Ser Pro Gly Met Arg Leu
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<210> 19648
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<400> 19648
Arg Ala Arg Pro Val Gly Val Trp Ser Thr
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<210> 19649
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Gly Thr Met Trp Arg Ala Ser Pro Gly Met
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<210> 19650
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<400> 19650
Trp Trp Arg Leu Met Gly Thr Met Trp Arg
1 5 10

<210> 19651
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<400> 19651
Phe Pro Val Asp Leu Arg Leu Pro Pro Trp
1 5 10

<210> 19652
<211> 10
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<220>
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<400> 19652
Ala Pro Arg Ala Arg Pro Val Gly Val Trp
1 5 10

<210> 19653
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<400> 19653
Arg Pro Val Gly Val Trp Ser Thr Leu Leu
1 5 10

<210> 19654

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Gly Ser Trp Ser Cys Asn Asp Gly Pro Leu
1 5 10

<210> 19655
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1 5 10

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Leu Ser Leu Val Gln Ala Pro Arg Thr Trp
1 5 10

<210> 19657
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1 5 10

<210> 19658
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1 5 10

<210> 19659
<211> 10
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<400> 19659
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1 5 10

<210> 19660
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<400> 19660
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<210> 19661
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<400> 19661
Leu Glu Thr Leu Ala Ser Pro Cys Gly Ala
1 5 10

<210> 19662
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<400> 19662
Leu Pro Pro Trp Cys Pro Cys Pro His Leu
1 5 10

<210> 19663
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<400> 19663
Gly Ala Gly Lys Met Glu Ala Ser Lys
1 5

<210> 19664
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<400> 19664
Ala Gly Lys Met Glu Ala Ser Lys Tyr
1 5

<210> 19665
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<400> 19665
Gly Lys Met Glu Ala Ser Lys Tyr Ile
1 5

<210> 19666
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<400> 19666
Lys Met Glu Ala Ser Lys Tyr Ile Met
1 5

<210> 19667
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<400> 19667
Ser Gly Ala Gly Lys Met Glu Ala Ser Lys
1 5 10

<210> 19668
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<400> 19668
Gly Ala Gly Lys Met Glu Ala Ser Lys Tyr
1 5 10

<210> 19669
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<400> 19669
Met Glu Ala Ser Lys Tyr Ile Met Gln Tyr
1 5 10

<210> 19670
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<400> 19670
Gly Lys Met Glu Ala Ser Lys Tyr Ile Met
1 5 10

<210> 19671
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Gly Glu Ser Gly Ala Gly Lys Met Glu Ala
1 5 10

<210> 19672
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Lys Ser Ser Ile Asn Asp Ala Ala Lys
1 5

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<210> 19732
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Tyr Ser Arg Arg Asn Gly Lys Gly Lys
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Tyr Ser Arg Arg Asn Gly Lys Gly Lys Lys
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Thr Leu Leu Glu Asn Leu Gln Asn Arg Phe
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Gln Thr His Leu Asn Thr Leu Glu Arg
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<210> 19757
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<210> 19758
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<400> 19778
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<210> 19798
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<210> 19799
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 19803
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<400> 19809
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<210> 19810
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<210> 19811
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<210> 19813
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<210> 19814
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<400> 19833
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Val Phe Thr Phe Gly Arg Thr Phe Arg
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1 5 10

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<400> 19842
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<210> 19843
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Ala Ala Ala Thr Pro Leu Pro Leu Val Lys
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Lys Lys Gly Pro Val Ser Pro Arg Asn Leu
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1 5 10

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Thr Leu Phe Asn Cys Leu Gly Leu Gly Ala
1 5 10

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<400> 19862
Ile Ile Lys Asp Thr Leu Phe Asn Cys Leu
1 5 10

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1 5

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1 5

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1 5

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<400> 19910
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 20458
Gln Ala Ser Pro Val Thr Phe Lys Lys
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<400> 20459
Leu Lys Gln Ala Ser Pro Val Thr Phe
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<210> 20460
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Lys Gln Ala Ser Pro Val Thr Phe Lys Lys
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<210> 20461
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Gly Asp Leu Ile Thr Leu Ala Asn Val Val
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<210> 20465
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<210> 20466
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<210> 20467
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Lys Arg Arg Arg Asn Leu Cys Gln Tyr
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<210> 20469
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1 5 10

<210> 20470
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<400> 20470
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<210> 20471
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 20473
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<400> 20473
Tyr Ser Tyr Asp Lys Asp Leu Glu Glu Leu
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<210> 20474
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Tyr Gln Asn Ala Lys Lys Ala His Lys
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<210> 20475
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<400> 20475
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<210> 20477
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1 5

<210> 20478
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1 5 10

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<210> 20484
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1 5 10

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<400> 20487

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1 5

<210> 20488
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<400> 20488
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<400> 20493
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1 5

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1 5 10

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1 5 10

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1 5 10

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1 5

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1 5

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<210> 20502
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1 5

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<400> 20510
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Lys Leu Val Val Val Gly Ala Asp Gly Val
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1 5 10

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<210> 20514
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<210> 20515
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Lys Leu Val Val Val Gly Ala Gly Arg
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Gly Arg Val Gly Lys Ser Ala Leu Thr Ile
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Leu Leu Leu Thr Pro Pro Arg Leu Arg
1 5

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Glu Glu Arg Pro Leu Leu Leu Leu Thr
1 5

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Leu Leu Thr Pro Pro Arg Leu Arg Glu Lys
1 5 10

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Lys Met Lys Ser Gln Met Gly Gln Val
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Ser Gln Met Gly Gln Val Gly Glu Lys
1 5

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Lys Leu Lys Lys Met Lys Ser Gln Met
1 5

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Met Lys Ser Gln Met Gly Gln Val Gly
1 5

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1 5 10

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Lys Leu Lys Lys Met Lys Ser Gln Met Gly
1 5 10

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peptide"

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Lys Met Lys Ser Gln Met Gly Gln Val Gly
1 5 10

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Lys Lys Met Lys Ser Gln Met Gly Gln Val
1 5 10

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Val Leu Pro Glu Trp Gly Ala Val Val
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1 5

<210> 20540
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Val Val Leu Pro Glu Trp Gly Ala Val Val
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<400> 20541
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Gln Val Val Leu Pro Glu Trp Gly Ala Val
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<400> 20545
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1 5

<210> 20546
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1 5 10

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Leu Pro Gly Ser His Val Ser Asn Asn Phe
1 5 10

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Phe Gln Ser Leu Tyr Gln Leu Trp Tyr

1 5

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Tyr Gln Leu Trp Tyr Gly His Ser Phe
1 5

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<400> 20658
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<400> 20670

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<400> 20684
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1 5

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<400> 20687
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1 5

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<400> 20690
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1 5 10

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<210> 20699
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1 5 10

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<210> 20704
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1 5

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<400> 20709
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<400> 20710
Lys Pro Leu Leu Lys Cys Ile Lys Leu
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Cys Ile Lys Leu Arg Tyr Lys Ser Cys
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<400> 20712
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<210> 20713
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<210> 20714
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Lys Ser His Tyr Glu Lys Ile Val Ile Lys
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Cys Gln Asn Ser Pro Leu Pro Phe Gln Trp
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Lys Gly Asn Met Gly Thr Glu Ser Met
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<400> 20731

Ser Lys Gly Asn Met Gly Thr Glu Ser Met
1 5 10

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Trp Leu Ala Ala Ile Leu Asn Asn Ala
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<210> 20733
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<400> 20733
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<210> 20734
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1 5 10

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1 5 10

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<400> 20746
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<210> 20751
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5

<210> 20850
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Ser Ser Val Ile Ile Gly Val Met Leu Val
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<210> 20912
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Cys Glu Asn Lys Thr Ser Ser Val Ile Ile
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<210> 20913
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1 5 10

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<210> 20947
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1 5 10

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<210> 21046
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Trp Ile Asn Ser Leu Leu Phe Val Ile Ile
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<210> 21047
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Ser Leu Leu Phe Val Ile Ile Ala Thr Leu
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<210> 21057

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<210> 21063
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1 5

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1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5

<210> 21938
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1 5

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<220>
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1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Gln Gln Val Pro Gly Lys Ile His Leu His
1 5 10

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Leu His His Ala Ala Arg Cys His Pro Leu
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1 5 10

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Trp Glu Ser Leu Arg Val Glu Glu Glu His

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1 5 10

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<400> 21973
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<400> 21974
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<400> 21982
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<400> 21984
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<400> 21985
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<400> 21987
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<210> 21988
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<400> 21988
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<400> 21991
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<400> 21993
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1 5 10

<210> 21994
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<400> 21994
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1 5

<210> 21995
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<400> 21995
Ser Ala Gly Arg Gly Arg Arg Ser Leu
1 5

<210> 21996
<211> 10
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<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 21996
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1 5 10

<210> 21997
<211> 10
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<213> Artificial Sequence

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<400> 21997
Cys Pro Ala Ala Thr Pro Gly Asn Ser Ala
1 5 10

<210> 21998
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<213> Artificial Sequence

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<400> 21998
Asn Ser Ala Gly Arg Gly Arg Arg Ser Leu
1 5 10

<210> 21999
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peptide"

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<400> 22002
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<210> 22003
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<400> 22003
Asn Lys Leu Val Gln Leu Asn Lys Leu Phe
1 5 10

<210> 22004
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<400> 22004
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<210> 22005
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<400> 22005
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<210> 22006
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<400> 22006
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<400> 22007
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<400> 22008
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<400> 22009
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<400> 22010
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<210> 22011
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<400> 22011
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1 5 10

<210> 22012
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<400> 22012

Asp Thr Pro Ala Trp Cys Trp Cys Val Ile
1 5 10

<210> 22013
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<400> 22013
Phe Glu Tyr Asp Thr Pro Ala Trp Cys Trp
1 5 10

<210> 22014
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<400> 22014
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<210> 22015
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 22015
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<210> 22212
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<400> 22605
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<210> 22606
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<400> 22610
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<400> 22666
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5

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<400> 22671
Leu Pro Pro His Ala Pro Leu Gly Leu
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1 5 10

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Val Leu His Ser Pro Glu Glu Trp Pro Ala
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Ala Leu Pro Asp Pro Ala Pro Ala Ala Val
1 5 10

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Arg Leu Pro Pro His Ala Pro Leu Gly Leu
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Gly Ala Arg Pro Leu Thr Gly Val Leu His
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<210> 22682
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Ala Val Arg Gln Pro Arg Pro Ala Pro Pro
1 5 10

<210> 22683
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<400> 22683

Ala Gly His Asp His Ala Glu Ala Gly Lys
1 5 10

<210> 22684
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<400> 22685
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<400> 22686
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<400> 22687
Arg Pro Ala Pro Pro Leu His His Arg Leu

1 5 10

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His His Arg Leu Pro Pro His Ala Pro Leu
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<400> 22690
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<400> 22691
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<400> 22694
Arg Val Trp Pro Ser Thr Thr Thr Leu
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1 5

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1 5

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1 5

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1 5

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<400> 22701
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1 5

<210> 22702
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<400> 22702
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1 5

<210> 22703
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<400> 22703
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1 5

<210> 22704

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<400> 22704
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1 5

<210> 22705
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<400> 22705
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1 5

<210> 22706
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1 5 10

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<400> 22866

Arg Ser Gln Lys Arg Glu Met Arg Arg Leu
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

<210> 22902
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1 5

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Met Lys Asp Ala His His Gly Gly Trp
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<210> 23009

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<400> 23037
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1 5 10

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1 5 10

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<210> 23071
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1 5 10

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1 5 10

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Tyr Met Leu Val Met His Asn Met Phe
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1 5

<210> 23098
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Thr Leu Pro Glu Thr Leu Arg Thr Ala
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Arg Thr Val Arg Arg Ser Ser Pro Arg
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<210> 23101
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Glu Thr Leu Arg Thr Ala Pro Arg Lys
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Arg Thr Ala Pro Arg Lys Ser Ser Leu
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<210> 23103
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Arg Lys Ser Ser Leu Met Pro Thr Lys
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1 5

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<400> 23106
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1 5

<210> 23107
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<400> 23107
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<210> 23108
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<400> 23108
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<210> 23110
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<400> 23110

His Pro Asn Met Glu Gly Leu Cys Leu
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<210> 23111
<211> 9
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<210> 23112
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<400> 23112
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<210> 23113
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<400> 23118
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<210> 23126
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<210> 23127
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<400> 23130
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<210> 23131

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1 5

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1 5

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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Phe Tyr Val Val Glu Glu Ile Leu Glu Ile
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Glu Ile Ile Phe Cys Phe Phe Ile Phe Phe
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Leu Val Ile Thr Gly Asn Gly Leu Tyr
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<210> 23158
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Gly Leu Tyr Pro Gly Asn Thr Thr Val
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<210> 23159
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<400> 23159
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Thr Leu Val Ile Thr Gly Asn Gly Leu Tyr
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Thr Thr Leu Val Ile Thr Gly Asn Gly Leu
1 5 10

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Thr Thr Asp Lys Lys Val Trp Leu Met
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Arg Lys Val Thr Thr Asp Lys Lys Val Trp
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Trp Leu Gln Glu Thr Thr Thr Gly Ser
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<400> 23167
Ala Trp Pro Arg Pro Cys Ala Ser Trp
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<220>
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Gly Ala Pro Trp Gly Ala Trp Pro Arg
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Trp Pro Arg Pro Cys Ala Ser Trp Leu
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<210> 23170
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<400> 23170
Ser Leu Gly Ala Pro Trp Gly Ala Trp
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<400> 23171

Phe Val Ser Leu Gly Ala Pro Trp Gly Ala
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Gly Ala Trp Pro Arg Pro Cys Ala Ser Trp
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Ala Leu Ala Arg Gln Ser Pro Val Ala

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<210> 23177
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1 5

<210> 23178
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<400> 23178
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<400> 23179
Ala Thr Leu Pro Ser Ala Phe Gln Lys
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<400> 23180
Ser Ser His Thr Val Leu Ser Asn Lys
1 5

<210> 23181
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<400> 23181
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<210> 23182
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<400> 23182
Ala Val Asn Phe Cys Trp Thr Thr Arg
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<400> 23186
Ser Phe Ala Thr Ala Thr Ala Thr Leu
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<400> 23187
Ala Ala Arg His Met Thr Thr Ala Met
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<400> 23190
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<400> 23191
Thr Thr Arg Thr Pro Thr Pro Ile His
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<400> 23192
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1 5

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Lys Thr Lys Ser Val Arg Pro Ser Phe
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23197
Lys Leu His Ile Thr Arg His Thr Arg
1 5

<210> 23198
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<400> 23198
Ile Thr Arg His Thr Arg Thr Trp Thr
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<210> 23199
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<400> 23199
His Thr Arg Thr Trp Thr Pro Arg Ser
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<210> 23200
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<400> 23200
Arg Thr Trp Thr Pro Arg Ser Ile Val
1 5

<210> 23201
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<400> 23201
Arg Ser Ile Val Arg Val Glu Tyr His
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<210> 23202
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<400> 23202
Arg Val Glu Tyr His Leu Ser Lys Ala
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<400> 23203
Leu Ser Lys Ala Ser Pro Leu Ser Ala
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<210> 23204
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<400> 23204
Trp Met Asn Trp Thr Ser Ala Ala Arg
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<400> 23205
Ala Phe Gln Lys Leu His Ile Thr Arg
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<210> 23206
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<400> 23206
Thr Trp Thr Pro Arg Ser Ile Val Arg
1 5

<210> 23207
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<400> 23207
Trp Thr Ser Ala Ala Arg His Met Thr
1 5

<210> 23208
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<400> 23208
Trp Thr Ala Val Asn Phe Cys Trp Thr
1 5

<210> 23209
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<400> 23209
Trp Thr Thr Arg Thr Pro Thr Pro Ile
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<210> 23210
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<400> 23210
Trp Thr Pro Arg Ser Ile Val Arg Val
1 5

<210> 23211
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<400> 23211
Arg Pro Arg Ser Trp Thr Ala Val Asn
1 5

<210> 23212
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23212
Thr Pro Ile His Thr Arg Ala Leu Ala
1 5

<210> 23213
<211> 9
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<400> 23213
Arg Pro Ser Phe Ala Thr Ala Thr Ala
1 5

<210> 23214
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<400> 23214
Tyr His Leu Ser Lys Ala Ser Pro Leu
1 5

<210> 23215
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<400> 23215
Ala Thr Ala Thr Leu Pro Ser Ala Phe
1 5

<210> 23216
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23216
Ala Gln Ala Pro Pro Trp Met Asn Trp
1 5

<210> 23217
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<400> 23217
Thr Ala Met Thr Arg Pro Arg Ser Trp
1 5

<210> 23218
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<400> 23218
Arg Gln Ser Pro Val Ala Ala Lys Thr
1 5

<210> 23219
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<400> 23219
Phe Gln Lys Leu His Ile Thr Arg His
1 5

<210> 23220
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<400> 23220
His Ile Thr Arg His Thr Arg Thr Trp
1 5

<210> 23221
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<400> 23221
Ser Lys Ala Ser Pro Leu Ser Ala Ser
1 5

<210> 23222
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<400> 23222
Leu Ser Ala Ser Ser His Thr Val Leu
1 5

<210> 23223
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<400> 23223
Val Glu Tyr His Leu Ser Lys Ala Ser
1 5

<210> 23224
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<400> 23224
Ala Met Thr Arg Pro Arg Ser Trp Thr Ala
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<210> 23225
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<400> 23225
Met Thr Arg Pro Arg Ser Trp Thr Ala Val
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<210> 23226
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Ala Leu Ala Arg Gln Ser Pro Val Ala Ala
1 5 10

<210> 23227
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Ala Thr Ala Thr Ala Thr Leu Pro Ser Ala
1 5 10

<210> 23228
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His Leu Ser Lys Ala Ser Pro Leu Ser Ala
1 5 10

<210> 23229
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Arg Thr Trp Thr Pro Arg Ser Ile Val Arg
1 5 10

<210> 23230
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1 5 10

<210> 23231
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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23232

Thr Ala Val Asn Phe Cys Trp Thr Thr Arg
1 5 10

<210> 23233
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Thr Ala Thr Leu Pro Ser Ala Phe Gln Lys
1 5 10

<210> 23234
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1 5 10

<210> 23235
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Arg Ser Trp Thr Ala Val Asn Phe Cys Trp
1 5 10

<210> 23236
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Cys Trp Thr Thr Arg Thr Pro Thr Pro Ile

1 5 10

<210> 23237
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23237
Ala Ala Arg His Met Thr Thr Ala Met Thr
1 5 10

<210> 23238
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23238
Thr Thr Arg Thr Pro Thr Pro Ile His Thr
1 5 10

<210> 23239
<211> 10
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<220>
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Arg Thr Pro Thr Pro Ile His Thr Arg Ala
1 5 10

<210> 23240
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<400> 23240
His Thr Arg Ala Leu Ala Arg Gln Ser Pro
1 5 10

<210> 23241
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Arg Ala Leu Ala Arg Gln Ser Pro Val Ala
1 5 10

<210> 23242
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1 5 10

<210> 23243
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Arg Gln Ser Pro Val Ala Ala Lys Thr Lys
1 5 10

<210> 23244
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23244
Lys Thr Lys Ser Val Arg Pro Ser Phe Ala
1 5 10

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<400> 23245
Lys Ser Val Arg Pro Ser Phe Ala Thr Ala
1 5 10

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<400> 23246
Ser Val Arg Pro Ser Phe Ala Thr Ala Thr
1 5 10

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<400> 23247
Lys Leu His Ile Thr Arg His Thr Arg Thr
1 5 10

<210> 23248
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<400> 23248
Ile Thr Arg His Thr Arg Thr Trp Thr Pro
1 5 10

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<400> 23249
His Thr Arg Thr Trp Thr Pro Arg Ser Ile
1 5 10

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<400> 23250
Arg Ser Ile Val Arg Val Glu Tyr His Leu
1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23251
Ser Ser His Thr Val Leu Ser Asn Lys Ala
1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23252
Pro Trp Met Asn Trp Thr Ser Ala Ala Arg
1 5 10

<210> 23253

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<400> 23253
His Met Thr Thr Ala Met Thr Arg Pro Arg
1 5 10

<210> 23254
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<400> 23254
Thr Pro Ile His Thr Arg Ala Leu Ala Arg
1 5 10

<210> 23255
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<400> 23255
Thr Ser Ala Ala Arg His Met Thr Thr Ala
1 5 10

<210> 23256
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<400> 23256
Trp Thr Ala Val Asn Phe Cys Trp Thr Thr
1 5 10

<210> 23257
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23257
Ala Pro Pro Trp Met Asn Trp Thr Ser Ala
1 5 10

<210> 23258
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<400> 23258
Ser Ala Ala Arg His Met Thr Thr Ala Met
1 5 10

<210> 23259
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Arg Pro Arg Ser Trp Thr Ala Val Asn Phe
1 5 10

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Thr Pro Thr Pro Ile His Thr Arg Ala Leu
1 5 10

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<400> 23261
Ser Pro Val Ala Ala Lys Thr Lys Ser Val
1 5 10

<210> 23262
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<400> 23262
Arg Pro Ser Phe Ala Thr Ala Thr Ala Thr
1 5 10

<210> 23263
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<400> 23263
Leu Pro Ser Ala Phe Gln Lys Leu His Ile
1 5 10

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Ser Pro Leu Ser Ala Ser Ser His Thr Val
1 5 10

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Met Asn Trp Thr Ser Ala Ala Arg His Met
1 5 10

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Thr Ala Thr Ala Thr Leu Pro Ser Ala Phe
1 5 10

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<400> 23267
Gly Leu Trp Gly Ala Gln Ala Pro Pro Trp
1 5 10

<210> 23268
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<400> 23268
Trp Met Asn Trp Thr Ser Ala Ala Arg His
1 5 10

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<400> 23269
Ala Lys Thr Lys Ser Val Arg Pro Ser Phe
1 5 10

<210> 23270
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<400> 23270
Pro Ser Phe Ala Thr Ala Thr Ala Thr Leu
1 5 10

<210> 23271
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<400> 23271
Phe Gln Lys Leu His Ile Thr Arg His Thr
1 5 10

<210> 23272
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<400> 23272
Leu His Ile Thr Arg His Thr Arg Thr Trp
1 5 10

<210> 23273
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<400> 23273
Lys Ala Ser Pro Leu Ser Ala Ser Ser His
1 5 10

<210> 23274
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<400> 23274
Thr Pro Arg Ser Ile Val Arg Val Glu Tyr
1 5 10

<210> 23275
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<400> 23275
Ile Gln Asn Tyr Arg Phe His Thr Ile
1 5

<210> 23276
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23276
Asn Tyr Gly Ile Gln Asn Tyr Arg Phe
1 5

<210> 23277
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23277
Gln Tyr Asn Tyr Gly Ile Gln Asn Tyr
1 5

<210> 23278
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23278
Tyr Asn Tyr Gly Ile Gln Asn Tyr Arg
1 5

<210> 23279
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Leu Gln Tyr Asn Tyr Gly Ile Gln Asn
1 5

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Tyr Asn Tyr Gly Ile Gln Asn Tyr Arg Phe
1 5 10

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peptide"

<400> 23281
Leu Gln Tyr Asn Tyr Gly Ile Gln Asn Tyr
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<400> 23282
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1 5 10

<210> 23283
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<400> 23283
Ile Gln Asn Tyr Arg Phe His Thr Ile Ser
1 5 10

<210> 23284
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<400> 23284
Gln Asn Tyr Arg Phe His Thr Ile Ser His
1 5 10

<210> 23285
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<400> 23285
Arg Met Ser Gly Asp Thr Trp Trp Cys
1 5

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<400> 23286
Thr Leu Glu Glu Arg Thr Ser Ser Val
1 5

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<400> 23287
Val Ile Ala Gly Ser Thr Pro Glu Arg
1 5

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<400> 23288
Arg Thr Ser Ser Val Ser Ile Val His
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<400> 23289
Thr Ser Ser Val Ser Ile Val His Arg
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<400> 23290
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1 5

<210> 23291
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<400> 23291
Lys Ser Thr Ser Ala Asn Ile Val Ile
1 5

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Thr Trp Trp Cys Thr Leu Glu Glu Arg
1 5

<210> 23293
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23293

Ile Val His Arg Asp Leu Gly Glu Arg
1 5

<210> 23294
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Ser Thr Ser Ala Asn Ile Val Ile Ala
1 5

<210> 23295
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<400> 23295
Lys Glu Lys Ser Thr Ser Ala Asn Ile
1 5

<210> 23296
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<212> PRT
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1 5

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1 5

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1 5

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1 5 10

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Pro Trp Arg Thr Ser Ala Met Pro Ser Ala
1 5 10

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Arg Thr Ser Ala Met Pro Ser Ala Met Gly
1 5 10

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Gln Gln Trp Val Asn Leu Arg Arg Gly Tyr
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Pro Thr Leu Cys Pro Ala His Pro Ala Arg
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1 5 10

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1 5 10

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<400> 23596
Gly Arg Ser Ser Arg Thr Thr Ser Gln Leu
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<400> 23610
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<210> 23611
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<210> 23612
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<210> 23613
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<400> 23615
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<210> 23619

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1 5 10

<210> 23639
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<400> 23659

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<400> 23670
Arg Ala Thr Ala Ala Ala Gly Ala Trp
1 5

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<400> 23671
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1 5

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<400> 23672
Arg Leu Gly Gly Pro Cys Pro Pro Ala Val
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Val Thr Arg Ala Ser Ala Pro Arg Ala Thr
1 5 10

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1 5 10

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<400> 23675
Ala Ser Ala Pro Arg Ala Thr Ala Ala Ala
1 5 10

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Arg Ala Thr Ala Ala Ala Gly Ala Trp Arg
1 5 10

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<400> 23677
Ala Trp Arg Gly Arg Arg Pro Pro Thr Ala
1 5 10

<210> 23678
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<400> 23678
Arg Gly Arg Arg Pro Pro Thr Ala Arg Ser
1 5 10

<210> 23679
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<400> 23679
Thr Ser Arg Ala Val Gly Arg Pro Pro Cys
1 5 10

<210> 23680

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<400> 23680
Arg Ala Val Gly Arg Pro Pro Cys Trp Arg
1 5 10

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<400> 23681
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1 5 10

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Ala Ala Ala Gly Ala Trp Arg Gly Arg Arg
1 5 10

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<400> 23683
Cys Pro Pro Ala Val Thr Arg Ala Ser Ala
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<210> 23684
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<400> 23684
Ala Pro Arg Ala Thr Ala Ala Ala Gly Ala
1 5 10

<210> 23685
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<400> 23685
Arg Pro Pro Thr Ala Arg Ser Ser Ala Thr
1 5 10

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<400> 23686
Gly Pro Pro Ser Ser Thr Ser Arg Ala Val
1 5 10

<210> 23687
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<400> 23687
Ala Arg Leu Gly Gly Pro Cys Pro Pro Ala
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<210> 23688
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<210> 23689
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<400> 23689
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1 5

<210> 23690
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<400> 23690
Arg Ala Arg Ile Cys Pro Gly Glu Asn
1 5

<210> 23691
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<400> 23691
Gln Asn Tyr Arg Lys Phe Arg Ala Arg
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<210> 23692
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1 5 10

<210> 23693
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<400> 23693
Arg Ala Arg Ile Cys Pro Gly Glu Asn Gln
1 5 10

<210> 23694
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<400> 23694
Glu Gln Asn Tyr Arg Lys Phe Arg Ala Arg
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<210> 23695
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<212> PRT
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<400> 23695
Arg Lys Phe Arg Ala Arg Ile Cys Pro Gly
1 5 10

<210> 23696
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<400> 23696
Ala Gly Phe Asp Leu Asp Trp Thr Leu
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<210> 23697
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<400> 23697
Trp Thr Leu Ile Thr Thr Arg Ser Gly Lys
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<210> 23698
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<400> 23698
Asp Leu Asp Trp Thr Leu Ile Thr Thr Arg
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<210> 23699
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<400> 23699
Gly Lys Val Ala Gly Phe Asp Leu Asp Trp
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<210> 23700
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<400> 23700
Gly Ile Met Glu Arg Pro Leu His Ile
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<210> 23701
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Ser Pro Trp Ser Gly Ile Met Glu Arg
1 5

<210> 23702
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<400> 23702
Ile Met Glu Arg Pro Leu His Ile Leu
1 5

<210> 23703
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<400> 23703
Gly Ile Met Glu Arg Pro Leu His Ile Leu
1 5 10

<210> 23704
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23704
Asp Ser Pro Trp Ser Gly Ile Met Glu Arg
1 5 10

<210> 23705
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<400> 23705
Met Glu Arg Pro Leu His Ile Leu Pro Trp
1 5 10

<210> 23706
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Asn Gln Ala Pro Phe Pro Pro Ser Lys
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<210> 23707
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<400> 23707
Leu Val Arg Leu Asn Gln Ala Pro Phe
1 5

<210> 23708
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<400> 23708
Leu Asn Gln Ala Pro Phe Pro Pro Ser Lys
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<210> 23709
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<400> 23709
Asn Gln Ala Pro Phe Pro Pro Ser Lys Arg
1 5 10

<210> 23710
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<400> 23710
Ala Pro Phe Pro Pro Ser Lys Arg Lys Met
1 5 10

<210> 23711
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23711
Asn Leu Val Arg Leu Asn Gln Ala Pro Phe
1 5 10

<210> 23712
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1 5 10

<210> 23713
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<400> 23713
Tyr Leu Arg Pro Pro Ser Thr Ala Thr
1 5

<210> 23714
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<400> 23714
Cys Leu Thr Ser Gly Ala Ala Ala Ala
1 5

<210> 23715
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<400> 23715
Thr Leu Pro Lys Leu Cys Leu Ala Leu
1 5

<210> 23716
<211> 9
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23716
Gly Met His Thr Gln Thr Ser Arg Ala
1 5

<210> 23717
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Trp Leu Ser Gln Asn Cys Leu Arg Ala
1 5

<210> 23718
<211> 9
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<400> 23718
Ser Gln Asn Cys Leu Arg Ala Pro Leu
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<210> 23719
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<400> 23719
Ser Ala Ser Ser Thr Arg Ser Ala Lys
1 5

<210> 23720
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<400> 23720

Ser Thr Arg Ser Ala Lys Trp Ala Thr
1 5

<210> 23721
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Lys Trp Ala Thr Ser Thr Gly Ala Arg
1 5

<210> 23722
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Gly Ala Arg Cys Leu Thr Ser Gly Ala
1 5

<210> 23723
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Ala Ala Cys Trp Arg Arg Cys Ser Ala
1 5

<210> 23724
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Arg Gly Arg Ala Arg Ser Pro Arg Val

1 5

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Arg Ala Arg Ser Pro Arg Val Arg Ser
1 5

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1 5

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1 5

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1 5

<210> 23730
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1 5

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Thr Ser Arg Ala Pro Gln Pro Ser Arg
1 5

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1 5

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1 5

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1 5

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Trp Met Thr Asn Leu Thr Thr Arg Arg
1 5

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<400> 23736
Asn Leu Thr Thr Arg Arg Ser Thr Arg
1 5

<210> 23737
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<400> 23737
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1 5

<210> 23738
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<400> 23738
Val Trp Leu Ser Gln Asn Cys Leu Arg
1 5

<210> 23739
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Arg Ala Pro Leu Thr Arg Thr Gly Arg
1 5

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<400> 23740
Thr Ala Thr Ala Pro Trp Thr Ser Ala
1 5

<210> 23741

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Ala Thr Ala Pro Trp Thr Ser Ala Ser
1 5

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<400> 23742
Ala Pro Trp Thr Ser Ala Ser Ser Thr
1 5

<210> 23743
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<400> 23743
Ser Pro Arg Val Arg Ser Ser Pro Val
1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23744
Val Pro Thr Pro Pro Ser Arg Thr Leu
1 5

<210> 23745
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<400> 23745
Ser Pro Pro Trp Trp Met Thr Asn Leu
1 5

<210> 23746
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<400> 23746
Ala Pro Gln Pro Ser Arg Ala Gln Thr
1 5

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<400> 23747
Arg Ser Ala Lys Trp Ala Thr Ser Thr
1 5

<210> 23748
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<400> 23748
Ala Lys Trp Ala Thr Ser Thr Gly Ala
1 5

<210> 23749
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<400> 23749
Ala Leu Ser Pro Pro Ser Pro Pro Trp
1 5

<210> 23750
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Ala Gln Thr Trp Arg Thr Ser Pro His
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<210> 23751
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23751
Pro Pro Ser Thr Ala Thr Ala Pro Trp
1 5

<210> 23752
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<400> 23752
Cys Glu Tyr Leu Arg Pro Pro Ser Thr
1 5

<210> 23753
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<400> 23753
Tyr Leu Arg Pro Pro Ser Thr Ala Thr Ala
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Thr Ser Ala Ser Ser Thr Arg Ser Ala Lys
1 5 10

<210> 23755
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<400> 23755
Arg Thr Leu Pro Lys Leu Cys Leu Ala Leu
1 5 10

<210> 23756
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<400> 23756
Ser Thr Ala Thr Ala Pro Trp Thr Ser Ala
1 5 10

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<400> 23757
Ser Thr Arg Ser Ala Lys Trp Ala Thr Ser
1 5 10

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<400> 23758
Ser Ala Lys Trp Ala Thr Ser Thr Gly Ala
1 5 10

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<400> 23759
Gly Ala Arg Cys Leu Thr Ser Gly Ala Ala
1 5 10

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<400> 23760
Ala Ala Ala Cys Trp Arg Arg Cys Ser Ala
1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23761
Cys Trp Arg Arg Cys Ser Ala Thr Ser Arg
1 5 10

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<400> 23762
Thr Ser Arg Gly Arg Ala Arg Ser Pro Arg
1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23763
Arg Gly Arg Ala Arg Ser Pro Arg Val Arg
1 5 10

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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23764
Arg Ala Arg Ser Pro Arg Val Arg Ser Ser
1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23765
Arg Ser Pro Arg Val Arg Ser Ser Pro Val
1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23766
Arg Val Arg Ser Ser Pro Val Pro Thr Pro
1 5 10

<210> 23767
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<400> 23767
Arg Ser Ser Pro Val Pro Thr Pro Pro Ser
1 5 10

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<400> 23768
Thr Thr Arg Arg Ser Thr Arg Arg Ser Cys
1 5 10

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peptide"

<400> 23769
Ser Thr Arg Arg Ser Cys Trp Thr Ser Pro
1 5 10

<210> 23770
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<400> 23770
Thr Ser Arg Ala Pro Gln Pro Ser Arg Ala
1 5 10

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<400> 23771
Arg Ala Gln Thr Trp Arg Thr Ser Pro His
1 5 10

<210> 23772
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23772
Thr Trp Arg Thr Ser Pro His Cys Gly Ile
1 5 10

<210> 23773
<211> 10
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23773
Cys Ser Ala Thr Ser Arg Gly Arg Ala Arg
1 5 10

<210> 23774
<211> 10
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<400> 23774
Trp Trp Met Thr Asn Leu Thr Thr Arg Arg
1 5 10

<210> 23775
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<400> 23775
Thr Asn Leu Thr Thr Arg Arg Ser Thr Arg
1 5 10

<210> 23776
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<400> 23776
Asn Leu Thr Thr Arg Arg Ser Thr Arg Arg
1 5 10

<210> 23777
<211> 10
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<400> 23777
Gln Thr Ser Arg Ala Pro Gln Pro Ser Arg
1 5 10

<210> 23778
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<400> 23778
Pro Val Trp Leu Ser Gln Asn Cys Leu Arg
1 5 10

<210> 23779
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<400> 23779
Trp Thr Ser Ala Ser Ser Thr Arg Ser Ala
1 5 10

<210> 23780
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<400> 23780
Arg Pro Pro Ser Thr Ala Thr Ala Pro Trp
1 5 10

<210> 23781
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<400> 23781

Thr Pro Pro Ser Arg Thr Leu Pro Lys Leu
1 5 10

<210> 23782
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<400> 23782
Ala Pro Gln Pro Ser Arg Ala Gln Thr Trp
1 5 10

<210> 23783
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<400> 23783
Ser Pro His Cys Gly Ile Asp Thr Pro Val
1 5 10

<210> 23784
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<400> 23784
Thr Pro Val Trp Leu Ser Gln Asn Cys Leu
1 5 10

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<400> 23785
Ala Pro Leu Thr Arg Thr Gly Arg Gly Leu

1 5 10

<210> 23786
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<400> 23786
Cys Glu Tyr Leu Arg Pro Pro Ser Thr Ala
1 5 10

<210> 23787
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<400> 23787
Ser Ala Ser Ser Thr Arg Ser Ala Lys Trp
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<400> 23788
Trp Ala Thr Ser Thr Gly Ala Arg Cys Leu
1 5 10

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Leu Ala Leu Ser Pro Pro Ser Pro Pro Trp
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<210> 23790
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Ala Leu Ser Pro Pro Ser Pro Pro Trp Trp
1 5 10

<210> 23791
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Arg Arg Ser Cys Trp Thr Ser Pro Gly Met
1 5 10

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Ala Gln Thr Trp Arg Thr Ser Pro His Cys
1 5 10

<210> 23793
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Leu Thr Ser Gly Ala Ala Ala Ala Cys Trp
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Leu Glu Lys Ile Pro Arg Gly Pro Ser Ala
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Phe Leu Pro Arg Ser Leu Arg Val Val
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Thr Ser Thr Thr Val Ser Ser Ser Trp
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<400> 23810
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<210> 23811
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<210> 23812
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<210> 23813
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<210> 23818
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<400> 23818
Leu Arg Trp Leu Lys Arg Asp Ser Tyr
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Trp Leu Lys Arg Asp Ser Tyr Leu Pro Val
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1 5 10

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1 5 10

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1 5

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Thr Leu Ala Thr Tyr Phe Val Ser Asp Ala
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Tyr Phe Val Ser Asp Ala Val Ala Thr Tyr
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5

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1 5 10

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<210> 23848
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Glu Glu Arg Arg Asn Met Gln Thr Ile Trp
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1 5 10

<210> 23862
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1 5

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1 5

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1 5 10

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1 5 10

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<400> 23886
Gly Pro Leu Lys Pro Ser Leu Gly His Trp
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1 5

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1 5

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1 5

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<400> 23890
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1 5 10

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1 5

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1 5

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<400> 24060
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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Gly Lys Lys Val Pro Pro Asn His Pro Leu
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1 5

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1 5

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Thr Pro Met Val Arg Trp Ala Ala Ala
1 5

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Met Val Arg Trp Ala Ala Ala Ser Lys Leu
1 5 10

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1 5 10

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Gly Gln Leu Thr Arg Ala Leu Ala Ile Leu
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<400> 24481
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<210> 24482
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Ser Thr Ala Ala Pro Val Ile Thr Ala
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Thr Pro Ala Pro Ala Ala Ser Ser Thr
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Ala Pro Ala Ala Ser Ser Thr Ala Ala
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Ala Ser Ser Thr Ala Ala Pro Val Ile
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<400> 24486
Thr Ala Ala Pro Val Ile Thr Ala Pro Thr
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<210> 24487
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<400> 24487
Thr Pro Ala Pro Ala Ala Ser Ser Thr Ala
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<210> 24488
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Ala Pro Ala Ala Ser Ser Thr Ala Ala Pro
1 5 10

<210> 24489
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Ala Ala Ser Ser Thr Ala Ala Pro Val Ile
1 5 10

<210> 24490
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<400> 24490
Leu Ser Trp Gly Thr Val Ser Pro Tyr
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<210> 24491
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<400> 24491
Tyr Leu Ser Trp Gly Thr Val Ser Pro
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<210> 24492
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Thr Val Ser Pro Tyr Ser Ala Met Ala
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<210> 24493
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<210> 24494
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<210> 24495
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<210> 24496
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Tyr Leu Ser Trp Gly Thr Val Ser Pro Tyr
1 5 10

<210> 24497
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Val Ser Pro Tyr Ser Ala Met Ala Thr Tyr
1 5 10

<210> 24498
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Trp Gly Thr Val Ser Pro Tyr Ser Ala Met
1 5 10

<210> 24499
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Thr Leu Asn Asn Asn Ile Met Leu Ile
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<210> 24500
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<210> 24501
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peptide"

<400> 24501
Arg Lys Thr Leu Asn Asn Asn Ile Met
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<210> 24502
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<400> 24502
Lys Thr Leu Asn Asn Asn Ile Met Leu Ile
1 5 10

<210> 24503
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<400> 24503
Thr Leu Asn Asn Asn Ile Met Leu Ile Lys
1 5 10

<210> 24504
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Asn Ile Met Leu Ile Lys Leu Ser Ser Arg
1 5 10

<210> 24505
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<400> 24505
Arg Lys Thr Leu Asn Asn Asn Ile Met Leu
1 5 10

<210> 24506
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<400> 24506
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<210> 24507
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<400> 24507
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<210> 24508
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<400> 24508
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<210> 24509
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1 5 10

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<400> 24510
Ala Gln Ile Ile Gly Gly His Gln Val
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<210> 24511
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Gln Val Thr Pro His Ser Arg Pro Tyr
1 5

<210> 24512
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His Gln Val Thr Pro His Ser Arg Pro Tyr
1 5 10

<210> 24513
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<400> 24513

Ala Gln Ile Ile Gly Gly His Gln Val Thr
1 5 10

<210> 24514
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<400> 24514
Gly Gly Met Arg Met Met Met Arg Arg
1 5

<210> 24515
<211> 9
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Gly Met Arg Met Met Met Arg Arg Thr
1 5

<210> 24516
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Arg Met Met Met Arg Arg Thr Arg Thr
1 5

<210> 24517
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<400> 24517
Met Met Met Arg Arg Thr Arg Thr Ser

1 5

<210> 24518
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<400> 24518
Met Met Arg Arg Thr Arg Thr Ser Cys
1 5

<210> 24519
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Gly Pro Gly Gly Met Arg Met Met Met
1 5

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1 5

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1 5 10

<210> 24522
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1 5 10

<210> 24523
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1 5 10

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1 5 10

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Pro Gln Gly Pro Gly Gly Met Arg Met Met
1 5 10

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Met Gly Ser Pro Glu Ile Leu Glu Lys
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Ser Glu Met Gly Ser Pro Glu Ile Leu
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Glu Met Gly Ser Pro Glu Ile Leu Glu Lys
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Ala His Ser Glu Met Gly Ser Pro Glu Ile
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1 5

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Gly Leu Tyr Ala Cys Ser Val Cys Asn Ser
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Cys Ser Val Cys Asn Ser Ala Thr Gly Lys
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<210> 24534

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Gln Tyr Gly Gly Ile Cys Ser Tyr Pro Val
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1 5 10

<210> 24539
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Ile Gln Thr Gln Ile Ile Ser Lys Lys
1 5

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Lys Asp Tyr Ile Gln Thr Gln Ile Ile
1 5

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1 5 10

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1 5 10

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1 5 10

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1 5

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1 5 10

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1 5 10

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1 5 10

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<210> 24561
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peptide"

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Asp Asp Phe Ser Lys Cys Met Ile Thr Phe
1 5 10

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Arg Ser Ile Ile Glu His Val Ala Ser Lys
1 5 10

<210> 24569
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1 5 10

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1 5 10

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<400> 24573
Ser Glu Ile Ser Val Gln His Val Thr Val
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<400> 24574

Val Gln His Val Thr Val Thr Gln Asp Thr
1 5 10

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Phe Leu Leu Lys Gly Ile Leu Ala Leu
1 5

<210> 24576
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Leu Leu Lys Gly Ile Leu Ala Leu Ala
1 5

<210> 24577
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<210> 24578
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Ala Leu Ala Ile Gly Pro Ala Gly Ala

1 5

<210> 24579
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Ala Ile Gly Pro Ala Gly Ala Leu Ala
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Ala Leu Ala Gly Pro Val Leu Thr Thr
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Phe Leu Leu Lys Gly Ile Leu Ala Leu Ala
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Leu Leu Lys Gly Ile Leu Ala Leu Ala Ile
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<210> 24600
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<210> 24601
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<210> 24602
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<210> 24603
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<210> 24604
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Ile Leu Ala Pro Phe Ser Gln Gly Val
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<210> 24614
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Leu Glu Thr Ile Leu Ala Pro Phe Ser
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

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<400> 24635

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1 5

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1 5 10

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1 5 10

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<400> 24672
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1 5 10

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1 5 10

<210> 24676
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1 5

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<400> 24684
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Phe His Phe Trp Val Asn Ile Phe Phe
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<400> 24687
Lys Met Phe His Phe Trp Val Asn Ile Phe
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<210> 24690
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<400> 24700
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<210> 24701
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<210> 24702
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<210> 24703
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<210> 24711
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<210> 24712
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<210> 24713
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<400> 24713
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1 5

<210> 24714
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<210> 24715
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<210> 24717

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1 5 10

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1 5 10

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Ser Leu Leu Asp Val Val Asp Lys Glu Ala
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Lys Asn Ala Lys Tyr Ile Ser Arg Leu
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Thr Ala Leu Phe His Thr Asp Asp Ile Lys
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Asp Ile Lys Asn Ala Lys Tyr Ile Ser Arg
1 5 10

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Ile Lys Asn Ala Lys Tyr Ile Ser Arg Leu
1 5 10

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Lys Asn Ala Lys Tyr Ile Ser Arg Leu Phe
1 5 10

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Gln Thr Gly Thr Gly Thr Gly Ala Arg
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Gln Lys Asn Phe Leu His Ile Ile Leu
1 5

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1 5 10

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1 5

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Glu Asn His Ser Phe Ser His Glu Arg
1 5

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1 5 10

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Gly Lys Tyr Glu Asn His Ser Phe Ser His
1 5 10

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1 5

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1 5 10

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1 5 10

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1 5

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1 5

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Cys Leu Met Val His Val Glu Ala Gln Tyr
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<400> 24771
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1 5

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1 5 10

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<210> 24775
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<210> 24816
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<210> 24839

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1 5 10

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<210> 24876
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<210> 24877
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Ala Thr Lys Arg Ser Lys Met Ser Lys
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Thr Ala Thr Lys Arg Ser Lys Met Ser Lys
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<210> 24889
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<210> 24891
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<400> 24896
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<210> 24897
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<210> 24898
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<210> 24900

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<210> 24901
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<400> 24907
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1 5 10

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<400> 24921
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1 5

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Leu Leu His Trp Val Ala Ala Tyr Phe
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<400> 24928
Arg Met Leu Leu His Trp Val Ala Ala Tyr
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Tyr His Arg Met Leu Leu His Trp Val Ala
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Thr Ser Tyr His Arg Met Leu Leu His Trp
1 5 10

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His Arg Met Leu Leu His Trp Val Ala Ala
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1 5

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Glu Ala Phe Ser Ser Leu Ala Leu Asp Ile
1 5 10

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1 5 10

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<210> 25024
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

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1 5 10

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Gln Asp His Ile Ser Phe Ile Ile Asn Leu

1 5 10

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1 5

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1 5

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1 5

<210> 25168
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<400> 25184

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<210> 25187
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1 5 10

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1 5 10

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1 5 10

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<210> 25613
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<210> 25615
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1 5

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1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 25801
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<400> 25809
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<400> 25810
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<210> 25811
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<400> 25811
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<210> 25814
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<400> 25814
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1 5 10

<210> 25815

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<400> 25815
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1 5 10

<210> 25816
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<400> 25816
Arg Pro Trp Arg Gly Thr Thr Arg Asn Cys
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<210> 25817
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Arg Thr Ser Glu Pro Arg Lys Val Leu Phe
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Leu Pro Arg Thr Ser Glu Pro Arg Lys Val
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Gln Ala Lys Ile Pro Leu Lys Asn Glu Lys
1 5 10

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Ala Lys Ile Pro Leu Lys Asn Glu Lys Leu
1 5 10

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<210> 25823
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Arg Trp Arg Cys Ser Lys Arg Ala Ser
1 5

<210> 25824
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<210> 25825
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1 5

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1 5 10

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1 5

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1 5

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<210> 25902
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<400> 25910
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<210> 25914
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Ile Leu Ile His His Arg Glu Asp Ile
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1 5 10

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1 5 10

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1 5 10

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Tyr Ile Gly Leu Lys Cys Leu Glu His Leu
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<400> 25960
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1 5 10

<210> 25980
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<400> 25986
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<400> 25988
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1 5 10

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Gln Ser Asp Trp Asn Asn Ser Leu Met
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<400> 26002
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1 5 10

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<400> 26005
Ser Arg Asp Gly Trp Gly Ala Met Ala Leu
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<210> 26006
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<400> 26007
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Arg Asp Ser Arg Asp Gly Trp Val Gly Tyr
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Arg Pro Arg Cys Ile Asn Met Thr Asp Thr
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Arg Cys Ile Asn Met Thr Asp Thr Gly Ile
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<210> 26022
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<210> 26024
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Ser Arg Phe Pro Trp Gly Pro Pro Pro
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<210> 26025
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<210> 26026
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<400> 26026
Gln Ser Gly Gly Phe Leu Pro Ser Arg Phe
1 5 10

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<400> 26028
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Ala Leu Leu Gly Thr Lys Val Ala Val
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1 5

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1 5 10

<210> 26039
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Gly Asp Ile Pro Ser Gln Phe Thr Trp

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Asp Ile Pro Ser Gln Phe Thr Trp Val Met
1 5 10

<210> 26047
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<400> 26047
Ser Thr Gly Ala Ser Arg Pro Leu Arg
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<210> 26048
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Ala Ser Arg Pro Leu Arg Thr Arg Arg
1 5

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1 5

<210> 26050
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<210> 26068
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1 5 10

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1 5 10

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1 5

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1 5

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1 5 10

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Lys Val Lys Asp Ser Ser Ser Glu Lys Arg
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<400> 26526

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1 5

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<400> 26540
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<400> 26587

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Cys His Met Val Glu Ile Ser Thr Pro Val
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Phe Met His Met Lys Leu Thr Lys Thr
1 5

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1 5

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1 5

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1 5 10

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1 5 10

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Gln Thr Phe Asn Ala Ser Tyr Asp Thr Lys
1 5 10

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1 5 10

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1 5

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1 5

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1 5

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1 5 10

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1 5

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Val Leu Leu Ile Met Thr Gly Thr Met
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<210> 26777
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1 5

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<400> 26787
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<400> 26790
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<210> 26801
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Ala Trp Leu Trp Leu Pro Phe Val Tyr Met
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<210> 26802
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1 5 10

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Cys Ile Gln Ile Ile Glu Gln Ser Arg
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Arg Leu Val Val Met Leu Gly Gly Ala
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<400> 26814
Leu Thr Arg Gly Phe Ser Tyr Val Arg
1 5

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Tyr Val Arg Arg His Arg His His Leu
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Arg His Arg His His Leu Trp Ser Gly
1 5

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1 5

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<400> 26818
Gly Phe Ser Tyr Val Arg Arg His Arg
1 5

<210> 26819
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<400> 26819
Cys Gln His Arg Asp Gly Gly Arg Leu
1 5

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<400> 26820
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<400> 26821
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<400> 26822
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1 5

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1 5 10

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1 5 10

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<400> 26827
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1 5 10

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Arg His Arg His His Leu Trp Ser Gly Ile
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1 5 10

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Phe Ser Tyr Val Arg Arg His Arg His His

1 5 10

<210> 26836
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<400> 26877
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<400> 26919
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<400> 26927
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<400> 27032
Pro Gln Arg Pro Ser Asn Ser Arg Lys Phe
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Ser Asn Ser Arg Lys Phe Gly Trp Gln Met
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<400> 27035
Trp Gln Met Arg Ala Ser Thr Pro Ala Pro
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Met Arg Ala Ser Thr Pro Ala Pro Cys Leu
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Ala Pro Cys Leu Thr His Cys Thr Phe Trp
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<210> 27039
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Asp Leu Arg Ala Leu Ala Trp Leu Arg
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Glu Glu Asp Leu Arg Ala Leu Ala Trp
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Asp Glu Glu Asp Leu Arg Ala Leu Ala Trp
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<400> 27042
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1 5 10

<210> 27043
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<400> 27043
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<210> 27045
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Tyr Phe Glu Arg His Thr Thr Phe Met
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Thr Thr Phe Met Asp Gly Lys Leu Met
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<210> 27057
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1 5

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1 5 10

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Tyr Leu Cys Ala Tyr Thr Tyr Phe Ile
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<400> 27085
Cys Thr Tyr Leu Cys Ala Tyr Thr Tyr Phe
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1 5

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1 5

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Cys Arg Arg Lys Ile Ser Asn Trp Ser Leu
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Asn Trp Ser Leu Lys Lys Val Pro Ala Leu
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Ala Glu Ala Glu Glu Leu Lys Pro Phe Leu
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<400> 27602
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<400> 27609
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<400> 27612
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<400> 27812
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1 5 10

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1 5 10

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1 5

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<400> 28100
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<400> 28401
Ser Leu Thr Arg Leu Leu His Thr Ser Leu
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Trp Trp Gly Ser Ser Val His Leu Ala Trp
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<400> 28408
Ser Leu Ser Leu His Gly Ser Ala Val Arg
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<400> 28410
Leu Ala Trp Ser Ser Gln Ser Leu Ser Leu
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<210> 28411
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<400> 28411
Gly Lys Asn Leu Met Lys Ser Pro Gln Trp
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<210> 28412
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<400> 28412
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<210> 28413
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<400> 28413
Val His Leu Ala Trp Ser Ser Gln Ser Leu
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<210> 28414
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Ser Gln Ser Leu Ser Leu His Gly Ser Ala
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<400> 28415
Ser Ala Val Arg Glu Asn His Pro Ser Leu
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<400> 28417

Thr Arg Leu Leu His Thr Ser Leu Cys Met
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1 5 10

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Arg Ile Arg Ser Leu Leu Glu Arg Gln Gly
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Lys Leu Gln Gln Ser Thr Ala Cys Val
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<210> 28499

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1 5

<210> 28794
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Asn Pro Tyr Val Arg Asn Arg Pro Pro Phe
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<400> 28795
Cys Ala Cys Ala Lys Ala Leu Lys Lys
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<210> 28796
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<400> 28796
Lys Cys Ala Cys Ala Lys Ala Leu Lys
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<210> 28797
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<400> 28797
Cys Lys Cys Ala Cys Ala Lys Ala Leu
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<210> 28798
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Arg Glu Asp Cys Lys Cys Ala Cys Ala
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<400> 28799
Cys Ala Cys Ala Lys Ala Leu Lys Lys Lys
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<400> 28800
Lys Cys Ala Cys Ala Lys Ala Leu Lys Lys
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<210> 28801
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Leu Cys Phe Ala Ser Arg Ile Arg Lys
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Cys Phe Ala Ser Arg Ile Arg Lys Ile
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<210> 28803
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<210> 28804

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<400> 28804
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<210> 28805
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1 5

<210> 28806
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<210> 28808
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Lys Lys Lys Met Pro Lys Leu Cys Phe Ala
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<210> 28809
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<400> 28810
Cys Phe Ala Ser Arg Ile Arg Lys Ile Arg
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<210> 28811
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<400> 28811
Met Pro Lys Leu Cys Phe Ala Ser Arg Ile
1 5 10

<210> 28812
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Lys Lys Lys Lys Met Pro Lys Leu Cys Phe
1 5 10

<210> 28813
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<400> 28813
Lys Lys Met Pro Lys Leu Cys Phe Ala Ser
1 5 10

<210> 28814
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<400> 28814
Tyr Pro Thr Leu Ala Ser Pro Ala Cys
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<210> 28815
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<400> 28815
Arg Leu Trp Phe Arg Glu Ala Glu Ile
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<210> 28816
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<400> 28816
Leu Trp Phe Arg Glu Ala Glu Ile Tyr
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<400> 28817
Ser Ser Arg Glu Glu Arg Leu Trp Phe
1 5

<210> 28818
<211> 9
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<400> 28818
Glu Glu Arg Leu Trp Phe Arg Glu Ala
1 5

<210> 28819
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<400> 28819
Phe Ser Ser Arg Glu Glu Arg Leu Trp
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<210> 28820
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Ser Ser Arg Glu Glu Arg Leu Trp Phe Arg
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<210> 28821
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Ile Phe Ser Ser Arg Glu Glu Arg Leu Trp
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<210> 28822
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<400> 28822
Lys Ile Phe Ser Ser Arg Glu Glu Arg Leu
1 5 10

<210> 28823
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1 5 10

<210> 28824
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Phe Ser Ser Arg Glu Glu Arg Leu Trp Phe
1 5 10

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<400> 28825
Arg Glu Glu Arg Leu Trp Phe Arg Glu Ala
1 5 10

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Arg Val Met Cys Thr Trp Leu Thr Met
1 5

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1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Trp Leu Thr Met Ala Pro Ser Cys Leu
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Leu Thr Met Ala Pro Ser Cys Leu Arg
1 5

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1 5

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1 5

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1 5

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1 5

<210> 28834
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Thr Ser Leu Thr Ser Thr Ser Ile Arg
1 5

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<400> 28835
Thr Ser Ile Arg Lys Gly Pro Gly Lys
1 5

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1 5

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<400> 28837
Ser Ala Arg Val Met Cys Thr Trp Leu
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Gly Thr Arg Met Arg Ala Gly Ser Val
1 5

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1 5

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1 5

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<400> 28842
Ser Ile Arg Lys Gly Pro Gly Lys Arg
1 5

<210> 28843
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<400> 28843
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1 5

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<400> 28844

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1 5

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1 5

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1 5

<210> 28847
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<400> 28847
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1 5

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<400> 28848
Thr Pro Arg Arg Arg Val Lys Val Cys

1 5

<210> 28849
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<210> 28850
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<220>
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<400> 28850
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<210> 28851
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<212> PRT
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Arg Arg Trp Ala Val Thr Pro Ala Trp
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1 5

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Arg Val Met Cys Thr Trp Leu Thr Met Ala
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Leu Thr Met Ala Pro Ser Cys Leu Arg Arg
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1 5 10

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Ser Thr Ser Ile Arg Lys Gly Pro Gly Lys
1 5 10

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1 5 10

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<400> 28858
Arg Val Lys Val Cys Ser Gly Ala Ala Gln
1 5 10

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Ser Ala Arg Val Met Cys Thr Trp Leu Thr
1 5 10

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<400> 28860
Gly Thr Arg Met Arg Ala Gly Ser Val Tyr
1 5 10

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1 5 10

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Ser Val Tyr Thr Gln Thr Arg Arg Arg Leu
1 5 10

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Gln Val Leu Asp Ala Thr Pro Arg Arg Arg
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Trp Leu Thr Met Ala Pro Ser Cys Leu Arg
1 5 10

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Trp Thr Ser Leu Thr Ser Thr Ser Ile Arg
1 5 10

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Thr Ser Ile Arg Lys Gly Pro Gly Lys Arg
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Asp Ala Ser Ala Pro Arg Arg Trp Ala Val
1 5 10

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Trp Ala Val Thr Pro Ala Trp Thr Ser Leu
1 5 10

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<400> 28870
Arg Leu Gly Asp Ala Ser Ala Pro Arg Arg
1 5 10

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Gln Pro Gln Ser Pro Pro Ser Ala Arg Val
1 5 10

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<400> 28872
Ala Pro Arg Arg Trp Ala Val Thr Pro Ala
1 5 10

<210> 28873
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<400> 28873
Thr Pro Ala Trp Thr Ser Leu Thr Ser Thr
1 5 10

<210> 28874
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<400> 28874
Arg Arg Val Lys Val Cys Ser Gly Ala Ala
1 5 10

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1 5 10

<210> 28876
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Ala Arg Val Met Cys Thr Trp Leu Thr Met
1 5 10

<210> 28877
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<400> 28877
Ala Trp Thr Ser Leu Thr Ser Thr Ser Ile
1 5 10

<210> 28878
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<400> 28878
Pro Pro Ser Ala Arg Val Met Cys Thr Trp
1 5 10

<210> 28879
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<400> 28879
Ser Val Trp Asp Ser Tyr Ala Glu Leu
1 5

<210> 28880
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<400> 28880
Glu Leu Arg Gln Leu Thr Leu Pro Arg
1 5

<210> 28881
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Tyr Ala Glu Leu Arg Gln Leu Thr Leu
1 5

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<400> 28883
Ser Tyr Ala Glu Leu Arg Gln Leu Thr Leu
1 5 10

<210> 28884
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<400> 28884
Leu Ser Val Trp Asp Ser Tyr Ala Glu Leu
1 5 10

<210> 28885
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<400> 28885
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1 5

<210> 28886
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<400> 28886
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1 5 10

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5 10

<210> 28890
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1 5

<210> 28892
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1 5 10

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Gly Ala Arg Gly Asp Phe Pro Thr Gly Lys
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<400> 28927
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Tyr Val Leu Ser Thr Leu Tyr Ser Leu
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<210> 28989
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<210> 29012
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<210> 29015
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<210> 29018
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<210> 29048

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Thr Ser Met Ser Pro Gly Pro Pro Cys Arg
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Arg Trp Leu Pro Gly Gly Gly Ser Pro Trp
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Lys Thr Arg Gly Glu Ala Met Gly Ser Gly
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Arg Gly Ser Gly Ala Ser Ser Phe Ile Arg
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<400> 29070
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1 5 10

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1 5 10

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1 5 10

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<400> 29075
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1 5 10

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peptide"

<400> 29076
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<210> 29077
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<400> 29077
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1 5 10

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1 5 10

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<400> 29086
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<400> 29087
Cys Pro Leu Val Leu Ser Phe Ala Ile
1 5

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Asn Ile Ser Leu Val Trp Cys Pro Leu Val
1 5 10

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<400> 29678
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Cys Thr Thr Ile His Tyr Asn Tyr Met Tyr
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<400> 29686
Thr Thr Ile His Tyr Asn Tyr Met Phe
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<400> 29687
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<400> 29698

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<210> 29702
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<210> 29703
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<400> 29703
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<210> 29706
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1 5 10

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<400> 29710
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<400> 29711
Asn Tyr Met Cys Asn Ser Ser Ala Trp
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<210> 29712
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<400> 29712
Tyr Asn Tyr Met Cys Asn Ser Ser Ala
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His Tyr Asn Tyr Met Cys Asn Ser Ser Ala
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<210> 29715
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<210> 29716
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<400> 29718
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<210> 29719

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<400> 29720
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Met Cys Asn Ser Ser Cys Met Cys Gly Met
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<400> 29734
Cys Met Cys Gly Met Asn Arg Arg Pro Ile
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Asp Gly Met Asn Arg Arg Pro Ile Leu
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<400> 29737
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Cys Met Asp Gly Met Asn Arg Arg Pro Ile
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<400> 29740
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<400> 29741
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<400> 29747
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1 5

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1 5

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<210> 30576
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<210> 30581
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Asp Val Val Pro Asp Trp Glu Thr His Leu
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<210> 30584
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1 5 10

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1 5 10

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1 5

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<210> 30613
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Thr His Met Asp Cys Leu Thr Gly Pro Leu
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Ala Leu His Leu Val Lys Pro Arg Val
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Ala Leu Val Ala Pro Arg Gly Leu Leu

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Val Leu His Gln Asn Leu Asp Pro Thr
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1 5 10

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1 5

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<210> 30688
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<210> 30699
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Val Lys Asn Ile Ile Tyr Val Leu Tyr
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1 5 10

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1 5

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1 5

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Leu Gln Ala Pro Ser Pro Ser Leu Trp
1 5

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1 5 10

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1 5 10

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<400> 30845
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1 5 10

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<210> 30912
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1 5 10

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1 5 10

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1 5 10

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<400> 30953
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<400> 30956
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<400> 30958
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<400> 30959
Asn Thr Trp Pro Arg Ser Thr Pro Met
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<210> 30960
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<400> 30960
Arg Pro Leu Arg Pro Pro Pro Pro Leu
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<400> 30961
Cys Pro Arg Ser Pro Tyr Arg Val Cys
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<400> 30967
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1 5

<210> 30971
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<210> 30972
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1 5

<210> 30974
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<210> 30976
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<220>
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<210> 30977
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<400> 30977
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<210> 30978
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Trp Leu Gly Val Ala Ala Ala Val Pro Leu
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<210> 30980
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Thr Ile Thr Gln Gly His Ser Ser Leu Lys
1 5 10

<210> 30983
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Gly Val Ala Ala Ala Val Pro Leu Gln Arg

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<210> 30984
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Ser Thr Gly Val Gly Tyr Leu Trp Met Arg
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<400> 30986
Gly Gly Arg Arg Trp Leu Gly Val Ala Ala
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<400> 30987
Leu Gly Ser Gly Val Trp Arg Pro Ala Lys
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Glu Met Arg Ser Gln Lys Arg Lys Gly Lys
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1 5 10

<210> 30990
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1 5 10

<210> 30992
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1 5 10

<210> 30993
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1 5 10

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1 5 10

<210> 30995
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Arg Ser Ser Arg Leu His Leu Ser Leu Ser
1 5 10

<210> 30996
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<400> 30996
Ser Ser Arg Leu His Leu Ser Leu Ser Ala
1 5 10

<210> 30997
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<400> 30997
Thr Trp Pro Arg Ser Thr Pro Met Glu Arg
1 5 10

<210> 30998
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<400> 30998
Glu Ala Ser Pro Ser Leu Ser Thr Gly Val
1 5 10

<210> 30999
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<400> 30999
Gln Thr Cys Pro Arg Ser Pro Tyr Arg Val
1 5 10

<210> 31000

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<400> 31000
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1 5 10

<210> 31001
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Met Pro Gly Gly Arg Arg Trp Leu Gly Val
1 5 10

<210> 31002
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<400> 31002
Arg Pro Pro Pro Pro Leu Gly Ser Gly Val
1 5 10

<210> 31003
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<400> 31003
Cys Pro Arg Ser Pro Tyr Arg Val Cys Leu
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<210> 31004
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<400> 31004
Met Glu Arg Arg Trp Arg Asn Gly Ser Val
1 5 10

<210> 31005
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<400> 31005
Ser Pro Ser Leu Ser Thr Gly Val Gly Tyr
1 5 10

<210> 31006
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<400> 31006
Arg Arg Trp Leu Gly Val Ala Ala Ala Val
1 5 10

<210> 31007
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<400> 31007
Ala Ala Ala Val Pro Leu Gln Arg Pro Leu
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<210> 31008
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<400> 31008
Leu Gln Arg Pro Leu Arg Pro Pro Pro Pro
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<210> 31009
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Ser Leu Ser Thr Gly Val Gly Tyr Leu Trp
1 5 10

<210> 31010
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<400> 31010
Leu Ser Thr Gly Val Gly Tyr Leu Trp Met
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<210> 31011
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<400> 31011
Gly Asn Thr Trp Pro Arg Ser Thr Pro Met
1 5 10

<210> 31012
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Gly Pro Gln Thr Cys Pro Arg Ser Pro Tyr
1 5 10

<210> 31013
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Tyr Arg Val Cys Leu Arg Ser Ser Arg Leu
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<400> 31014
Leu Arg Ser Ser Arg Leu His Leu Ser Leu
1 5 10

<210> 31015
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<400> 31015
Ser Arg Leu His Leu Ser Leu Ser Ala Trp
1 5 10

<210> 31016
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<400> 31016
Leu His Leu Ser Leu Ser Ala Trp Lys Leu
1 5 10

<210> 31017
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<400> 31017
Ser Ala Thr Ser Glu Ser Cys Ser Thr Ile
1 5 10

<210> 31018
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<400> 31018
Arg Leu Gln Ala Glu Thr Lys Leu Ile
1 5

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<400> 31019
Lys Leu Ile Asn Arg Val Asn Ser Thr
1 5

<210> 31020
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31020
Ala Glu Thr Lys Leu Ile Asn Arg Val
1 5

<210> 31021
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<400> 31021
Lys Leu Ile Asn Arg Val Asn Ser Thr Tyr
1 5 10

<210> 31022
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Ala Met Glu Arg Leu Gln Ala Glu Thr Lys
1 5 10

<210> 31023
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31023
Met Glu Arg Leu Gln Ala Glu Thr Lys Leu
1 5 10

<210> 31024
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31024
Thr Leu Thr Pro His Ile Gly Pro Lys
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<210> 31025
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<400> 31025
Glu Val Val Thr Leu Thr Pro His Ile
1 5

<210> 31026
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<400> 31026
Leu Thr Pro His Ile Gly Pro Lys Val
1 5

<210> 31027
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<400> 31027
Asp Glu Val Val Thr Leu Thr Pro His
1 5

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<400> 31028
Thr Leu Thr Pro His Ile Gly Pro Lys Val
1 5 10

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Val Thr Leu Thr Pro His Ile Gly Pro Lys
1 5 10

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Thr Pro His Ile Gly Pro Lys Val Ser Leu
1 5 10

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<400> 31031
Asp Glu Val Val Thr Leu Thr Pro His Ile
1 5 10

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<400> 31032
Ala Leu Cys Thr Pro Gln Pro Pro Ala
1 5

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<400> 31033
Cys Thr Pro Gln Pro Pro Ala Ser Thr Lys
1 5 10

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Lys Glu Ala Phe Gly Pro Gln Ala Leu Cys
1 5 10

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His Asn Val Thr Ser Trp Pro Gly Lys
1 5

<210> 31036
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Gln Gln Gln Gln Gln His Asn Val Thr
1 5

<210> 31037
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<400> 31037
Gln Gln Gln Gln His Asn Val Thr Ser
1 5

<210> 31038
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<400> 31038
Gln Gln Gln His Asn Val Thr Ser Trp
1 5

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<400> 31039
Asn Val Thr Ser Trp Pro Gly Lys Gln Val
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<210> 31040
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<400> 31040

Gln Gln Gln Gln Gln Gln His Asn Val
1 5 10

<210> 31041
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<400> 31041
Gln Gln Gln Gln Gln Gln His Asn Val Thr
1 5 10

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<400> 31042
Gln Gln Gln Gln His Asn Val Thr Ser Trp
1 5 10

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Gln Gln His Asn Val Thr Ser Trp Pro Gly
1 5 10

<210> 31044
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1 5 10

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<400> 31045
Pro Glu Glu Ser Gly Leu Glu Glu Leu
1 5

<210> 31046
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<400> 31046
Leu Glu Glu Leu Gly Ala Glu Glu Glu Met
1 5 10

<210> 31047
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<400> 31047
Glu Glu Ser Gly Pro Glu Glu Ser Gly Leu
1 5 10

<210> 31048
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Arg Pro Arg Pro Val Leu Arg Leu Val
1 5

<210> 31049
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<400> 31049
Pro Val Leu Arg Leu Val Asn Ser Arg
1 5

<210> 31050
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Leu Pro Ile Ser His Cys Gln Cys Ile Leu
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Cys Thr Glu Ala Val Phe Tyr Tyr Trp
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<210> 31411
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<210> 31412
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Lys Trp Asn Lys Lys Met Leu Thr Ala
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Trp Asn Lys Lys Met Leu Thr Ala Leu
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Ala Leu Pro Pro Ala Met Thr Ala Met Cys
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Met Thr Ala Met Cys Gly Tyr Gly Ile Arg
1 5 10

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1 5 10

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Leu Thr Ala Leu Pro Pro Ala Met Thr Ala
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Lys Phe Lys Glu Leu Leu Met Gln Lys
1 5

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Ala Gln Lys Arg Lys Tyr Lys Lys Phe
1 5

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<210> 31539
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<400> 31605
Leu Val Arg Asn His Thr Ser Val Thr
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1 5

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Thr Gln Ala Ala Ile Arg Asp Ile Leu
1 5

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1 5 10

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1 5 10

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<400> 31638
Trp Glu Met Lys Tyr Thr Ser Glu Ala Val
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<400> 31639
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1 5 10

<210> 31640
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31640
Glu Gln Leu Ala Ala Lys Ala Glu Arg
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<210> 31641
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<400> 31641
Ala Lys Ala Glu Arg Asp Gln Pro Leu
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Glu Gln Arg Ala Glu Gln Leu Ala Ala Lys
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<400> 31643
Ile Ser Tyr Ser Arg Glu Gly Glu Tyr
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<400> 31644
Leu Ser Ile Glu Ile Ser Tyr Ser Arg
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Ile Leu Leu Ser Ile Glu Ile Ser Tyr
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Ile Glu Ile Ser Tyr Ser Arg Glu Gly
1 5

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1 5 10

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Leu Leu Ser Ile Glu Ile Ser Tyr Ser Arg
1 5 10

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<400> 31650

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Glu Glu Ile Leu Leu Ser Ile Glu Ile Ser
1 5 10

<210> 31652
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Lys Asp Asn Lys Asn Asn Phe Ser Pro Lys
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Lys His Ile Lys Asp Asn Lys Asn Asn Phe
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Lys Glu Lys Glu Glu Ile Thr His Ile

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Gln Gln Arg Lys Glu His Gln Arg Arg Phe
1 5 10

<210> 31657
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Lys Leu Phe Glu Phe Met His Lys Thr
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<210> 31658
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Lys Leu Phe Glu Phe Met His Lys Thr His
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Val Asn Lys Leu Phe Glu Phe Met His Lys
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<210> 31662
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<210> 31663
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<210> 31671

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1 5 10

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Ser Ala Lys Val Trp Ser Arg Thr Ala Tyr
1 5 10

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Gly Leu Arg His Ser Ser Ala Lys Val Trp
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1 5

<210> 31680
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1 5

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1 5

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<210> 31692
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1 5

<210> 31693
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Ile Ser Met Thr Thr Ile Ser Arg Ala
1 5

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<400> 31694
Leu Tyr Gly Ser Tyr Pro Pro Ala Arg
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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1 5

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<400> 31696
His Ser Ala Gly Leu Ser Pro Gly Ala
1 5

<210> 31697
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<400> 31697
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1 5

<210> 31698
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1 5

<210> 31699
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<400> 31700
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<210> 31701
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<400> 31701
Leu Leu His Pro Gln Trp Ala Pro His
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<400> 31702
Gly Ser Val Met Ser Cys Ser Leu Leu
1 5

<210> 31703
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<400> 31703
Met Thr Thr Ile Ser Arg Ala Thr Trp
1 5

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<400> 31704
Met Pro Pro Leu Leu His Pro Gln Trp
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<210> 31705
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<400> 31705
Arg Leu Met Ala Pro Val Gly Ser Val Met
1 5 10

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<400> 31706
Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala
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Gly Leu Ser Pro Gly Ala Cys Arg Pro Ala
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<210> 31708
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<400> 31708
His Leu Tyr Gly Ser Tyr Pro Pro Ala Arg
1 5 10

<210> 31709
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<400> 31709
Thr Met Pro Pro Leu Leu His Pro Gln Trp
1 5 10

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<400> 31710
Thr Gly Arg Thr Pro Thr Thr Arg Leu Met
1 5 10

<210> 31711
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<400> 31711

Ala Ser Ala Cys Thr Met Pro Pro Leu Leu
1 5 10

<210> 31712
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<400> 31712
Ser Tyr Pro Pro Ala Arg Gln Pro Ser Arg
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<400> 31713
Thr Cys Ile Ser Met Thr Thr Ile Ser Arg
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<210> 31714
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<400> 31714
Thr Pro Thr Thr Arg Leu Met Ala Pro Val
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<400> 31715
Gln Pro Ser Pro Ala Ser Ala Cys Thr Met

1 5 10

<210> 31716
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<400> 31716
His Pro Gln Trp Ala Pro His Ser Ala Gly
1 5 10

<210> 31717
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<400> 31717
Ala Pro His Ser Ala Gly Leu Ser Pro Gly
1 5 10

<210> 31718
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<400> 31718
Arg Pro Ala Cys Thr Cys Ile Ser Met Thr
1 5 10

<210> 31719
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Phe His Leu Tyr Gly Ser Tyr Pro Pro Ala
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<210> 31720
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<400> 31720
Pro Gln Trp Ala Pro His Ser Ala Gly Leu
1 5 10

<210> 31721
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<400> 31721
Ser Met Thr Thr Ile Ser Arg Ala Thr Trp
1 5 10

<210> 31722
<211> 10
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<400> 31722
Met Pro Pro Leu Leu His Pro Gln Trp Ala
1 5 10

<210> 31723
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<400> 31723
Arg Phe Arg Arg Gly Pro Leu Arg Gln
1 5

<210> 31724
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<400> 31724
Arg Pro Arg Phe Arg Arg Gly Pro Leu
1 5

<210> 31725
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<400> 31725
Arg Pro Arg Phe Arg Arg Gly Pro Leu Arg
1 5 10

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<400> 31726
Arg Phe Arg Arg Gly Pro Leu Arg Gln Arg
1 5 10

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<400> 31727
Arg Trp Cys Pro His Pro Ser Ser Thr
1 5

<210> 31728
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<400> 31728
His Pro Ser Ser Thr Asp Gly Gly Leu
1 5

<210> 31729
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Cys Glu Ala Pro Gly Leu Pro Thr Ser
1 5

<210> 31730
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Gly Gln Arg Pro Arg Arg Trp Cys Pro His
1 5 10

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Arg Pro Arg Arg Trp Cys Pro His Pro Ser
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Ala Pro Gly Leu Pro Thr Ser Ser Ser Leu
1 5 10

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<400> 31733
Arg Arg Trp Cys Pro His Pro Ser Ser Thr
1 5 10

<210> 31734
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<400> 31734
Cys Glu Ala Pro Gly Leu Pro Thr Ser Ser
1 5 10

<210> 31735
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Lys Thr Ser Thr Pro Leu Thr Ser Ile
1 5

<210> 31736
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Ser Ile Ser Pro Arg Trp Pro Ser Leu
1 5

<210> 31737
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<400> 31760
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1 5

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1 5 10

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<210> 31806
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1 5 10

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1 5 10

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<210> 31812
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<210> 31815
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Leu Ala Pro Gln Ala Trp Trp Pro Ala
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<210> 31816
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1 5

<210> 31817
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31817
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1 5

<210> 31818
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<400> 31818
Trp Trp Pro Ala Arg Arg Gly Pro Leu
1 5

<210> 31819
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<400> 31819
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1 5

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<400> 31820
Gln Ala His Pro Gln Val Pro Ala Leu
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<400> 31821
Val Pro Ala Leu Ala Pro Gln Ala Trp
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Ala Trp Trp Pro Ala Arg Arg Gly Pro Leu
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1 5 10

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Leu Gln Asn Leu Ile Ile Ser Ala Gln
1 5

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1 5 10

<210> 31835
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<210> 31915

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1 5

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<400> 31935
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1 5

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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31936
Arg Lys Arg Arg Arg Met Thr Met Met
1 5

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<400> 31937
Thr Lys Ala Leu Pro Arg Gln Thr Ile
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<210> 31938
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<400> 31938
Ser Gln Arg Arg Pro Ile Gln Thr Pro
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<210> 31939
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31939
Ser Arg Leu Ala Val Leu Ala Ile Trp
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<210> 31940
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31940
Thr Met Met Thr Arg Arg Thr Leu Leu Thr
1 5 10

<210> 31941
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<400> 31941
Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr
1 5 10

<210> 31942
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<400> 31942
Ser Leu Thr Pro Ser Arg Leu Ala Val Leu
1 5 10

<210> 31943
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<400> 31943
Met Thr Arg Arg Thr Met Thr Thr Thr Lys
1 5 10

<210> 31944
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<400> 31944
Lys Met Met Met Met Arg Arg Thr Lys Arg
1 5 10

<210> 31945
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<400> 31945
Met Met Met Met Arg Arg Thr Lys Arg Arg
1 5 10

<210> 31946
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<400> 31946
Met Met Met Arg Arg Thr Lys Arg Arg Arg
1 5 10

<210> 31947
<211> 10
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31947
Met Met Thr Arg Arg Thr Leu Leu Thr Lys
1 5 10

<210> 31948
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<400> 31948
Met Thr Arg Arg Thr Leu Leu Thr Lys Lys
1 5 10

<210> 31949
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<400> 31949
Met Thr Thr Thr Lys Met Met Met Met Arg
1 5 10

<210> 31950
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31950
Thr Thr Thr Lys Met Met Met Met Arg Arg
1 5 10

<210> 31951
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<400> 31951
Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys
1 5 10

<210> 31952
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<400> 31952
Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg
1 5 10

<210> 31953
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<400> 31953
Arg Thr Met Thr Thr Thr Lys Met Met Met
1 5 10

<210> 31954
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31954
Met Met Arg Arg Thr Lys Arg Arg Arg Arg
1 5 10

<210> 31955
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31955

Met Arg Arg Thr Lys Arg Arg Arg Arg Lys
1 5 10

<210> 31956
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31956
Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg
1 5 10

<210> 31957
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31957
Arg Arg Arg Lys Arg Arg Arg Met Thr Met
1 5 10

<210> 31958
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<400> 31958
Lys Arg Arg Arg Met Thr Met Met Thr Arg
1 5 10

<210> 31959
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31959
Arg Arg Arg Met Thr Met Met Thr Arg Arg

1 5 10

<210> 31960
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<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31960
Arg Met Thr Met Met Thr Arg Arg Thr Leu
1 5 10

<210> 31961
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<212> PRT
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<400> 31961
Met Thr Met Met Thr Arg Arg Thr Leu Leu
1 5 10

<210> 31962
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31962
Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu
1 5 10

<210> 31963
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31963
Leu Thr Lys Lys Thr Cys Leu Thr Pro Arg
1 5 10

<210> 31964
<211> 10
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31964
Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala
1 5 10

<210> 31965
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<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31965
Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile
1 5 10

<210> 31966
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31966
Arg Gln Thr Ile Ser Gln Arg Arg Pro Ile
1 5 10

<210> 31967
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31967
Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala
1 5 10

<210> 31968
<211> 10
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31968
Thr Pro Ser Arg Leu Ala Val Leu Ala Ile
1 5 10

<210> 31969
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31969
Arg Arg Lys Arg Arg Arg Met Thr Met Met
1 5 10

<210> 31970
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<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31970
Arg Met Thr Arg Arg Thr Met Thr Thr Thr
1 5 10

<210> 31971
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<400> 31971
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1 5 10

<210> 31972
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1 5 10

<210> 31973
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1 5 10

<210> 31974
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<400> 31974
Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro
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<210> 31975
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<400> 31975
Ile Gln Thr Pro Pro Gly Thr Ser Leu Thr
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<210> 31976

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<400> 31976
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1 5

<210> 31977
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<400> 31977
Ser Leu Thr Pro Ser Arg Leu Ala Val
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<210> 31978
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<400> 31978
Cys Leu Thr Pro Arg Thr Ser Ala Ala
1 5

<210> 31979
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<400> 31979
Lys Met Met Met Met Arg Arg Thr Lys
1 5

<210> 31980
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Met Met Met Met Arg Arg Thr Lys Arg
1 5

<210> 31981
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<400> 31981
Met Met Met Arg Arg Thr Lys Arg Arg
1 5

<210> 31982
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<400> 31982
Met Thr Arg Arg Thr Leu Leu Thr Lys
1 5

<210> 31983
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31983
Thr Thr Thr Lys Met Met Met Met Arg
1 5

<210> 31984
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<400> 31984
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1 5

<210> 31985
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31985
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1 5

<210> 31986
<211> 9
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31986
Arg Met Thr Arg Arg Thr Met Thr Thr
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<210> 31987
<211> 9
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<400> 31987
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<210> 31988
<211> 9
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31988
Thr Arg Arg Thr Met Thr Thr Thr Lys
1 5

<210> 31989
<211> 9
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31989
Arg Thr Met Thr Thr Thr Lys Met Met
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<210> 31990
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<400> 31990
Met Met Arg Arg Thr Lys Arg Arg Arg
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<210> 31991
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<400> 31991
Arg Thr Lys Arg Arg Arg Arg Lys Arg
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<400> 31992
Arg Arg Arg Met Thr Met Met Thr Arg
1 5

<210> 31993
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31993
Met Thr Met Met Thr Arg Arg Thr Leu
1 5

<210> 31994
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31994
Arg Thr Ser Ala Ala Thr Lys Ala Leu
1 5

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<400> 31995
Met Thr Thr Thr Lys Met Met Met Met
1 5

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<400> 31996
Gln Thr Ile Ser Gln Arg Arg Pro Ile
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<210> 31997
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<400> 31997
Arg Arg Lys Arg Arg Arg Met Thr Met
1 5

<210> 31998
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31998
Thr Leu Leu Thr Lys Lys Thr Cys Leu
1 5

<210> 31999
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 31999
Ile Gln Thr Pro Pro Gly Thr Ser Leu
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<210> 32000
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32000
Arg Arg Thr Met Thr Thr Thr Lys Met
1 5

<210> 32001
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32001
Thr Met Thr Thr Thr Lys Met Met Met
1 5

<210> 32002
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32002
Arg Lys Arg Arg Arg Met Thr Met Met
1 5

<210> 32003
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32003
Thr Lys Ala Leu Pro Arg Gln Thr Ile
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<210> 32004
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peptide"

<400> 32004
Ser Gln Arg Arg Pro Ile Gln Thr Pro
1 5

<210> 32005
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32005
Ser Arg Leu Ala Val Leu Ala Ile Trp
1 5

<210> 32006
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32006
Thr Met Met Thr Arg Arg Thr Leu Leu Thr
1 5 10

<210> 32007
<211> 10
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32007
Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr
1 5 10

<210> 32008
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32008
Ser Leu Thr Pro Ser Arg Leu Ala Val Leu
1 5 10

<210> 32009
<211> 10
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32009
Met Thr Arg Arg Thr Met Thr Thr Thr Lys
1 5 10

<210> 32010
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32010
Lys Met Met Met Met Arg Arg Thr Lys Arg
1 5 10

<210> 32011
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<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32011
Met Met Met Met Arg Arg Thr Lys Arg Arg
1 5 10

<210> 32012
<211> 10
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32012
Met Met Met Arg Arg Thr Lys Arg Arg Arg
1 5 10

<210> 32013
<211> 10
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32013
Met Met Thr Arg Arg Thr Leu Leu Thr Lys
1 5 10

<210> 32014
<211> 10
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32014
Met Thr Arg Arg Thr Leu Leu Thr Lys Lys
1 5 10

<210> 32015
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32015
Met Thr Thr Thr Lys Met Met Met Met Arg
1 5 10

<210> 32016
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32016

Thr Thr Thr Lys Met Met Met Met Arg Arg
1 5 10

<210> 32017
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32017
Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys
1 5 10

<210> 32018
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32018
Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg
1 5 10

<210> 32019
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32019
Arg Thr Met Thr Thr Thr Lys Met Met Met
1 5 10

<210> 32020
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32020
Met Met Arg Arg Thr Lys Arg Arg Arg Arg

1 5 10

<210> 32021
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32021
Met Arg Arg Thr Lys Arg Arg Arg Arg Lys
1 5 10

<210> 32022
<211> 10
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32022
Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg
1 5 10

<210> 32023
<211> 10
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32023
Arg Arg Arg Lys Arg Arg Arg Met Thr Met
1 5 10

<210> 32024
<211> 10
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32024
Lys Arg Arg Arg Met Thr Met Met Thr Arg
1 5 10

<210> 32025
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32025
Arg Arg Arg Met Thr Met Met Thr Arg Arg
1 5 10

<210> 32026
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32026
Arg Met Thr Met Met Thr Arg Arg Thr Leu
1 5 10

<210> 32027
<211> 10
<212> PRT
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<220>
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<400> 32027
Met Thr Met Met Thr Arg Arg Thr Leu Leu
1 5 10

<210> 32028
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32028
Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu
1 5 10

<210> 32029
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32029
Leu Thr Lys Lys Thr Cys Leu Thr Pro Arg
1 5 10

<210> 32030
<211> 10
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32030
Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala
1 5 10

<210> 32031
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32031
Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile
1 5 10

<210> 32032
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<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 32032
Arg Gln Thr Ile Ser Gln Arg Arg Pro Ile
1 5 10

<210> 32033
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<400> 32033
Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala
1 5 10

<210> 32034
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<400> 32034
Thr Pro Ser Arg Leu Ala Val Leu Ala Ile
1 5 10

<210> 32035
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<400> 32036
Arg Met Thr Arg Arg Thr Met Thr Thr Thr
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<210> 32037

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<400> 32037
Thr Arg Arg Thr Met Thr Thr Thr Lys Met
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Arg Arg Thr Met Thr Thr Thr Lys Met Met
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Thr Met Thr Thr Thr Lys Met Met Met Met
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<210> 32047
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<400> 32047
Phe Leu Met Lys Lys Gln Pro Ser Lys
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Lys Gln Pro Ser Lys Val Arg Arg Lys
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Lys Val Arg Arg Lys Glu Ala His Gly
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Leu Met Lys Lys Gln Pro Ser Lys Val Arg
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<210> 32063
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Ala Lys Arg Gln Arg Gln Trp Gln Trp
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<210> 32076
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<400> 32077

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1 5 10

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Lys Gln Phe Phe Gly Arg Val Ile Lys Ala
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<210> 32087
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Cys Thr Arg Ala Ile Asn Asn Lys Gln Phe
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<210> 32088
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<400> 32088
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<210> 32089
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<400> 32089
Leu Gly Asn Pro His Ser Arg Ser Trp
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<210> 32090
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<210> 32091
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Tyr His Ile Glu Phe Leu Gly Asn Pro His
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<210> 32092
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Phe Leu Gly Asn Pro His Ser Arg Ser Trp
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<210> 32093
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<210> 32094
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Leu Leu Asp Phe Leu Gly Leu Val Gln Leu
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Phe Leu Gly Leu Val Gln Leu Gly Gln Leu
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<210> 32098

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Gly Leu Val Gln Leu Gly Gln Leu Leu Ile
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<210> 32100
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<210> 32102
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Cys Gln His Cys Pro Leu Val Ala Trp
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<210> 32103
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Trp Ala Trp Cys Gln His Cys Pro Leu Val
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1 5 10

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1 5

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1 5

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1 5 10

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1 5 10

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<210> 32120
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Gln Ser Ala Ser Lys Asn Gly Asn Lys
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1 5

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<400> 32130
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1 5

<210> 32131
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<400> 32131
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<210> 32132
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<400> 32132
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1 5

<210> 32133
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1 5

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<400> 32382

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<210> 32383
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<400> 32387
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<210> 32388
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<400> 32388
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<210> 32389
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1 5

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<210> 32403

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1 5

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Ala Pro Arg Pro Thr Ala Pro Ser Thr
1 5

<210> 32406
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<400> 32406
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1 5

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<400> 32409
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1 5

<210> 32410
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<400> 32410
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<210> 32411
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1 5

<210> 32413
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<400> 32413
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1 5

<210> 32414
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Leu Pro Pro Arg Leu Cys Ala Arg Ala
1 5

<210> 32415
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1 5 10

<210> 32416
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<400> 32416
Arg Thr Ala Arg Ala Ala Gly Ala Ala Arg
1 5 10

<210> 32417
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Arg Thr Thr Pro Ala Ala Arg Cys Ala Arg
1 5 10

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<400> 32418
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1 5 10

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1 5 10

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1 5 10

<210> 32421
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 32426
Arg Trp Arg Ser Arg Arg Arg Pro Pro Ser
1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 32431
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1 5 10

<210> 32433
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<400> 32433
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<400> 32434
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Cys Ser Arg Ala Arg Ala Arg Ala Pro Ala
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<400> 32437
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Ala Ala Arg Arg Pro Gly Ser Ser Pro Gly
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Arg Ala Leu Arg Ala Ser Ser Ala Arg Ser
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1 5 10

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<400> 32443

Arg Ala Gly Pro Arg Arg Pro Pro Ala Arg
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Arg Ala Arg Pro Arg Ala Pro Glu Arg Ala
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Arg Ala Arg Arg Gly Leu Gly Ala Arg Pro
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Arg Gly Leu Gly Ala Arg Pro Arg Pro Arg

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Thr Thr Arg Arg Thr Thr Pro Ala Ala Arg
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1 5 10

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Cys Ala Arg Pro Ala Thr Ser Ala Ser Ala
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Ala Thr Arg Pro Thr Pro Cys Thr Ser Gly
1 5 10

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Leu Gly Arg Pro Arg Pro Arg Pro Pro Leu
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 32486
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1 5 10

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<400> 32487
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1 5 10

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<400> 32489
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1 5 10

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<400> 32490
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1 5 10

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1 5 10

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<400> 32492
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Arg Pro Arg Pro Arg Thr Ala Arg Ala Ala
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Arg Pro Arg Thr Ala Arg Ala Ala Gly Ala
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 32504

Arg Pro Pro Leu Pro Pro Arg Leu Cys Ala
1 5 10

<210> 32505
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<400> 32505
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1 5 10

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1 5 10

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Arg Arg Ser Trp Pro Arg Cys Pro Ser Trp
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<400> 32510
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1 5 10

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1 5 10

<210> 32512
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Glu Pro Trp Pro Arg Met Glu Ala Ala Ala
1 5 10

<210> 32513
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<400> 32513
Ala Glu Pro Trp Pro Arg Met Glu Ala Ala
1 5 10

<210> 32514
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Ala Glu Ala Glu Ala Ala Pro Ala Ser Pro
1 5 10

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<400> 32515
Pro Glu Ala Glu Ala Glu Ala Ala Pro Ala
1 5 10

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Arg Pro Asn Phe Gln Ser Ala Ala Leu
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<400> 32518
Ala Arg Ser Tyr Glu Asp Arg Pro Asn Phe
1 5 10

<210> 32519
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1 5 10

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1 5 10

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Leu Val Ile Tyr Gln Thr His Ala Asp Arg
1 5 10

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Val Ile Tyr Gln Thr His Ala Asp Arg Leu
1 5 10

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Ser Asn Arg Tyr Asn Glu Ile Met Lys
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<400> 32527
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1 5

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<400> 32528
Arg Tyr Asn Glu Ile Met Lys Ala Met
1 5

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1 5 10

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Asn Arg Tyr Asn Glu Ile Met Lys Ala Met
1 5 10

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<400> 32531
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1 5

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<400> 32532
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1 5

<210> 32533
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Lys Leu Gly Gln Ile Ile Met Lys Lys
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<400> 33615
Ile Met Lys Pro Lys Arg Asp Gly Tyr
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<400> 33617
Thr Val His Cys Met His Leu His Glu Lys
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<210> 33618
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His Met Ser Ser Leu Ser His Ile Ser Ala
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<210> 33625
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<210> 33626
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<210> 33629
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Phe Leu Leu Leu Leu Val Val Phe Leu
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<210> 33637
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<210> 33638
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<400> 33638
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Val Leu His Glu Cys Asn Ser Ser Tyr Ile
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Tyr Leu Asp Phe Gly Ile His Ser Gly Ala
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Tyr Leu Asp Phe Gly Ile His Ser Gly
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Gly Thr Gly Val Met Ile Cys Ala Tyr
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<210> 33684

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Leu Pro Ala Leu Arg Phe Ile Gly Leu
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Met Pro Ala Leu Arg Arg Ser Ala Val
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Leu Leu Thr Trp His Ala Ala Met Leu Lys
1 5 10

<210> 33689
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Arg Ser Ser Ile Met Lys Pro Lys Arg
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<210> 33690
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Phe Leu Leu Leu Thr Leu Pro Lys Val
1 5

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Arg Val Arg Asp Met Lys Cys Leu Met
1 5

<210> 33692
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1 5 10

<210> 33693
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Gly Leu Asn Pro Leu Pro Asp Val Gln Val
1 5 10

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1 5

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1 5 10

<210> 33697
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1 5 10

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1 5 10

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<210> 33700
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<210> 33701
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<400> 33701
Tyr Leu Asn Ser Gly Ile His Ser Gly
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1 5 10

<210> 33703
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1 5 10

<210> 33704
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<400> 33704
Arg Glu Thr Phe His Leu Val Ser Glu Met
1 5 10

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<400> 33705
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1 5 10

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<210> 33707
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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<400> 33709
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1 5 10

<210> 33710
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<400> 33710
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1 5

<210> 33711
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<400> 33711
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<210> 33718
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<210> 33730
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<210> 33731
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<210> 33732
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<210> 33733
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6xHis tag"

<400> 33733
His His His His His His
1 5

CLAIMS

1. A pharmaceutical composition comprising:

(i) a polypeptide comprising at least one amino acid sequence comprising at least 8 contiguous amino acids of:
RRLSAARRAGTSCANCQTTTTTLWRLEEECQWGPCLQCLWALLQASQY (SEQ ID NO: 1300),

(ii) a nucleic acid encoding the polypeptide,

(iii) antigen presenting cells (APCs) comprising (i) or (ii), or

(iv) T cells stimulated with APCs comprising (i) or (ii); and

a pharmaceutically acceptable carrier.

2. A pharmaceutical composition according to Claim 1, in which the at least one amino acid sequence binds to a protein encoded by an HLA allele.

3. A pharmaceutical composition according to Claim 1 or 2, in which the at least one amino acid sequence binds to a protein encoded by an HLA-A, HLA-B or HLA-C allele with a K_D of less than 500 nM.

4. A pharmaceutical composition according to Claim 1, 2 or 3, in which the at least one amino acid sequence binds to a protein encoded by a class II HLA allele with a binding affinity of less than 1000 nM.

5. A pharmaceutical composition according to any preceding claim, in which the polypeptide is from 8 to 50 amino acids in length.

6. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence CLQCLWALL (SEQ ID NOs: 13428, 13809).

7. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence QWGPCLQCL (SEQ ID NO: 13810).

8. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence TTTTTLWRL (SEQ ID NO: 13811).

9. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence WALLQASQY (SEQ ID NOs: 13429, 13812).

10. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence EECQWGPCL (SEQ ID NO: 13813).

11. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence QWGPCLQCLW (SEQ ID NO: 13814).

12. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence LWALLQASQY (SEQ ID NOs: 13431, 13815).

13. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence QTTTTTLWRL (SEQ ID NO: 13816).

14. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence CQWGPCLQCL (SEQ ID NOs: 13817).

15. A pharmaceutical composition according to Claim 5, in which the polypeptide comprises an amino acid sequence LQCLWALLQA (SEQ ID NOs: 13433, 13818).

16. A pharmaceutical composition according to Claim 5, in which the pharmaceutical composition comprises (iv).

17. A pharmaceutical composition according to Claim 5, in which the pharmaceutical composition comprises (i) or (ii).

18. A pharmaceutical composition according to Claim 5, further comprising an adjuvant or an immunomodulator.

19. A pharmaceutical composition according to Claim 5, in which the pharmaceutical composition is an immunogenic composition.

20. A pharmaceutical composition according to Claim 5, in which the pharmaceutical composition is a vaccine composition.

21. A pharmaceutical composition for use in treating or preventing a cancer, in which the pharmaceutical composition is an immunogenic composition or a vaccine composition, comprising:

(i) an isolated neoantigenic polypeptide comprising at least one amino acid sequence comprising a tumor-specific neoepitope, in which the tumor-specific neoepitope is an amino acid sequence selected from the group consisting of CLQCLWALL (SEQ ID NO: 13809), QWGPCLQCL (SEQ ID NO: 13810), TTTTTLWRL (SEQ ID NO: 13811), WALLQASQY (SEQ ID NO: 13812), EECQWGPCL (SEQ ID NO: 13813), QWGPCLQCLW (SEQ ID NO: 13814), LWALLQASQY (SEQ ID NO: 13815), QTTTTTLWRL (SEQ ID NO: 13816), CQWGPCLQCL (SEQ ID NO: 13817), and LQCLWALLQA (SEQ ID NO: 13818),

(ii) a nucleic acid encoding (i),

(iii) antigen presenting cells (APCs) comprising (i) or (ii), or

(iv) T cells stimulated with (iii); and

a pharmaceutically acceptable carrier.

22. A pharmaceutical composition according to any preceding claim, for treating or preventing a tumor in a subject in need thereof.

23. A pharmaceutical composition according to Claim 22, in which the subject has a GATA3 frameshift mutation.

24. A pharmaceutical composition according to Claim 22, in which the tumor is breast cancer.

25. A pharmaceutical composition according to Claim 24, in which the breast cancer is non-metastatic breast cancer, metastatic breast cancer, HER-2-positive breast cancer, stage I breast cancer, stage II breast cancer, stage IIA breast cancer or operable stage IIC breast cancer.

26. A pharmaceutical composition according to any of Claims 22 to 25, in which the pharmaceutical composition is to be administered as a combination therapy with an additional cancer therapy, in which the additional cancer therapy is a check point inhibitor, surgery, chemotherapy, or a targeted therapy.

27. Use of a pharmaceutical composition according to any of Claims 1 to 21, in the manufacture of a medicament for treating or preventing a tumor in a subject in need thereof.

28. Use according to Claim 27, in which the subject has a GATA3 frameshift mutation.

29. Use according to Claim 27, in which the tumor is breast cancer.

30. Use according to Claim 29, in which the breast cancer is non-metastatic breast cancer, metastatic breast cancer, HER-2-positive breast cancer, stage I breast cancer, stage II breast cancer, stage IIA breast cancer or operable stage IIC breast cancer.

31. Use according to any of Claims 27 to 30, in which the pharmaceutical composition is to be administered as a combination therapy with an additional cancer therapy, in which the additional cancer therapy is a check point inhibitor, surgery, chemotherapy, or a targeted therapy.