

METHODS OF DIAGNOSING AND TREATING CERVICAL CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit of priority of MX/a/2019/005940 filed May 21, 2019, the entire contents of which is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

[0002] The present invention relates generally to methods of diagnosing and treating cervical cancer in a subject and more specifically to biomarkers used to diagnose cervical cancer.

BACKGROUND INFORMATION

[0003] Cervical cancer (CC) is one of the most common cancers among women worldwide. Among the risk factors related to this disease are infection with the human papilloma virus (HPV), the microbiome, risky sexual behavior, multiparity, smoking, prolonged use of hormonal contraceptives and environmental factors. Cervical cancer is a disease of slow and progressive evolution. It is preceded by cervical intraepithelial neoplasms, which are the lesions considered to be the prelude to this condition. These malignancies or injuries can occur even 10 years before cervical cancer develops.

[0004] Human papillomavirus infection (HPV) causes more than 90% of cases. Other risk factors include smoking, a weak immune system, birth control pills, starting sex at a young age, and having many sexual partners, but these are less important. Cervical cancer typically develops from precancerous changes over 10 to 20 years. About 90% of cervical cancer cases are squamous cell carcinomas, 10% are adenocarcinoma, and a small number are other types. Diagnosis is typically by cervical screening followed by a biopsy. Medical imaging is then done to determine whether or not the cancer has spread.

[0005] Current methods of diagnosing cervical cancer are invasive. The most common method of diagnosing cervical cancer is by a smear screening with Papanicolaou staining, i.e. Pap smear. There is a need for non-invasive methods of detecting cervical cancer.

SUMMARY OF THE INVENTION

[0006] The present invention is based on the seminal discovery that a collection of biomarkers can be used for the diagnosis of cervical cancer.

[0007] In one embodiment, the present invention is directed to methods of detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat Shock Protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof; and diagnosing cervical cancer based on the detection of the at least one polypeptide.

[0008] In one aspect, the sample is selected from the group consisting of blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair. In certain aspects the sample is a blood sample and the subject is human.

[0009] In another aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In an additional aspect, the at least one polypeptide is a polypeptide having at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 and a fragment thereof.

[0010] In a further aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay. In a specific aspect, the detecting is by lateral flow assay. In one aspect, the method also includes

administering a treatment to the subject. In an additional aspect, the treatment is surgery, radiation, chemotherapy, targeted therapy and/or immunotherapy.

[0011] In another embodiment, the present invention provides a method of diagnosing cervical cancer in a subject by detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin 1, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate protein 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof; and diagnosing cervical cancer based on the detection of at least one polypeptide.

[0012] In one aspect, the sample is blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair. In certain aspects, the sample is a blood sample and the subject is human.

[0013] In an additional aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Cognate thermal shock protein 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In a further aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having an amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0014] In another aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay. In a specific aspect, the detecting is by lateral flow assay. In one aspect, the method also includes administering a treatment to the subject. In certain aspects, the treatment is surgery, radiation, chemotherapy, targeted therapy and/or immunotherapy.

[0015] In an additional embodiment, the present invention provides a method of treating cervical cancer in a subject in need thereof, the method is detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof; diagnosing cervical cancer based on the detection of the at least one polypeptide; and administering a treatment to the subject. In one aspect, the sample is a blood sample.

[0016] In an additional aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In a further embodiment, the at least one polypeptides is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof

and at least one polypeptide with at least about 70% sequence identity to a polypeptide with an amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0017] In another aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow or immunoassay. In a specific aspect, the detecting is by lateral flow assay. In an additional aspect, the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy.

[0018] In a further aspect, the chemotherapy is Cisplatin, Carboplatin, Paclitaxel, Topotecan, docetaxel, ifosfamide, 5-fluorouracil, irinotecan, gemcitabine or mitomycin. In certain aspects, the targeted therapy is bevacizumab and the immunotherapy is pembrolizumab.

[0019] In a further embodiment, the present invention provides methods of predicting a response to treatment for a subject having cervical cancer by detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof; and predicting a response to treatment based on the detection of the at least one polypeptide.

[0020] In one aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In another aspect, the at least one

polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0021] In an additional aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow or immunoassay. In a further aspect, the detecting is by lateral flow assay. In certain aspects, the treatment is surgery, radiation, chemotherapy, targeted therapy and immunotherapy.

[0022] In another embodiment, the present invention provides methods for determining the stage of cervical cancer in a subject in need thereof by detecting at least one polypeptide in a sample from the subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof; and determining the stage of cervical cancer in the subject based on the detection of the at least one polypeptide.

[0023] In one aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In another aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the

amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0024] In an additional aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical assay or immunoassay. In a specific aspect, the detecting is by lateral flow assay. In a further aspect, the method also includes administering a treatment to the subject. In certain aspects, the treatment is surgery, radiation, chemotherapy, targeted therapy or immunotherapy. In one aspect, the cervical cancer is stage I, stage II, stage III or stage IV.

[0025] In one embodiment, the present invention provides a kit with a sample collection unit; a lateral flow device; and instructions for using the lateral flow device.

[0026] In one aspect, the lateral flow device detects at least one polypeptide selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof.

[0027] In an additional aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In a further aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a

polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0028] In another aspect, the lateral flow device detects the at least one polypeptide by an immunoassay. In one aspect, the sample collection unit collects a blood sample.

[0029] In an additional aspect, the present invention provides a use of the detection of at least one polypeptide for the diagnosis of cervical cancer in a subject in need thereof, wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof.

[0030] In a further aspect, the at least one polypeptide is detected in a sample from the subject and the sample is a blood sample. In another aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0031] In another aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow or immunoassay. In certain aspects, the detecting is by lateral flow assay.

BRIEF DESCRIPTION OF THE DRAWINGS

[0032] Figure 1 shows the workflows to obtain secreted proteins *in vivo* or *ex vivo*.

[0033] Figure 2 is a graph showing the growth kinetics of cell lines with and without fetal bovine serum (FBS).

[0034] Figure 3A show analysis of the cervical cancer line secretome and its negative control. Figure 3B illustrates the number of total protein in each cell line, the number of unique protein, and the protein shared between cell lines. Figure 3C is a graphical representation of the data presented in Figure 3B.

[0035] Figure 4A shows a dotplot graph illustrating the label-free quantification (LFQ) of 200 CC cell line secretome proteins vs. their negative control. Figure 4B is a graph bar representing the expression profile of proteins of interest. Figure 4C is a heat map illustrating the label-free quantification (LFQ) of 200 CC cell line secretome proteins vs. their negative control.

[0036] Figure 5A illustrates the workflow to collect blood and serum samples. Figure 5B illustrate the western blot analysis of FPS (farnesyl pyrophosphatase) in mouse sera. Figure 5C illustrates the quantification of the data presented in Figure 5B.

[0037] Figure 6A illustrates the validation of the candidate protein Farnesyl pyrophosphate synthase in the sera of patients with CC. Figure 6B illustrates the level of Farnesyl pyrophosphate synthase protein detected in the sera of control patients. Figure 6C illustrates the quantification of the data presented in Figures 6A and 6B.

[0038] Figure 7A illustrates the validation of the candidate protein Farnesyl pyrophosphate synthase in precancerous cervical lesions. Figure 7B illustrates the validation of the candidate protein Ankyrin-3 in precancerous cervical lesions. Figure 7C illustrates the quantification of the data presented in Figures 7A and 7B.

[0039] Figure 8A illustrates the detection of Farnesyl pyrophosphate synthase by western blot in the sera of patients with pre-cancerous lesions L1. Figure 8B illustrates the detection of Farnesyl pyrophosphate synthase by western blot in the sera of patients with pre-cancerous lesions L2. Figure 8C illustrates the detection of Farnesyl pyrophosphate synthase by western blot in the sera of control patients. Figure 8D illustrates the quantification of the data provided in Figure 8A-8C.

[0040] Figure 9A illustrates the detection of Ankyrin-3 by western blot in the sera of patients with pre-cancerous lesions L1. Figure 9B illustrates the detection of Ankyrin-3 by western blot in the sera of patients with pre-cancerous lesions L2. Figure 9C illustrates the detection of Ankyrin-3 by western blot in the sera of control patients. Figure 9D illustrates the quantification of the data provided in Figure 9A-9C.

DETAILED DESCRIPTION OF THE INVENTION

[0041] The present invention is based on the seminal discovery that a collection of biomarkers can be used for the diagnosis of cervical cancer.

[0042] Before the present compositions and methods are described, it is to be understood that this invention is not limited to particular compositions, methods, and experimental conditions described, as such compositions, methods, and conditions may vary. It is also to be understood that the terminology used herein is for purposes of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only in the appended claims.

[0043] As used in this specification and the appended claims, the singular forms “a”, “an”, and “the” include plural references unless the context clearly dictates otherwise. Thus, for example, references to “the method” includes one or more methods, and/or steps of the type described herein which will become apparent to those persons skilled in the art upon reading this disclosure and so forth.

[0044] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

[0045] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, it will be understood that modifications and variations are encompassed within the spirit and scope of the instant disclosure. The preferred methods and materials are now described.

[0046] Cervical cancer (CC) is one of the most common cancers among women worldwide. Among the risk factors related to this disease are infection with the human papilloma virus (HPV), the microbiome, risky sexual behavior, multiparity, smoking, prolonged use of hormonal

contraceptives and environmental factors. Cervical cancer is a disease of slow and progressive evolution. It is preceded by cervical intraepithelial neoplasms, which are the lesions considered to be the prelude to this condition.

[0047] These lesions are generally asymptomatic, making it difficult to detect the disease in a timely manner, so if they are not detected by any of the conventional methods, there is a risk that they will develop to the state of CC. Due to this, the diagnosis of neoplastic lesions or cancer in early stages, from HPV infection, is extremely important to be able to channel and treat these cases in a timely and adequate manner.

[0048] Currently the gold standard for the diagnosis of CC is the Pap test, while for the detection of HPV the most widely used method is detection by PCR and sequencing of the viral genome. Although both methods are an international benchmark, these tests have technical limitations, since highly trained personnel, facilities and specialized equipment are required; Furthermore, it is not easily accessible to the entire female population and the existence of socio-cultural beliefs prevent women from making diagnoses.

[0049] Molecular biomarkers would help in the detection of cervical cancer using non-invasive methods. These biomarkers will serve as detection, prognosis, or follow-up of treatment of preneoplastic lesions and cancers in early stages based on patient serum samples. Thus being able to decrease the incidence of the disease that continues to be a public health problem in many low and high income countries.

[0050] Due to all of the above, there is an urgent need to develop new and simpler disease detection methods that are applicable in early detection, specific, highly sensitive, inexpensive, and easily accessible to the population.

[0051] The methods, compositions, and kits disclosed herein may be used for the diagnosis, prognosis, and/or monitoring the status or outcome of a cancer in a subject. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer comprises determining the malignancy or malignant potential of the cancer or tumor. Alternatively, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer comprises determining the stage of the cancer. The diagnosing, predicting, and/or monitoring the status or outcome of a cancer can comprise determining the tumor grade. Alternatively, the diagnosing, predicting, and/or monitoring the status or outcome of a cancer comprises assessing the risk of developing a cancer. In some embodiments, the diagnosing, predicting, and/or monitoring the status or outcome of a

cancer includes assessing the risk of cancer recurrence. In some embodiments, diagnosing, predicting, and/or monitoring the status or outcome of a cancer may comprise determining the efficacy of treatment.

[0052] In one embodiment, the present invention is directed to methods of detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat Shock Protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-147 or a fragment thereof; and diagnosing cervical cancer based on the detection of the at least one polypeptide. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof.

[0053] As used herein, the terms “detect”, “detecting” or “detection” may describe either the general act of discovering or discerning or the specific observation of a polypeptide. Detecting may comprise determining the presence or absence of a polypeptide. Detecting may comprise quantifying a polypeptide. For example, detecting comprises determining the expression level of a polypeptide. For example, the polypeptide may comprise at least a portion of the polypeptides disclosed herein.

[0054] The polypeptides or biomarkers of the present invention can be detected by any method that can be used for the specific detection and/or identification of a protein, peptide, fragment thereof, variant thereof, or mutant thereof. Examples of method of detecting protein include, but are not limited to: spectrometry methods, such as high-performance liquid chromatography (HPLC), partition chromatography, normal-phase chromatography, displacement chromatography, reversed-phase chromatography (RPC), size-exclusion chromatography, ion-exchange chromatography, bioaffinity chromatography, aqueous normal-phase chromatography,

liquid chromatography–mass spectrometry (LC/MS); and antibody dependent or immunoassay based methods, such as enzyme-linked immunosorbent assay (ELISA), direct ELISA, sandwich ELISA, competitive ELISA, reverse ELISA, protein immunoprecipitation (direct or indirect), individual protein immunoprecipitation (IP), protein complex immunoprecipitation (Co-IP), chromatin immunoprecipitation (ChIP), RNP Immunoprecipitation (RIP), immunoelectrophoresis, western blot, and protein immunostaining. The polypeptides or biomarkers of the present invention can also be detected using protein microarrays, lateral flow assays or vertical flow assays. In certain aspects, the polypeptides or biomarkers are detected using a lateral flow assay. A lateral flow assay is typically an immunoassay either a sandwich assay or competitive assay. Typically these assays use a conjugated gold, carbon or colored latex nanoparticles. Multiplexed assays may also be performed using these methods.

[0055] As used herein, the term “subject” refers to any organisms that are screened using the diagnostic methods and treated using the treatment methods described herein. Such organisms preferably include, but are not limited to, mammals (e.g., murines, simians, equines, bovines, porcines, canines, felines, and the like), and most preferably includes humans.

[0056] The term “diagnosed,” as used herein, refers to the recognition of a disease by its signs and symptoms, or genetic analysis, pathological analysis, histological analysis, and the like. Specifically, the term refers to the diagnosis or detection of cervical cancer.

[0057] The biomarkers of the present invention serve various functions within cells.

[0058] Farnesylpyrophosphate synthase (FPPS), also known as Dimethylallyltranstransferase (DMATT) or as farnesyl diphosphate synthase (FDPS), is an enzyme that in humans is encoded by the FDPS gene and catalyzes the transformation of dimethylallylpyrophosphate (DMAPP) and isopentenyl pyrophosphate (IPP) into farnesylpyrophosphate (FPP).

[0059] Neurofibromin 1 (NF1) is a gene in humans that is located on chromosome 17. NF1 codes for neurofibromin, a GTPase-activating protein that negatively regulates RAS/MAPK pathway activity by accelerating the hydrolysis of Ras-bound GTP. NF1 has a high mutation rate and mutations in NF1 can alter cellular growth control, and neural development, resulting in neurofibromatosis type 1 (NF1, also known as von Recklinghausen syndrome).

[0060] Glyceraldehyde 3-phosphate dehydrogenase (abbreviated as GAPDH or less commonly as G3PDH) (EC 1.2.1.12) is an enzyme of ~37kDa that catalyzes the sixth step of glycolysis and thus serves to break down glucose for energy and carbon molecules. In addition to

this long established metabolic function, GAPDH has recently been implicated in several non-metabolic processes, including transcription activation, initiation of apoptosis, ER to Golgi vesicle shuttling, and fast axonal, or axoplasmic transport.

[0061] Protein 1 containing fibronectin domain type III also known as Fibronectin type III domain containing protein-1 may be an activator of G protein signaling. Protein 1 containing fibronectin domain type III is encoded by the FNDC1 gene.

[0062] Eukaryotic initiation factor 4A-I is an ATP-dependent RNA helicase which is a subunit of the eIF4F complex involved in cap recognition and is required for mRNA binding to ribosome. In the current model of translation initiation, eIF4A unwinds RNA secondary structures in the 5'-UTR of mRNAs which is necessary to allow efficient binding of the small ribosomal subunit, and subsequent scanning for the initiator codon. The protein is encoded by the EIF4A1 gene.

[0063] L-lactate dehydrogenase chain B is involved in step 1 of the subpathway that synthesizes (S)-lactate from pyruvate. The protein is encoded by the LDHB gene.

[0064] Nuclear heterogeneous Ribonucleoprotein A1, also known as heterogeneous nuclear ribonucleoprotein A1, is involved in the packaging of pre-mRNA into hnRNP particles, transport of poly(A) mRNA from the nucleus to the cytoplasm and may modulate splice site selection. May bind to specific miRNA hairpins. Binds to the IRES and thereby inhibits the translation of the apoptosis protease activating factor APAF1. Nuclear heterogeneous Ribonucleoprotein A1 is encoded by the HNRNPA1 gene.

[0065] 1-like protein 1 polycystic kidney disease, also known as polycystic kidney disease protein 1-like 1, is a component of a ciliary calcium channel that controls calcium concentration within primary cilia without affecting cytoplasmic calcium concentration. Forms a heterodimer with PKD2L1 in primary cilia and forms a calcium-permeant ciliary channel that regulates sonic hedgehog/SHH signaling and GLI2 transcription. Does not constitute the pore-forming subunit. Also involved in left/right axis specification downstream of nodal flow: forms a complex with PKD2 in cilia to facilitate flow detection in left/right patterning. Encoded by the PKD1L1 gene.

[0066] Heat Shock Protein Cognate 71 kDa is a molecular chaperone implicated in a wide variety of cellular processes, including protection of the proteome from stress, folding and transport of newly synthesized polypeptides, activation of proteolysis of misfolded proteins and the formation and dissociation of protein complexes. Plays a pivotal role in the protein quality control system, ensuring the correct folding of proteins, the re-folding of misfolded proteins and

controlling the targeting of proteins for subsequent degradation. This is achieved through cycles of ATP binding, ATP hydrolysis and ADP release, mediated by co-chaperones. The co-chaperones have been shown to not only regulate different steps of the ATPase cycle of HSP70, but they also have an individual specificity such that one co-chaperone may promote folding of a substrate while another may promote degradation. The affinity of HSP70 for polypeptides is regulated by its nucleotide bound state. In the ATP-bound form, it has a low affinity for substrate proteins. However, upon hydrolysis of the ATP to ADP, it undergoes a conformational change that increases its affinity for substrate proteins. HSP70 goes through repeated cycles of ATP hydrolysis and nucleotide exchange, which permits cycles of substrate binding and release. The HSP70-associated co-chaperones are of three types: J-domain co-chaperones HSP40s (stimulate ATPase hydrolysis by HSP70), the nucleotide exchange factors (NEF) such as BAG1/2/3 (facilitate conversion of HSP70 from the ADP-bound to the ATP-bound state thereby promoting substrate release), and the TPR domain chaperones such as HOPX and STUB1. Acts as a repressor of transcriptional activation. Inhibits the transcriptional coactivator activity of CITED1 on Smad-mediated transcription. Component of the PRP19-CDC5L complex that forms an integral part of the spliceosome and is required for activating pre-mRNA splicing. May have a scaffolding role in the spliceosome assembly as it contacts all other components of the core complex. Binds bacterial lipopolysaccharide (LPS) and mediates LPS-induced inflammatory response, including TNF secretion by monocytes. Participates in the ER-associated degradation (ERAD) quality control pathway in conjunction with J domain-containing co-chaperones and the E3 ligase STUB1. Interacts with VGF-derived peptide TLQP-21. This protein is encoded by the HSPA8 gene.

[0067] Ankyrin 3 is found in skeletal muscle and is required for costamere localization of DMD and betaDAG1 (By similarity). Membrane-cytoskeleton linker. The protein may participate in the maintenance/targeting of ion channels and cell adhesion molecules at the nodes of Ranvier and axonal initial segments. Regulates KCNA1 channel activity in function of dietary Mg^{2+} levels, and thereby contributes to the regulation of renal Mg^{2+} reabsorption. Ankyrin-3 is encoded by the ANK3 gene.

[0068] Rho 23 GTPase-activating protein, also known as Rho GTPase activating protein 23, is part of the RHO family of small GTPases which are involved in signal transduction through transmembrane receptors, and they are inactive in the GDP-bound form and active in the GTP-bound form. GTPase-activating proteins, such as ARHGAP23, inactivate RHO family proteins by

stimulating their hydrolysis of GTP. Rho GTPase-activating protein 23 is encoded by the ARHGAP23 gene.

[0069] Keratins are the major structural proteins in epithelial cells, forming a cytoplasmic network of 10 to 12 nm wide intermediate filaments and creating a scaffold that gives cells the ability to withstand mechanical and non-mechanical stresses. There are two types of cytoskeletal and microfibrillar keratin, I (acidic) and II (neutral to basic), i.e. Cytoskeletal Keratin 78 type II, also known as keratin, type II cytoskeletal 78. Cytoskeletal keratin 78 type II is encoded by the KRT78 gene.

[0070] Alpha 3 collagen chain (VI), also known as collagen alpha-3 (VI) chain, acts as a cell-binding protein. Collagen alpha-3(VI) chain is encoded by the COL6A3 gene.

[0071] Beta subunit of proteasome type-5, also known as Proteasome subunit beta type-5 and 20S proteasome subunit beta-5 is a protein that in humans is encoded by the PSMB5 gene. This protein is one of the 17 essential subunits (alpha subunits 1–7, constitutive beta subunits 1–7, and inducible subunits including beta1i, beta2i, beta5i) that contributes to the complete assembly of 20S proteasome complex. In particular, proteasome subunit beta type-5, along with other beta subunits, assemble into two heptameric rings and subsequently a proteolytic chamber for substrate degradation. This protein contains "chymotrypsin-like" activity and is capable of cleaving after large hydrophobic residues of peptide. The eukaryotic proteasome recognized degradable proteins, including damaged proteins for protein quality control purpose or key regulatory protein components for dynamic biological processes. An essential function of a modified proteasome, the immunoproteasome, is the processing of class I MHC peptides. Beta subunit of proteasome type - 5 is encoded by the PSMB5 gene.

[0072] Heterogeneous nuclear ribonucleoprotein (hnRNP) that associates with nascent pre-mRNAs, packaging them into hnRNP particles. The hnRNP particle arrangement on nascent hnRNA is non-random and sequence-dependent and serves to condense and stabilize the transcripts and minimize tangling and knotting. Packaging plays a role in various processes such as transcription, pre-mRNA processing, RNA nuclear export, subcellular location, mRNA translation and stability of mature mRNAs. Forms hnRNP particles with at least 20 other different hnRNP and heterogeneous nuclear RNA in the nucleus. Involved in transport of specific mRNAs to the cytoplasm in oligodendrocytes and neurons: acts by specifically recognizing and binding the A2RE (21 nucleotide hnRNP A2 response element) or the A2RE11 (derivative 11 nucleotide

oligonucleotide) sequence motifs present on some mRNAs, and promotes their transport to the cytoplasm. Specifically binds single-stranded telomeric DNA sequences, protecting telomeric DNA repeat against endonuclease digestion (By similarity). Also binds other RNA molecules, such as primary miRNA (pri-miRNAs): acts as a nuclear 'reader' of the N6-methyladenosine (m6A) mark by specifically recognizing and binding a subset of nuclear m6A-containing pri-miRNAs. Binding to m6A-containing pri-miRNAs promotes pri-miRNA processing by enhancing binding of DGCR8 to pri-miRNA transcripts. Involved in miRNA sorting into exosomes following sumoylation, possibly by binding (m6A)-containing pre-miRNAs. Acts as a regulator of efficiency of mRNA splicing, possibly by binding to m6A-containing pre-mRNAs. Plays also a role in the activation of the innate immune response. Mechanistically, senses the presence of viral DNA in the nucleus, homodimerizes and is demethylated by JMJD6. In turn, translocates to the cytoplasm where it activates the TBK1-IRF3 pathway, leading to interferon alpha/beta production. Heterogeneous nuclear ribonucleoproteins A2/B1 is a protein that in humans is encoded by the HNRNPA2B1 gene.

[0073] Histone H2B type 1-B is a core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling. Histone H2B type 1-B is encoded by the H2BC3 gene.

[0074] Homolog of DnaJ subfamily C member 13, also known as DnaJ homolog subfamily C member 13, is involved in membrane trafficking through early endosomes, such as the early endosome to recycling endosome transport implicated in the recycling of transferrin and the early endosome to late endosome transport implicated in degradation of EGF and EGFR. Involved in the regulation of endosomal membrane tubulation and regulates the dynamics of SNX1 on the endosomal membrane; via association with WASHC2 may link the WASH complex to the retromer SNX-BAR subcomplex. DnaJ homolog subfamily member 13 is encoded by the DNAJC13 gene.

[0075] Enolase 3 (ENO3), more commonly known as beta-enolase (ENO- β), is an enzyme that in humans is encoded by the ENO3 gene. This gene encodes one of the three enolase isoenzymes found in mammals. This isoenzyme is found in skeletal muscle cells in the adult where it may play

a role in muscle development and regeneration. A switch from alpha enolase to beta enolase occurs in muscle tissue during development in rodents. Mutations in this gene have been associated with glycogen storage disease. Alternatively spliced transcript variants encoding different isoforms have been described.

[0076] Glutathione S-transferases (GSTs) are a family of enzymes that play an important role in detoxification by catalyzing the conjugation of many hydrophobic and electrophilic compounds with reduced glutathione. Based on their biochemical, immunologic, and structural properties, the soluble GSTs are categorized into four main classes: alpha, mu, pi, and theta. The glutathione S-transferase pi gene (GSTP1) is a polymorphic gene encoding active, functionally different GSTP1 variant proteins that are thought to function in xenobiotic metabolism and play a role in susceptibility to cancer, and other diseases. Glutathione S-transferase P is an enzyme that in humans is encoded by the GSTP1 gene.

[0077] Glutathione S-transferase Mu 3 may govern uptake and detoxification of both endogenous compounds and xenobiotics at the testis and brain blood barriers. Glutathione S-transferase Mu 3 is encoded by the GSTM3 gene.

[0078] The amino acid sequences for the biomarkers of the present invention and variants thereof are shown in Table 1.

Table 1

Protein name /SEQ ID NO.	Amino acid sequence
Farnesyl pyrophosphate synthase (FDPS) SEQ ID NO:1	MPLSRWLRSVGVFLLPAPYWAPRRRWLGSRLRPSLVHGYPVLAW HSARCWCQAWTEEPALCSSLRMNGDQNSDVYAQEKQDFVQHFS QIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVA FRELVEPRKQDADSLQRAWTVGWCVELLQAFFLVADDIMDSSLTR RGQICWYQKPGVGLDAINDANLLEACIYRLKLKYCREQPYLNLIE LFLQSSYQTEIGQTLDLLTAPQGNVDLVRFTKRYKSIVKYKTAFY SFYLPAAAAMYMAGIDGEEKHANAKKILLEMGEFFQIQDDYDLDF GDPSVTGKIGTDIQDNKCSWLVVQCLQRATPEQYQILKENYQKE AEKVARVKALYEELDLPAVFLQYEEDSYSHIMALIEQYAAPLPPAV FLGLARKIYKRRK
Neurofibromin 1 (NF1) SEQ ID NO:2	MAAHRPVEWVQAVVSRFDEQLPIKTGQQNTHTKVSTEHNKECLIN ISKYKFSLVISGLTTILKNVNNMRIFGEAAEKNLYLSQLILDLEK LAGQPKDTMRLDETMLVKQLLPEICHLHTCREGNQHAELRNSA SGVLFSLSCNNFNAVFSRISTRLQELTVCSNVDVHDIELLYQINV DCAKLKRLKETAFAFKALKKVAQLAVINSLEKAFWNWVENYPD EFTKLYQIPQTDMAECAEKLFDLVDGFAESTKRKAADVWPLQILLI LCPEIIQDISKDVVDENNMNKKLFLDSLRLKALAGHGGSRQLTESAA IACVKLCKASTYINWEDNSVIFLLVQSMVVDLKNLLFNPSKPFSSRG SQPADVDLMIDCLVSCFRISPHNNQHFQICLAQNSPSTFHYVLVNS LHRIITNSALDWPKIDAVYCHSVELRNMFGETLHKAVQCGGAHP AIRMAPSLTFKEKVTSLKFKEKPTDLETRSYKYLLLSMVKLIHADP

	<p> KLLLCNPRKQGPETQGSTAELITGLVQLVPQSHMPEIAQEAMEALL VLHQLDSIDLWNPDAVETFWISSQMLFYICKKLTSHQMLSSTEIL KWLREILICRNKFLKKNKQADRSSCHFLLFYGVGCDIPSSGNTSQM SMDHEELLRTPGASLRKKGKGNSSMDSAAGCSGTPPICRQAQTKLE VALYMFLWNPDEAVLVAMSCFRHLCEEADIRCGVDEVSVHNLL PNYNTFMEFASVSNNMMSTGRAALQKRVMMALLRRIEHPTAGNTEA WEDTHAKWEQATKLILNYPKAKMEDGQAAESLHKITVKKRMSHV SGGGSIDLSDTDSLQEWINMTGFLCALGGVCLQQRSNSGLATYSPP MGPVSEKSGSMISVMSSEGNADTPVSKFMDRLLSLMVCNHEKVG LQIRTNVKDLVGLELSPALYPMLFNKLNKNTISKFFDSQGVLLTDT NTQFVEQTIAIMKNLLDNHTEGSSEHLGQASITMMLNLVRYVRV LGNMVHAIQIKTKLCQLVEVMMARRDDLSFCQEMKFRNKMVEYL TDWVMGTSNQAADDDVKCLTRDLQASMEAVVSLLAGLPLQPEE GDGVELMEAKSQLFLKYFTLFMNLNDCSEVEDESAQTGGRKRG MSRRLASLRHCTVLAMSNLLNANVDSGLMHISGLGYHKDLQTRA TFMEVLTKILQQGTEFDTLAETVLADRFERLVELVTMMGDQGELPI AMALANVVPSCSQWDELARVLVTLFDSRHLLYQLLWNMFKEVEL ADSMQTLFRGNLASKIMTFCFKVYGATYLOKLLDPLLRIVITSSD WQHVSFEVDPTRLEPSESLEENQRNLLQMTKEFFHAISSSEFPQ LRSVCHCLYQATCHSLNKAIVKEKKENKKS SVVSQRFPQNSIGAV GSAMFLRFINPAIVSPYEAGILDKKPPPRIERGLKLSKILQSIANHV LFTKEEHMRPFNDFVKSNFDAARRFFLDIASDCPTSDAVNHSLSFIS DGNVLALHRLWNQEKIGQYLSSNRDHKA VGRPFDKMATLLA YLGPPEHKPVADTHWSSLNLTSSKFEFMRTHQVHEKEEFKALKT LSIFYQAGTSKAGNPIFYVARRFKTGQINGDLLIYHVLTKPYY AKPYEIVVDLTHTGPSNRFKTDFLSKWFVVPFGFAYDNVSAVYIY NCNSWVREYTKYHERLLTGLKGSKRLVFIDCPGKLAEHIEHEQQK LPAATLAL EEDLKV FHNALKLAHKDTKVSIVKGSTAVQVTS AERT KVLGQSVFLNDIYYASEIEEICLV DENQFTLTIANQGTPLTFMHQEC EAIVQSIHIRTRELWELSQPDSIPQHTKIRPKDVP GTLLNIALNLGSSD PSLRSAAYNLLCALTCTFNKIEGQLLETSGLCIPANNLTFIVSISK LAANEPHLTLEFLEECISGFSKSSIELKHLCLEYMTWPWLSNLVRFC HNDDAKRQRTAILDKLITMTINEKQMYPSIQAKIWGSLGQITDLL DVVLDSFIKTSATGGLGSIKAEVMADTAVALASGNVVLVSSKVG RMCKIIDKTCLSPPTLEQHLMWDDIAILARYMLMLSFNNSLDVA AHLPYLFHVVTFLVATGPLSLRASTHGLVINIHSCTCSQLHFSEET KQVLRSLTEFSLPKFYLLFGISKVKSAAVIAFRSSYRDRSFSPGSYE RETFALTSLETVTEALLEIMEACMRDIPTCKWLDQWTELAQRFAF QYNPSLQPRALVFGCISKRVSHGQIKQIIRILSKALESCLKGPDY NSQVLIEATVIALTKLQPLLNKDSPLHKALFWVAVAVLQLDEVNL YSAGTALLEQNLHTLDSLRFNDKSP EEFVMAIRNPLEWHCKQMD HFVGLNFNSNFALVGHLLKGYRHPSAIVARTVRILHTLLTLVN KHRNCDKFEVNTQSVAYLAALLTVSEEVRSRCSLKHKRSLLLTDIS MENVPMDTYPIHHGDPSTYRTLKETQPWSSPKGSEGYLAATYPTVG QTSRARKSMSLDMGQPSQANTKKLLGTRKSFHLSIDTKAPKRQ EMESGITTPPKMRRVAETDYEMETQRISSSQQPHLRKVS VSES NV LLDEEVLTDPKIQALLTVLATLVKYTTDEFDQRILEYLA EASV V FPKVFPVVHNLLDSKINTLLSLCQDPNLLNPIHGIVQSVVYHEESPP QYQTSYLSQSGFNGLWRFAGPFSKQTQIPDYAELIVKFLDALIDTY LPGIDEETSEESLLTPTSPYPPALQSQLSITANLNSNMTSLATSQH SPGIDKENVELSPTTGHCNSGRTRHGSASQVQKQRSAGSFKRNSIK KIV </p>
Glyceraldehyde-3 phosphate dehydrogenase (GAPDH)	<p> MGKVKVG VNGFGRIGRLVTRAAFNSGKVDIVAINDPFIDLNYMVY MFQYDSTHGKFHGTVKAENGKLVINGNPITIFQERDPSKIKWGDA GA EYVVESTGVFTTMEKAGAH LQGGAKRVIISAPSADAPMFVMG </p>

SEQ ID NO:3	VNHEKYDNSLKIISNASCTTNCLAPLAKVIHDNFGIVEGLMTTVHA ITATQKTVDPGSGKLWRDGRGALQNIIPASTGAAKAVGKVIPELNG KLTGMAFRVPTANVSVDLTCRLEKPAKYDDIKKVVKQASEGPL KGILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVKLISWYDN EFGYSNRVVDLMAHMASKE
Protein 1 containing fibronectin domain type III or Fibronectin Type III Domain Containing protein 1 (FNDC1) SEQ ID NO:4	MAPEAGATLRAPRRLSWAALLLLAALLPVASSAAASVDHPLKPRH VKLLSTKMGLKVTWDPPKDATSRPVEHYNIAYGKSLKSLYIKVN AETYSFLIEDVEPGVVYFVLLTAENHSGVSRPVYRAESPPGGEWIEI DGFPIKGPFPNETVTEKEVPNKPLRVVRSSDDRLSVAWKAPRLS GAKSPRRSRGFLGYGESGRKMNYVPLTRDERTHEIKKLASESVY VVSLSQSMNSQGRSQPVYRAALTKRKISEEDELDPDDISVRVMSS QSVLVSWVDPVLEKQKKVVASRQYTVRYREKGEARWDYKQIA NRRVLIENLIPDVTVEFAVRISQGERDGKWSTSVFQRTPEAPTAP ENLNVWPVNGKPTVVAASWDALPETEGKVKEYILSYAPALKPFG AKSLTYPGDTTSALVDGLQPGERYLFKIRATNRRGLGPHSKAFIVA MPTTSKADVEQNTEDNGKPEKPEPSSPSRAPASSQHPSVPASPQG RNAKDLLLDLKNKILANGGAPRKPLRAKKAEELDLQSTEITGEEE LGSREDSMSPSDTQDQKRTLPPSRHGHSSVAPGRTAVRARMPA LPRREGVDKPGFSLATQPRPGAPPSASASPAHHASTQGTSHRPSLP ASLNDNDLVDSDEDERAVGSLHPKGAFAPQRPALSPSRQSPSSVLR DRSSVHPGAKPASPARRTPHSGAAEEDSSASAPPSRLSPPHGGSSRL LPTQPHLSSPLSKGGKDGEDAPATNSNAPSRSTMSSSVSSHLSRTQ VSEGAESDGEHGDGDREDGGRQAEATAQTLRARPASGHFHL RHKPFAANGRSPSRFSIGRGPRLQPSSSPQSTVPSRAHPRVPSHDS HPKLSSGIHGDEEDEKPLPATVVNDHVPSSSRQPIRSGWEDLRSP QRGASLHRKEPIPENPKSTGADTHPQGKYSSLASKAQDVQQSTDA DTEGHSPKAQPGSTDRHASPARPPAARSQQHPSVPRRMTPGRAPQ QQPPPPVATSQHHPGPQSRDAGRSPSQPRLSLTQAGRPRPTSQGRS HSSSDPYTASSRGMLPTALQNQDEDAQGSYDDSTEVEAQDVRA AHAARAKEAAASLPKHQQVESPTGAGAGGDHRSQRGHAAASPARP SRPGGPQSRARVPSRAAPGKSEPPSKRPLSSKSQQSVSAEDDEED AGFFKGGKEDLLSSSVPKWPSSSTPRGGKDADGSLAKEEREPAIAL APRGGSLAPVKRPLPPPGSSPRASHVPSRLPPRSAATVSPVAGTHP WPQYTTRAPPGHFSTTPMLSLRQRMHARFRNPLSRQPARPSYRQ GYNGRPNVEGKVLPGSNGKPNGQRIINGPQGTKVWVDLDRGLVL NAEGRYLQDSHGNPLRIKLG DGRTIVDLEGTVPVSDGLPLFGQG RHGTPLANAQDKPILSLGGKPLVGLEVIKKTTHPPTTTMQPTTTTT LPTTTTPRPTTATRRTTTTTRRTTTRRPTTTVTRTTTPTPTTT PIPTCPPGTLEHDDDGNLIMSSNGIPECYAEDEFSGLETDTAVPT EEAYVIYDEDEYEFETSRPPTTTEPSTTATTPRVIEEGAISFPEEFD LAGRKRFBVAPYVTYLNKDPSAPCSLTDALDHFQVDSLDEIIPNDLK KSDLPPQHAPRNITVVAVEGCHSFVVDWDKATPGDVVTGYLVYS ASYEDFIRNKWSTQASSVTHLPIENLKPNTTRYFYFVQAQNPBGY PISPSVSFVTESDNPLL VVRPPGGEPIWIPFAFKHDPSTYDCHGRQY VKRTWYRKFBVGVLCNSLRYKIYLSNLDKDTFYSIGDSWGRGED HCQFVDSHLDGRTGPQSYVEALPTIQGYRQYRQEPVRFNGIFGT PYYYVGWYECGVSIPGKW
Eukaryotic initiation factor 4A-I (EIF4A1) SEQ ID NO:5	MSASQDSRSRDNGPDGMEPEGVIESNWNIEVDSFDDMNLSESLR GIYAYGFEPKSAIQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQ IELDLKATQALVLAPTRELAQQIQKVMALGDYMGASCHACIGGT NVRAEVQKLQMEAPHIIVGTGRVFDMLNRRYLSPKYIKMFVLDE ADEMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLEVTKKFM RDPILIRLKKKEELTLEGIRQFYINVEREEWKDLTCLDLYETLTITQA VIFINTRRKVDWLTEKMHARDFTVSAMHGDMDQKERDVIMREFR

	SGSSRLITTDLLARGIDVQQVSLVINYLPTNRENYIHRIGRGGRF GRKGVAINMVTEEDKRTLRLDIETFYNTSIEEMPLNVADLI
L-lactate dehydrogenase chain B (LDHB) SEQ ID NO:6	MATLKEKLIAPVAEEEEATVPNNKITVVGVGQVGMACAISILGKSLA DELALVDVLEDKLGEMMDLQHGSFLQTPKIVADKDYSVTANS KIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVVS NPVDILTYVTWKLKSLPKHRVIGSGCNLDSARFRLMAEKLGIHPS SCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNSEN WKEVHKMVVESAYEVIKLGKGTNWAIGLSVADLIESMLKNLSRIH PVSTMVKGMYGIENEVFLSLPCILNARGLTSVINQKLKDDEVAQLK KSADTLWDIQDKDL
Nuclear heterogeneous Ribonucleoprotein A1 (HNRNPA1) SEQ ID NO:7	MSKSESPKEPEQLRKLFIGGLSFETTDSELRSHFEQWGTLTDCVVM RDPNTRSRGFGFVYATVEEVDAAAMNARPHKVDGRVVEPKRAV SREDSQRPGAHLTVKKIFVGGIKEDTEHHLRDYFEQYQKIEVIEIM TDRGSGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNCEVRKALS KQEMASASSSQGRSGSGNFGGGRGGGFGGNDNFGRGGNFSGRG GFGGSRGGGGYGGSGDGYNGFGNDGGYGGGGPGYSGGSRGYGS GGQGYGNQGSYGGSGSYDSYNNGGGGGFGGSGSGNFGGGGSY NDFGNYNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGG YGGSSSSSYGSGRRF
Polycystic kidney disease protein 1- like 1 (PKD1L1) SEQ ID NO:8	MAEEAAQNISDDQERCLQAACCLSFGGELSVSTDKSWGLHLCSCS PPGGGLWVEVYANHVLLMSDGKCGCPWCALNGKAEDRESQSPSS SASRQKNIWKTTEAALSVMNEKTQAVVNEKTQAPLDCQNTSADRI PHKPFIIARAWSSGGPRFHHRRRLCATGTADSTFSALLQLCGTSDAA APCSLKMEASCCVLRLLCCAEDVATGLLPGTVMETPTKVARPTQ TSSQRVPLWPISHFPTSPRSSHGLPPGIPRTPSFTASQSGSEILYPPTQ HPPVAILARNSDNFMNPVLNCSLEVEARAPPNLGFRVHMASGEAL CLMMDFGDSSGVEMRLHNMSEAMAVTAYHQYSKGIFFHLLHFQL DMSTYKEAETQNTTLNVYLCQSENSCLESDSPSNLYELISAFVTK GVYMLKAVIYNFHFHTEVELGPYYVEIGHEAVSAFMNSSSVHDE VLVFADSQVNQKSTVVIHHFSPISYNVSFISQTVQVGDQAWHSM VWYKMQSVSVYTNGTVFATDITFTAVTKETIPLEFEWYFGEDP PVRTTSRISIKRLSIPQWYRVMVKASNRMSVSEPHVIRVQKKIV ANRLTSPSSALVNASVAFECWINFGTDVAYLWDFGDTVSLGSSS SSHVYSREGEFTVEVLAFFNNVSASTLRQQLFIVCEPCQPPLVKNMG PGKVQIWRSPVRLGVTFAAVFCDISQGLSYTNWLMDSGGLPVS LPAAVDTHRQTLILPSHTLEYGNYTALAKVQIEGSVVYSNYCVGLE VRAQAPVSVISEGTHLFFSRTTSSPIVLRGTQSFDPDDPGATLRYHW ECATAGSPAHPCFDSSTAHLDAAPTVSFEAQWLSDSYDQFLVM LRVSSGGRNSSETRVFLSPYPDSAFRFVHISWVSFKDTFVNWNDEL SLQAMCEDCSEIPNLSYSWDLFLVNATEKNRIEVPFCRVVGLLGLS GLGAISESSQLNLLPTEPGTADPDATTPFSREPSPTLGGPATSA GTPTEPMTGVYWIPAGDSAVLGEAPEEGSLDLEPGPQSKGSLMT GRSERSQPTHSPDPLSDFEAYYSIQEAIPSGGGRQPAKDTSFPGSG PSLSAEESPGDGDNLVDPSLSAGRAEPVLMIDWPKALLGRAVFQ YSSSGITEQVTIKPYSLSSGETYVLQVSVASKHGLLGKAQLYLT NPAPRDMACQVQPHHGLEAHTVFSVFCMSGKPDFHYEFSYQIGN SKHTLYHGRDTQYYFVLPAGEHLDNYKVMVSTEITDGKSKVQP CTVVVTVLPYHGNDCLEDLYNSSLKNLSTLQLMGYSYTEIRNYIT VITRILSRLSKEDKTASCNQWSRIQDALISSVCRLAFVDQEEMIGSV LMLRDLVSFSNKLGFMSAVLILKYTRALLAQGQFSGPFVIDKGVR ELIGLISRVWEVSEQENSKEEVYRHEEGITVISDLLLGCLSLNHVST GQMEFRTLLHYNLQSSVQSLGVSQVHLPGLAGHSPAGAETQSPC YISQLILFKKNPYPGSQAPGQIGGVVGLNLYTCSSRRPINRWLRKP

	<p>VMVEFGGEDGLDNRNKTTFVLLRDKVNLHQFTELSNPQESLQIE IEFSEKPVTRAFPVMLLVRFSEKPTPSDFLVKQIYFWDESIVQIYIPAA SQKDASVGYLSLLDADYDRKPPNRYLAKAVNYTVHFQWIRCLFW DKREWKSERFSPQPGTSPEKVNCSYHRLAAFALLRRKLKASFEVS DISKLQSHPENLLPSIFIMGSVILYGFVAKSRQVDHHEKKKAGYIF LQEASLPGHQLYAVVIDTGFRAPARLTSKVYIVLCGDNGLSETKEL SCPEKPLFERNRHTFILSAPAQLGLLRKIRLWHD SRGPSPGW FISH VMVKELHTGQGWFFPAQCWLSAGRHDGRVERELTCLQGGLGFR KLFYCKFTEYLEDFHVWLSVYSRPSSRYLHTPRLTVSFSLLCVYA CLTALVAAGGQEQPHLDVSPTLGSFRVGLLCTLLASPGAQLLSLLF RLSKEAPGSARVEPHSPLRGGAQTEAPHGPNSWGRIQDAQEPRKQP ASAILSGSGRAQRKAASDNGTACPAKQLQVHGADHSRTSLMGKSH CCPHQTAPSSGLEGLMPQWSRALQPWWSSAVWAICGTASLACSL GTGFLAYRFGQEQCVQWLHLLSLSVCCIFITQPLMVCLMALGFA WKRRADNHFFTESLCEATRDLDSELAERSWTRLPFSSSCSIPDCAG EVEKVLAAARQQARHLRWAHPPSKAQLRGTRQRMRESRTRAALR DISMDILMLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGL RNIADWWDWSLTLLDGLYPGGTSPARVPGAQPGALGKCYLIGS SVIRQLKVFPRLCKPPRPFSAIEDSIPTCSPEVGGPENPYLIDPEN QNVTLNGPGGCGTREDCVLSLGRTRTEAHTALSRLRASMWIDRST RAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIFRSDS ALQYHMLPQLVFLALSLIHL CVQLYRMMDKGVL SYWRKPRNWL EL SVVGVSLTY AVSGHL VTLAGDVTNQFHRGLCRAFMDLTLMA SWNQRARWLRGILLFLTLKCVYLPGIQNTMASCSSMMRHSLSIF VAGLVGALMLAALSHLHRFLSMWVLPPTFTDAFPGLLFHPPRR SQKDCLLGLSKSDQRAMACYFGILLIVSATLCFGMLRGFLMTLPQ KRKSQSKSFVRLKDVTA YMWKVL TFLRLETPKLEEAEMVENH NYYLDEFANLLDELLMKINGLSDSLQLPLEKTSNNTGEARTEESP LVDISSYQAAEPADIKDF</p>
<p>Cognate thermal shock protein 71 kDa or heat shock protein cognate 71 kDa (HSPA8) SEQ ID NO:9</p>	<p>MSKGAVIDGLGTTYSVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFD AKRLIGRRFDDA VVQSDMKH WPFMVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNVAVTVPAYFNDSQRQATKDA GTIAGLNVLRINEPTA AAIAYGLDKKVGAEARNVLIFDLGGGTDFVSILTIEDGIFEVKSTAGD THLGGEDFDNRMVNHFAIEFKRKHKDISENKRAVRLRTACERA KRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVE KALRDAKLDKSIHDI VLVGGSTRIPKIQKLLQDFNGKELNKSINP DEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVM TVLIKRNNTIPTKTQTFTTYSQDNQPGVLIQVYEGERAMTKDNNLL GKFEITGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITIT NDKGRLSKEDIERMVQEA EKYKAEDEKQRDKVSSKNSLESYAFN MKATVEDEKLQGKINDEKQKILDKCNEIINWLDKNQTAEEKEEFE HQQKELEKVCNPIITKLYQSAGGMPGGMPPGGFPGGAPSGGASS GPTIEEVD</p>
<p>Anikirina-3 or Ankyrin-3 (ANK3) SEQ ID NO:10</p>	<p>MAHAASQLKKNRDLEINAE EEPKRRKHKRKS RDRKKKSDANAS YLRAARAGHLEKALDYIKNGVDINICNQNLNALHLASKEGHVEV VSELLQREANVDAATKKGN TALHIASLAGQAEVVKVLVTNGANV NAQSQNGFTPLYMAAQENHLEVVKFLLDNGASQSLATEDGFTPLA VALQQGHDQVVSLLLENDTKGKVRLPALHIAARKDDTKAAALLL QNDNNADVESKSGFTPLHIAAHYG NIN VATLLLNRAAAVDFTARN DITPLHVASKRGNANMVKLLDRGAKIDAKTRDGLTPLHCGARSG HEQVVEMLLDRAAPILSKTKNGLSPLHMA TQGDHLNVCVQLLLQH NVPVDDVTNDYLTALHVA AHCGHYKVAKVLLDKKANPNKALN GFTPLHIACKKNRIKVMELLLKHGASIQAVTESGLTPIHVA AFMGH</p>

	<p> VNIVSQLMHHGASPNTTNVRGETALHMAARSGQAEVVRYLVQDG AQVEAKAKDDQTPLHISARLGKADIVQQLLQQGASPNAATTSGYT PLHLSAREGHEDVAAFLLDHGASLSITTKKGFTPLHVAAKYGKLE VANLLLQKSASPDAAGKSGLTPLHVAAHYDNQKVALLLLDQGAS PHAAAKNGYTPLHIAAKKNQMDIATTLLEYGADANAVTRQGIASV HLAAQEGHVDMSVLLGRNANVNLSNKSGLTPLHLAAQEDRVNV AEVLVNQGAHVDAQTKMGYTPLHVGCHYGNIKIVNFLQHSKAV NAKTKNGYTPLHQAAQQGHTHIINVLLQNNASPNETLVNGNTALG IARRLGYSVVDTLKIVTEETMTTTTVTEKHKMNVPETMNEVLDM SDDEVKANAPEMLSDGEYISDVEEGEDAMTGDTDKYLGPQDLK ELGDDSLPAEGYMGFSLGARSASLSRFSDDRSYTLNRSSYARDSM MIEELLVPSKEQHLTFTREFDSDSLRHYSWAADTLDNVNLVSSPIH SGFLVSFMDARGGSMRGRHHGMRIIPPRKCTAPTRITCRLVKR HKLANPPPMVEGEGLASRLVEMGPAGAQLGPVIVEIPHFGSMRG KERELIVLRSENGETWKEHQFDSKNEDLTELNGMDEELDSPEELG KKRICRIITKDFPQYFVAVVSRIKQESNQIGPEGGILSSTTVPLVQASFP EGALTKRIRVGLQAQVPDEIVKKILGNKATFSPIVTVEPRRRKFHK PITMTIPVPPPSGEGVSNGYKGDTPNLRLLCSITGGTSPAQWEDIT GTTPLTFIKDCVSFTTNVSARFWLADCHQVLETVGLATQLYRELIC VPYMAKFVVFAMNDPVESSLRCFCMTDDKVDKTLEQQENFEEV ARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPF SIKIRDTSQEPGRLSFLKEPKTTKGLPQTAVCNLNTLPAHKKETE SDQDDEIEKTDRRQSFASLALRKRYSYLTPGMIERSTGATRSLPTT YSYKPPFSTRPYQSWTTAPITVGPAGSGFTSLSSSSNTPSASPLKS IWSVSTPSPIKSTLGASTTSSVKSISDVASPIRSFRTMSSPIKTVVSQS PYNIQVSSGTLARAPAVTEATPLKGLASNSTFSSRTSPVTTAGSLLE RSSITMTPPASPKSNINMYSSSLPFSIITSAAPLISSPLKSVVSPVKS AVDVISSAKITMASSLSPPVKQMPGHAVALVNGSISPLKYPSSSTL INGCKATATLQEKISSATNSVSSVSAATDTEKVFSTTTAMPFSP RSYVSAAPSAFQSLRTPSASALYTSLGSSISATTSSTVTSIITVPVYSV VNVLEPALKKLPDSNSFTKSAALLSPIKTLTTETHPQPHFSRTSSP VKSSLFLAPSALKLSTPSSLSSSQEILKDVAEMKEDLMRMTAILQTD VPEEKPFQPELPKEGRIDDEEPFKIVEKVKEDLVKVEILKKDVCVD NKGSPKSPKSDKGHSPEDDWIEFSSEEIREARQQAASQSPSPERV QVKAKAASEKDYNLTKVIDYLTNDIGSSSLTNLKYKFEDAKKDGE ERQKRVLKPAIALQEHKLMPPASMRSTSEKELCKMADSFSGTD TILESPDDFSQHDQDKSPLSDSGFETRSEKTPSAPQSAESTGPKPLFH EVPIPPVITETRTEVVHVIRSYDPSAGDVPQTQPEEPVSPKPSPTFME LEPKPTTSSIKEKVKAFQMKASSEDDHNRVLSKGMRVKEETHITT TTRMVYHSPPGGEGASERIEETMSVHDIMKAFQSGRDPSELAGLF EHKSAVSPDVHKSAEETSAQHAEKDNQMKPKLERIIEVHIEKGNQ AEPTVIRETKKHPEKEMYVYQKDLSRGDINLKDFLPEKHDAFPC SEEQQQEEEEELTAEESLPSYLESSRVNTPVSQEEDSRPSSAQLISD DSYKTLKLLSQHSIEYHDDDELSELRGESYRFAEKMLLSEKLDVSHS DTEESVTDHAGPPSSELQGS DKRSREKIATAPKKEILSKIYKDVSEN GVGKVS KDEHFDKVTVLHYS GNVSSPKHAMWMRFTEDRLDRGR EKLIYEDRVDRTVKEAEEKL TEVSQFFRDKTEKLNDELQSPEKKAR PKNGKEYSSQSPTSSSPEKVLLTELLASNDEWVKARQHGPDPGQGF PKAEEKAPSLPSSPEK MVL SQQTEDSKSTVEAKGSISQSKAPDGPQ SGFQLKQSKLSSIRLKFEQGTHAKSKDMSQEDRKSDGQSRIPVKKI QESKLPVYQVFAREKQQAIDLPDES VSVQKDFMVLKTKDEHAQS NEIVVNDSGSDNVKKQRTEMSSKAMPDSFSEQQAKDLACHITSDL ATRGPWDKKVFRTWESSGATNNKSQKEKLSHVLVHDVRENHIGH PESKSVDQKNEFMSVTERERKLLTNGSLSEIKEMTVKSPSKKVLYR EYVVKEGDHPGGLLDQPSRRSESAVSHIPVRVADERRMLSSNIPD GFCEQSAFPKHELSQLSQSSMSKETVETQHFNSIEDEKVTYSEISK </p>
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	<p>VSKHQSYVGLCPPLEETETSPTKSPDSLEFSPGKESPSSDVFHDSPID GLEKLAPLAQTEGGKEIKTLPVYVSFVQVGKQYEKEIQQGGVKKII SQUECKTVQETRGTFTYTTROQKQPPSPQGSPEDDTLEQVSFLDSSGK SPLTPETPSSEEVSYEFTSKTPDLSLIAIYPGKPSPIPEVSESEEEEEQA KSTSLKQTTVEETAVEREMPNDVSKDSNQRPKNNRVAYIEFP PPPP LDADQIESDKKHHYLPEKEVDMIEVNLQDEHDKYQLAEPVIRVQP PSPVPPGADVSDSSDDESIYQVPVKKYTFKLKEVDDEQKEKPKAS AEKASNQKELESNGSGKDNEFGLGLDSPQNEIAQNGNNDQSITECS IATTAEFSHDTDATEDSLDGYDLQDEDDGLTESDSKLPQAMEIKK DIWNTEGILKPADRSFSQSKLEVIEEEGKVGPDDEKPPSKSSSSEKT PDKTDQKSGAQFFTLGRHPDRSVFPDITYFSYKVDEEFATPFKTV TKGLDFDPWSNNRGDDEVFDSKSREDETKPFGLAVEDRSPATTPD TTPARTPTDESTPTSEPNPFPFHEGKMFEMTRSGAIDMSKRDFVEE RLQFFQIGEHTSEGKSGDQGEQDKSMVTATPQPQSGDITVETNLE RNVETPTVEPNPSIPTSGECQEGTSSSGSLEKSAAATNTSKVDPKLR TPIKMGISASTMTMKKEGPGEITDKIEAVMTSCQGLENETITMISNT ANSQMGVRPHEKHDFQKDNFNNNNNLDSSITQTDNIMSNIVLTEH SAPTCTTEKDNPVKVSSGKKTGVLQGHCVRDQKQVLGEQKQTKKE LIGIRQKSKLPIKATSPKDTFPPNHMSNTKASKMKQVSQSEKTKAL TTSSCVDVKSRIPVKNTHRDNIIVRKACATQKQGGQPEKGAKQL PSKLPVKVRSTCVTTTTTTATTTTTTTTTTTTCTVKVRKSQLKEV CKHSIEYFKGISGETLKLVDRLSEEEKKMQSELDEEEESTSRNTSL ETSRGGQPSVTTKSARDKKTEAAPLKSSEKAGSEKRSSRRTPGQS PCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNFLIS QSFMLLKKWVTRDGKNATTDALTSVLTKNRIVTLLEGPIFDYD NISGTRSFADENNVFHDVPDVGWQNETSSGNLESCAARRVTGGLL DRLDDSPDQCRDSITSYLKGEAGKFEANGSHTTEITPEAKTKSYFPES QNDVGKQSTKETLKPKEHSGHVEEPASPLAAYQKSLEETSKLIIEE TKPCVPVSMKKMSRTSPADGKPRLSLHEEEGSSGSEQKQGEFGKV KTKKEIRHVEKKSHS</p>
<p>Rho 23 or Rho GTPase-activating protein 23 (ARHGAP23) SEQ ID NO:11</p>	<p>MNGVAFCLVGIIPRPEPRPPQLPLGPRDGCSPRRPFPWQGPRTLL YKSPQDGFGLTLRHFIYPPESA VHC SLKEEENGGRGGGPSRYRL EPMDTIFVKNVEDGPAHRAGLRTGDRLVKVNGESVIGKTYSQVI ALIQNSDDTLELSIMPKDEDILQLAYSQDAYLKGNEPYSGEARSIP PPICYPKRTYAPPARA STRATMVPEPTSALPSDPRSPA AWSDPGLR VPPAARAHLDNSSLGMSQPRPSPGAFPHLSSEPRTPRAFPEPGSRVP PSRLECQQALSHWLSNQVPRRAGERRCPAMAPRARSASQDRLEEV AAPRPWPCSTSQDALSQLGQEGWHRARSDDYLSRATRSALGPG ALVSPRFERCGWASQRSSARTPACPTRDLPGPQAPPPSGLQGLDDL GYIGYRSYSPSFQRRTGLLHALSFRDSPFGGLPTFNLAQSPASFPPE ASEPVRVRPEPSTRALEPPAEDRGDEVVLRQKPPTGRKVQLTPAR QMNLGFGDESPEPEASGRGERLGRKVAPLATTEDSLASIPFIDEPTS PSIDLQAKHVPASAVVSSAMNSAPVLGTSPSSPTFTFTLGRHYSQD CSSIKAGRSSYLLAITTERS KSCDDGLNTFRDEGRVLRRLPNRIPS LRMLRSFFT DGLSDSWGTSEDADAPSKRHSTSDLSDATFS DIRREG WLYYKQILTKKGKAGSGLRQWKRVYAALRARSLSLSKERREPG PAAAGAAAAGAGEDEAAPVCIGSCLVDISYSETKRRHVRLTTAD FCEYLFQAE DRDDMLGWIRAIENSRAEGEDPGCANQALISKLN DYRKVSHSSGPKADSSPKGSRGLGGLKSEFLKQSAARGLRTQDLP AGSKDDSAAPKTPWGINIIKKNKKAAPRAFGVRLEECQPATENQ RVPLIVAACCRIVEARGLESTGIYRVPGNNAVVSSLQEQLNRGPGD INLQDERWQDLNVISSLLKSFFRKLPEPLFTDDKYND FIEANRIEDA RERMRTLRLKLRDLPGHYETLKLFLVGHKTIADHSEKNKMEPRN LALVFGPTLVRTSEDNMTDMVTHMPDRYKIVETLIQHSDWFFSDE EDKGERTPVGDKEPQAVPNIEYLLPNIGRTVPPGDPGSDSTTCSSAK</p>

	SKGSWAPKKEPYAREMLAISFISAVNRKRKKRREARGLGSSTDDD SEQUEAHKPGAGATAPGTQERPQGPLPGAVAPEAPGRSLPPAAPEER PAADTRSIIVSGYSTLSTMDRSVCSGASGRRAGAGDEADDERSELS HVETDTEGAAGAGPGGRLTRRPSFSSHLMPCDTLARRRLARGRP DGEGAGRGGPRAPEPPGSASSSSQESLRPPAAALASRPSRMEALRL RLRGTADDMLAVRLRRPLSPETRRRRSSWRRHTVVVQSPPLTDLNF NEWKELGGGGPPEPAGARAHSDNKDSGLSSLESTKARAPSSAASQ PPAPGDTGSLQSQPPRRSAASRLHQCL
Cytoskeletal Keratin 78 type II or Keratin, type II cytoskeletal 78 (KRT78) SEQ ID NO:12	MSLSPCRAQRGFSARSACSARSGRSRGGFSSRGGFSSRLNSFGG CLEGSRGSTWGS GGRLGVRFGEWGGPGLSLCPGGIQEVTINQNL LTPKIEIDPQFQVVRTQETQEIRTLNNQFASFIDKVRFLQQNKVL ETKWHLLQQQGLSGSQGLEPVFEACLDQLRKQLEQLQGERGAL DAELKACRDQEEYKSKYEEEEAHRRATLENDFVVLKDDVDGVFL SKMELEGKLEALREYL YFLKHLNEEELGQLQTQASDTSVVLSDMN NRYLDFSSIITEVRYEYIARSSKAEAEALYQTKYQELQVSAQLH GDRMQETKVQISQLHQEIQRQLQSQTENLKKQNASLQAAITDAEQR GELALKDAQAKVDELEAALRMAKQNLARLLCEYQELTSTKLSLD VEIATYRRLLEGEECRMSGECTSQVTISSVGGSAVMSGGVGGGLG STCGLGSGKSPGSCCTSI VTGGSNILGSGKDPVLDSCSVSGSSAG SSCHTILKKTVESSLKTSITY
Alpha-3 collagen chain (VI) or Collagen type VI, alpha 3 (COL6A3) SEQ ID NO:13	MRKHRHLPLVAVFCLFLSGFPTTHAQQQQADVKNAAAADIIFLVD SSWTIGEEHFLVREFLYDVVKSLAVGENDFHFALVQFNGNPHTTE FLLNTYRTRKQEVLSHISNMSYIGGTNQTGKGLEYIMQSHLTAAAGS RAGDGVPPQVIVVLTGDHSGDGLALPSAELKSADVNVFAIGVEDAD EGALKEIASEPLNMHMFNLENFTSLHDIVGNLVSCVHSSVSPERAG DTETLKDITAQDSADIIFLIDGSNNTGSVNFVILDFLVNLEKLPIG TQQIRVGVVQFSDPEPTMFSLDTYSTKAQVLGAVKALGFAGGELA NIGLALDFVVENHFTRAGGSRVEEGVPQVLVLISAGPSSDEIRYGV VALKQASVSFGLGAQAASRAELQHIAATDDNLVFTVPEFRSFGDLQ EKLLPYIVGVAQRHIVLKPPTIVTQVIEVNRDIVFLVDGSSALGLA NFNAIRDFIAKVIQRLEIGQDLIQVAVAQYADTVRPEFYFNTHPTKR EVITAVRKMKPLDGSALYTGSA LDFVRNNLFTSSAGYRAAEGIPKL LVLTITGGKSLDEISQAQELKRSSIMAF AIGNKGADQAELEEIAFDS SLVFIPAEFRAAPLQGMPLGLLAPLRTLSTGTPVHNSNRDIIFLLDGS ANVGKTNFPYVRDFVMNLVNSLDIGNDNIRVGLVQFSDTPVTEFS LNTYQTKSDILGHLRQLQLQGGSGLNTGSALSYYVYANHFTEAGGS RIREHVPQLLLLLTAGQSEDSYLQAANALTRAGILTF CVGASQANK AELEQIAFNPSLVYLMDDFSSLPALPQQLIQPLTTYVSGGVEEVPLA QPESKRDI LFLFDGSANLVGQFPVVRDFLYKIIDE LNVKPEGTRIAV AQYSDDVKVESRFDEHQSKPEILNLVKRMKIKTGKALNLGYALDY AQRYIFVKSAGSRIEDGVLQFLVLLVAGRSSDRVDGPASN LKQSGV VPFIFQAKNADPAELEQIVLSPAFILAAESLPKIGDLHPQIVNLLKSV HNGAPAPVSGEKDVVFLLDGSEGVRS GFPLKEFVQRVVESLDVG QDRVRVAVVQYSDRTRPEFYLN SYMNKQDVVNAV RQLTLLGGPT PNTGA ALEFVLRN ILVSSAGSRITEGVPQLLIVLTADRSGDDVRNPS VVVKRGGAVPIGIGIGNADITEMQTISFIPDFAVAIPTFRQLGT VQQ VISERV TQLTREELSRLQPVLQPLSPGVGGKRDV VFLIDGSQSAGP EFQYVRTLIERLVDYLDVGFDTTRVAVIQFSDDPKVEFLLNAHSSK DEVQNAVQRLRPKGGRQINVGNAL EYVSRNIFKRPLGSRIEEGVQP FLVLISGKSDDEVDDPAVELKQFGVAPFTIARNADQEELVKISLSP EYVFSVSTFRELP SLEQKLLTPITLTSEQIQKLLASTRYPPPAVESD AADIVFLIDSSEGV RPDGF AHIRDFVSRIVRRLNIGPSKVRVGVVQF SNDVFPEFYLKTYRSQAPVLD AIRRLRLRGGSPLNTGKALEFVARN

	<p>LFVKSAGSRIEDGVPQHLVLVLGGKSQDDVSRFAQVIRSSGIVSLG VGDRNIDRTELQTITNDPRLVFTVREFRELPNIEERIMNSFGPSAATP APPGVDTPPPSRPEKKKADIVFLLDGSINFRDSSFQEVLRVSEIVD TVYEDGDSIQVGLVQYNSDPTDEFFLKDFSTKRQIIDAINKVYKKG GRHANTKVGLEHLRVNHFVPEAGSRDLQRPQIAFVITGGKSVED AQDVSLALTQRGVKVFVAVGVRNIDSEEVGKIASNSATAFRVGNVQ ELSELSEQVLETLHDAMHETLCPGVTDAAKACNLDVILGFDGSRD QNVFVAQKGFESKVDAILNRISQMHRVSCSGGRSPTVRVSVVANT PSGPVEAFDFDEYQPEMLEKFRNMRSOHPYVLTEDTLKVYLNKFR QSSPDSVKVVIHFTDGDADGLADLHRASENLRQEGVRALILVGLE RVVNLERLMHLEFGRGFMYDRPLRLNLLDLDYELAEQLDNIAEKA CCGVPCCKCSGQRGDRGPIGSIGPKGIPGEDGYRGYPGDEGGPGERG PPGVNGTQGFQGPCGQRGVKGSRGFPGEKGEVGEIGLDGLDGEDG DKGLPGSSGEKGNPGRRGDKGPRGEKGERGDV GIRDPGNPGQDS QERGPKGETGDLGPMGVPRDGVPGGPGETGKNGGFGRRGPPGA KGNKGGPGQPGFEQEQTRGAQGPAGPAGPPGLIGEQQISGPRGS GGAAGAPGERGRTGPLGRKGEPGEPGPKGGIGNRGPRGETGDDGR DGVGSEGRRGKKGERGFGYPGPKGNPGEPLNGTTGPKGIRGRR GNSGPPGIVGQKGDGPYPGPAGPKGNRGDSIDQCALIQSIKDKCPC CYGPLECPVFPTLAFALDTSEGVNQDTFGRMRDVVLSIVNDLTIA ESNCPRGARVAVVTYNNEVTTEIRFADSKRKSVLDDKIKNLQVAL TSKQQSLETAMSFVARNTFKRVRNGFLMRKVAVFFSNTPTRASQ LREAVLKLSDAGITPLFLTRQEDRQLINALQINNTAVGHALVLPAG RDLTDFLENVLTCHVCLDICNIDPSCFGFSWRPSFRDRRAAGSDVD IDMAFILDSAETTTLQFNEMKKYIAYLVRQLDMSPDPKASQHFAR VAVVQHAPSESVDNASMPPVKVEFSLTDYGSKEKLVDFLSRGMTQ LQGTRALGSAIEYTIENVFESAPNPRDLKIVVLMLTGEVPEQQLEEA QRVILQAKCKGYFFVVLGIGRKNVNIKEVYTFASEPNDVFFKLVDKS TELNEEPLMRFGRLLPSFVSSENAFYLSPIRQCDWFQGDQPTKN LVKFGHKQVNVPNNTSSPTSNPVTITTKPVTITTKPVTITTKPVTIT TKPVTIINQPSVKPAAAKPAPAKPVAAPVATKMATVRPPVAVKP ATAAKPVAAPAAVRPPAAAAAKPVATKPEVPRPQAAPAAATKP ATTKPMVKMSREVQVFEITENSAKLHWERAEPGPYFYDLTVTSA HDQSLVLKQNLTVTDRIVIGLLAGQTYHVAVVCYLR SQVRATYH GSFSTKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVISVMGT</p>
<p>Beta subunit of proteasome type-5 or Proteasome subunit beta type-5 (PSMB5) SEQ ID NO:14</p>	<p>MALASVLERPLPVNQRGFFGLGGRADLLDLGPGSLSDGLSLAAPG WGVPEEPGIEMLHGTTTLAFKFRHGVIVAADS RATAGAYIASQTV KKVIEINPYLLGT MAGGAADCSFWERLLARQCRIYELRNKERISVA AASKLLANMVYQYKGMGLSMGMTMICGWDKRGPLYVDSEGNR ISGATFSVSGSVYAYGVMDRGYSYDLEVEQAYDLARRAIYQATY RDAYS GGA VNL YHVREDGWIRVSSDNVADLHEKYS GSTP</p>
<p>Heterogeneous nuclear ribonucleoproteins A2/B1 (HNRNPA2B1) SEQ ID NO:15</p>	<p>MEKTLETVPLERKKREKEQFRKLFIGGLSFETTEESLRNYEQWGK LTDCVVMRDPASKRSRGFGVTFSSMAEVD AAMAARPHSIDGRV VEPKRAVAREESGKPGAHVTVKKLFVGGIKEDTEEHRLRDYFEEY GKIDTIEITDRQSGKKRGFGVTFDDHDPVDKIVLQKYHTINGHNA EVRKALS RQEMQEVQSSRSRGGNFGFGDSRGGGGNFGPGPGSNF RGGSDGYGSGRGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYG GGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNYNQGPSN YGPMKSGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY</p>

<p>Histone H2B type 1-B</p> <p>(HIST1H2BB)</p> <p>SEQ ID NO:16</p>	<p>MPEPSKSAPAPKKGSKKAITKAQKKDGKKRKRSRKESYSIYVYKV LKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITS REIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK</p>
<p>homolog of DnaJ subfamily C member 13</p> <p>or DnaJ homolog subfamily C member 13</p> <p>(DNAJC13)</p> <p>SEQ ID NO:17</p>	<p>MNIIRENKDLACFYTTKHSWRGKYKRVFSVGTHAITTYNPNTLEV TNQWPYGDICISIPVGKGQGTEFNLTRKGGSGKKSETLKFSTEHR ELLTEALRFRTDFSEGKITGRRYNCYKHHWSDSRKPVILEVTPGGF DQINPATNRVLCSDYRNIIEGFVDLSYQGGFCILYGGFSRLHLFA SEQREEIISAIHDAGNYIGISLRIRKEPLEFEQYLNLRFGKYSTDESI TSLAEFVVQKISPRHSEPVKRVLALTETCLVERDPATYNIATLKPLG EVFALVCDSENQPLFTIEFIKGQVRKYSSTERDSSLASLLDGVRASG NRDVCVKMTPTHKGQRWGLLSMPVDEEVESLHLRFLATPPNGNF ADAVFRFNANISYSGVLHAVTQDGLFSENKEKLINNAITALLSQEG DVVASNAELESQFQAVRRLVASKAGFLAFTQLPKFRERLGVKVVV ALKRSNNGIIHAAVDMLCALMCPMHDDYDLRQEQLNKASLLSSK KFLENLLEKFNSHVDHGTGALVISSLLDFTFALCAPYSETTEGQQF DMLLEMVASNGRTLFLKLFQHPSMAIIKAGLVMKAIIEEGDKIEAT KMQELALSEGALPRHLHTAMFTISSDQRMILTNRQLSRHLVGLWTA DNATATNLLKRILPPGLLAYLESSDLVPEKDAARMHVRDNVKIAM DQYGGFNKVPWQRLAGKAAKEVEKFAKEKVDLVLMHWRDRM GIAQKENINQKPVVLRKRRQRIKIEANWDLFYRFGQDHARSNLI WNFKTREELKDTLESEMRAFNDRELGSANVISWNHHEFEVKYEC LAEIIGIDYYLRLLLEEDENEESGSIKRSYEFFNELYHRFLTPKV NMKCLCLQALAIYVGRCHIEIGPFTDTRYIIGMLERCTDKLERDRLI LFLNKLILNKKNVKDLMDSNIGIRILVDLLTLAHLHVSRAVPLQSN VIEAAPDMKRESEKEWYFGNADKERSGPYGFHEMQELWTKGML NAKTRCWAQGMGDWRPLQSIPLKWCLLASGQAVLNEDLATLI LNMLITMCGYFPSRDQDNAIIRPLPKVKRLSDSTCLPHIQLLTFD PILVEKVAIILYHIMQDNPQLPRLYLSGVFFIMMYTGSNVLPVAR FLKYTHTKQAFKSEETKGQDIFQRSILGHILPEAMVCYLENYEPEKF SEIFLGEFDTPEAIWSSEMRRLMIEKIAAHLADFTPRLQSNTRALYQ YCPPIINYPQLENELFCNIYYLKQLCDTLRFPDWPIKDPVKLLKDTL DAWKKEVEKKPPMMSIDDAYEVLNLPQGGQPHDESKIRKAYFRL AQKYHPDKNPEGRDMFEKVNKAYEFLCTKSAKIVDGPDPENIILIL KTQSILFNHRKEDLQPYKYAGYPMLIRTITMETSDDLFSKESPLLP AATELAFHTVNCALNAEELRRENGLEVLEAFSRCVAVLTRASK PSDMSVQVCGYISKCYSVAAQFECEKREKITEMPSIIKDLCRVLYFG KSIPRVAALGVECVSSFAVDFWLQTHLFQAGILWYLLGFLFNVDY TLEESGIQKSEETNQEVANSLAKLSVHALSRLGGYLAEQATPEN PTIRKSLAGMLTPYVARKLAVASVTEILKMLNSNTESPYLIWNNST RAELLEFLSQENMIKKGDCDKTYGSEFVYSDHAKELIVGEIFVR VYNEVPTFQLEVPKAFAASLLDYIGSQAQYLHTFMAITHAAKVESE QHGDRLPRVEMALEALRNVIKYNPGSESECIGHFKLIFSLLRVHGA GQVQQLALEVVNIVTSNQDCVNNIAESMVLSSLLALLHSLPSSRQL VLETLYALTSTKIIEAMAKGALIYLLDMFCNSTHPQVRAQTAE FAKMTADKLIGPKVRITLMKFLPSVFMAMDNRNPEAAVHIFEGTH ENPELIWNDNSRDKVSTTVREMMLEHFKNQQDNPEANWKLPEDF AVVFGEAEGELAVGGVFLRIFIAQPAWVLRKPREFLIALLEKLT EKNPNPHGETLETMTATVCLFSAQPQLADQVPPLGHLPKVIQAMN HRNNAIPKS AIRVIHALSENELCVRAMASLETIGPLMNGMKKRADT VGLACEAINRMFQKEQSELVAQALKADLVPYLLKLEGGIGLENLD SPAATKAQIVKALKAMTRSLQYGEQVNEILCRSSVWSAFKDQKHD LFISESQTAGYLTGPGVAGYLTAGTSTSVMSNLPPPVDHEAGDLGY QT</p>

Beta enolase (ENO3) SEQ ID NO:18	MAMQKIFAREILDSRGNPTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRYLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPLYRHI ADLAGNPDILPVP AFNVINGGSHAGNKLAMQEFMILPVGASSFKE AMRIGAEVYHHLKGVIKAKYGKD ATNVGDEGGFAPNILENEAL ELLKTAIQAAGYPDKVVIGMDVAASEFYRNGKYDLDFKSPDDPAR HITGEKLGELYKSFINKYPVVSIEDPFDQDDWATWTSFLSGVNIQIV GDDLTVTNPKRIAQAVEKKACNCLLLKVNQIGSVTESIQACKLAQS NGWGVMSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKY NQLMRIEEALGDKAIFAGRKFRNPKAK
Glutathione S-transferase P (GSTP1) SEQ ID NO:19	MPPYTVVYFVRGRCAALRMILLADQGQSWKEEVTVTVETWQEGS LKASCLYGQLPKFQDGLTLYQSNILRHLGRITGLYKGDQEEAA LVD MVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETL LSQNQGGKTFIVGDQISFADYNLLDLLIHEVLAPGLDAFPLLSAY VGRLSARPKLKAFLASPEYVNLPIGNGKQ
Glutathione S-transferase Mu 3 (GSTM3) SEQ ID NO:20	MCESSMVLGYWDIRGLAHAIRLLEFTDTSYEEKRYTCGEAPDY DRSQWLDVKFKLDLDFPNLPYLLDGKNKITQSNAILRYIARKHNM CGETEEEEKIRVDIENQVMDFRITQLRLCYSSDHEKLKPQYLEELPG QLKQFSMFLGKFSWFAGEKLTVDFTYDILDQNRIFDPKCLDEFP NLKAFMCRFEALEKIAAYLQSDQFCKMPINNMAQWGNKPVK
Farnesyl pyrophosphate synthase Variant 2 SEQ ID NO:21	MPLSRWLRSVGVFLLPAPYWAPRERWLGSLRRPSLVHGYPVLAW HSARCWCQAWTEEPRALCSSLRMNGDQNSDVYAEKQDFVQHFS QIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVA FRELVEPRKQDADSLQRAWTVGWCVELLQAFFLVADDIMDSSLTR RGQICWYQKPGVGLDAINDANLLEACIYRLLKLYCREQPYLNLIE LFLQSSYQTEIGQTLDLLTAPQGNVDLVRFTKRYKSIVKYKTAFFY SFYLPAAAAMYMAGIDGEKEHANAKKILLEMGEFFQIQDDYDLDF GDPSVTGKIGTDIQDNKCSWL VVQCLQRATPEQYQILKENYGQKE AEKVARVKALYEELDLPAVFLQYEEDSYSHIMALIEQYAAPLPPAV FLGLARKIYKRRK
Farnesyl pyrophosphate synthase Variant 3 SEQ ID NO:22	MNGDQNSDVYAEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARL KEVLEYNAIGGKYNRGLTVVVAFRELVEPRKQDADSLQRAWTVG WCVELLQAFFLVADDIMDSSLTRRGQICWYQKPGVGLDAINDANL LEACIYRLLKLYCREQPYLNLIELFLQSSYQTEIGQTLDLLTAPQG NVDLVRFTKRYKSIVKYKTAFFYSFYLPAAAAMYMAGIDGEKEHA NAKKILLEMGEFFQIQDDYDLDFGDPSVTGKIGTDIQDNKCSWL VV QCLQRATPEQYQILKENYGQKEAEKVARVKALYEELDLPAVFLQY EEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK
Farnesyl pyrophosphate synthase Variant 4 SEQ ID NO:23	MNGDQNSDVYAEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARL KEVLEYNAIGGKYNRGLTVVVAFRELVEPRKQDADSLQRAWTVG WCVELLQAFFLVADDIMDSSLTRRGQICWYQKPGVGLDAINDANL LEACIYRLLKLYCREQPYLNLIELFLQSSYQTEIGQTLDLLTAPQG NVDLVRFTKRYKSIVKYKTAFFYSFYLPAAAAMYMAGIDGEKEHA NAKKILLEMGEFFQIQDDYDLDFGDPSVTGKIGTDIQDNKCSWL VV QCLQRATPEQYQILKENYGQKEAEKVARVKALYEELDLPAVFLQY EEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK
Farnesyl pyrophosphate synthase Variant 5	MDSSLTRRGQICWYQKPGVGLDAINDANLLEACIYRLLKLYCREQ PYLNLIELFLQSSYQTEIGQTLDLLTAPQGNVDLVRFTKRYKSIV KYKTAFFYSFYLPAAAAMYMAGIDGEKEHANAKKILLEMGEFFQIQ

SEQ ID NO:24	DDYDLDFGDPSVTGKIGTDIQDNKCSWLVVQCLQRATPEQYQILK ENYQGKEAEKVARVKALYEELDPAVFLQYEEDSYSHIMALIEQY AAPLPPAVFLGLARKIYKRRK
Farnesyl pyrophosphate synthase Variant 6 SEQ ID NO:25	MNGDQNSDVYAQEKQDFVQHFSQIVRVLTEDEMGHPEIGDAIARL KEVLEYNAIGGKYNRGLTVVVAFRELVEPRKQDADSLQRAWTVG WCVELLQAFFLVADDIMDSSLTRRGQICWYQKPGVGLDAINDANL LEACIYRLLKLYCREQPYLNLIELFLQSSYQTEIGQTLDLLTAPQG NVDLVRFTKRYKSIVKYKTAFYSFYLPAAAMYMAGIDGEKEHA NAKKILLEMGEFFQIQDDYDLDFGDPSVTGKIGTDIQDNKCSWLVV QCLQRATPEQYQILKENYQGKEAEKVARVKALYEELDPAVFLQY EEDSYSHIMALIEQYAAPLPPAVFLGLARKIYKRRK
Farnesyl pyrophosphate synthase Variant 7 SEQ ID NO:26	MPLSRWLRSVGVFLLPAPYWAPRERWLGSLRRPSLVHGYPVLAW HSARCWCQAWTEEPALCSSLRMNGDQNSDVYAQEKQDFVQHFS QIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVA FRELVEPRKQDADSLQRAWTVGWCVELLQAFFLVADDIMDSSLTR RGQICWYQKPGVGLDAINDANLLEACIYRLLKLYCREQPYLNLIE LFLQSSYQTEIGQTLDLLTAPQGNVDLVRFTKRYKSIVKYKTAFY SFYL
Farnesyl pyrophosphate synthase Variant 8 SEQ ID NO:27	MPLSRWLRSVGVFLLPAPYWAPRERWLGSLRRPSLVHGYPVLAW HSARCWCQAWTEEPALCSSLRMNGDQNSDVYAQEKQDFVQHFS QIVRVLTEDEMGHPEIGDAIARLKEVLEYNAIGGKYNRGLTVVVA FRELVEPRKQDADSLQRAWTVGWCVELLQAFFLVADDIMDS
Neurofibromin 1 Variant 2 SEQ ID NO:28	MAAHRPVEWVQAVVSRFDEQLPIKTGQQNTHTKVSTEHNKECLIN ISKYKFSLVISGLTTILKNVNNMRIFGEAAEKNLYLSQIILDTEKCL LAGQPKDTMRLDETMLVKQLLPEICHLHTCREGNQHAELRNSA SGVFLSLSNCFNAVFSRISTRLQELTVCSNVDVHDIELLQYINV DCAKLRLLKETAFKFKALKKVAQLAVINSLEKAFWNWVENYYPD EFTKLYQIPQTDMAECAEKLFDLVDGFAESTKRKAADVWPLQIILLI LCPEIIQDISKDVVDENNMNKKLFLDSLRLKALAGHGGSRQLTESAA IACVKLCKASTYINWEDNSVIFLLVQSMVVDLKNLLFNPSKPFSSRG SQPADVDLMIDCLVSCFRISPHNNQHFICLAQNSPSTFHYVLVNS LHRIITNSALDWWPKIDAVYCHSVELRNMFGETLHKAVQCGGAHP AIRMAPSLTFKEKVTSLKFKEKPTDLETRSYKYLSSMVKLIHADP KLLLCNPRKQGPETQGSTAELITGLVQLVPQSHMPEIAQEAMEALL VLHQDLSIDLWNPDPVETFWISSQMLFYICKKLTSHQMLSSTEIL KWLREILICRNKFLKKNKQADRSSCHFLFYGVGCDIPSSGNTSQM SMDHEELLRTPGASLRKKGKGNSSMDAAGCSGTPPICRQAQTKLE VALYMFLWNPDEAVLVAMSCFRHLCEEADIRCGVDEVSVNLL PNYNTFMEFASVSNMSTGRAALQKRVMAALLRRIEHPHTAGNTEA WEDTHAKWEQATKLILNYPKAKMEDGQAAESLHKTIVKRRMSHV SGGGSIDLSDTSLQEWINMTGFLCALGGVCLQQRNSGLATYSPP MGPVSEKSGSMISVMSSEGNADTPVSKFMDRLLSLMVCNHEKVG LQIRTNVKDLVGLSPALYPMLFNKLKNTISKFFDSQGGVLLTDT NTQFVEQTIAIMKNLLDNHTEGSSEHLGQASIE TMMLNLVRYVRV LGNMVHAIQIKTKLCQLVEVMMARRDDL SFCQEMKFRNKMVEYL TDWVMGTSNQAADDDVKCLTRDLQASMEAVVSLLAGLPLQPEE GDGVELMEAKSQLFLKYFTLFMNLNDCSEVEDESAQTGGRKRG MSRRLASLRHCTVLA MSNLLNANVDSGLMH SIGLYHKDLQTRA TFMEVLTKILQQGTEFDTLAETVLADRFERLVELVTMMGDQGELPI AMALANVVPSCSQWDELARVLVTLFDSRHLLYQLLWNMFKEVEL ADSMQTLFRGNSLASKIMTFCFKVYGATYQLKLLDPLL RIVITSSD WQHVSFEVDPTRLEPSESLEENQRNLLQMTEKFFHAISSSEFPQ

	<p> LRSVCHCLYQVVSQRFPQNSIGAVGSAMFLRFINPAIVSPYEAGILD KKPPPRIERGLKLSKILQSIANHVLFTKEEHMRPFNDFVKSNFDA ARFFLDIASDCPTSDAVNHSLSFISDGNVLALHRLWNNQEKIGQ YLSSNRDHKA VGRRPFDKMATLLAYLGPPEHKPVADTHWSSLNL TSSKFEEFMTRHQVHEKEEFKALKTL SIFYQAGTSKAGNPIFYVA RRFKTGGINGDILLIYHVLLTLKPYYAKPYEIVVDLTHTGPSNRFKT DFLSKWFVVPGFAYDNVSAVYIYNCNSWVREYTKYHERLLTGL KGSKRLVFIDCPGKLA EHIEHEQQKLP AATLAEEDLKVFHNAKL AHKDTKVSIVGSTAVQVTS AERTKVLGQSVFLNDIYYASEIEICL VDENQFTLTIANQGTPLTFMHQECEAIVQSIHIRTWELSQPDSIPQ HTKIRPKDVP GTLLNIALNLGSSDPSLRSAAYNLLCALCTCFNLKI EGQLLETSGLCIPANNTLFIVSISKTLAANEPHLTLEFLEECISGFSKS SIELKHLCLEYMTWPWLSNLVRFCKHNDDAKRQRTAIDDKLITMTI NEKQMYPSIQAKIWGSLGQITDLLDVVLD SFIKTSATGGLGSIKAE VMADTAVALASGNVKLVSSKVIGRMCKIIDKTCLSPTPTLEQHLM WDDIAILARYMLMLSFNNSLDVA AHLPLYLFHVVTFLVATGPLSLR ASTHGLVINIHSCTCSQLHFSEETKQVLRSLTEFSLPKFYLLFGIS KVKSAAVIAFRSSYRDRSFSPGSEYERETFALTSLETVTEALLEIMEA CMRDIPCTCKWLDQWTELAQRFAFQYNPSLQPRALVVFGCISKRVS HGQIKQIIRILSKALESCLKGPD TYNSQVLEATVIALTKLQPLLND SPLHKALFWVAVAVLQLDEVNLYSAGTALLEQNHLTDLRLIFND KSPEEVFMAIRNPLEWHCKQMDHFVGLNFNSNFNALVGHLLKG YRHPSAIVARTVRILHTLLTVNKHRCNDKFEVNTQSVAYLAALL TVSEEVSRCSLKHRSKLLTDISMENVPMDTYPIHHGDPYSYRTLK ETQPWSSPKGSEGYLAATYPTVGQTS PRARKSMSLDMGQPSQANT KKL LGTRK SFDHLISDTKAPKRQEMESGITTPPKMRRVAETDYEM ETQRISSSQPHLRKVSVSESNVLLDEEVLTDPKIQALLTVLATL VKYTTDEFDQRILYEYLAEASVVPKVPVHNLLDSKINTLLSLC QDPNLLNPIHGIVQSVVYHEESPQYQTSYLSQSFNGLWRFAGPF SKQTQIPDYAELIVKFLDALIDTYLPGIDEETSEESLLTPTSPYPAL QSQLSITANLNSNSMTSLATSQHSPGIDKENVELSPTTGHCNSGR RHGSASQVQKQRSAGSFKRNSIKKIV </p>
<p>Neurofibromin 1 Variant 3</p> <p>SEQ ID NO:29</p>	<p> MAAHRPVEWVQAVVSRFDEQLPIKTGQQTHTK VSTEHNKECLIN ISKYKFSLVISGLTTILKNVNNMRIFGEAAEKNLYLSQLIILDTEK LAGQPKDTMRLDETMLVKQLLPEICHFLHTCREGNQHAELRNSA SGVFLSLSNNAFVSRISTRQLQELTVCSNVDVHDIELLYQYIN DCAKLKRLKETA FKFALKKVAQLAVINSLEKAFWNWVENYPD EFTKLYQIPQDMAECAEKLFDLVDGFAESTKRKA AVWPLQIILLI LCPEI IQDISKDVVDENNMNKKFLDSLRLKALAGHGGSRQLTESAA IACVKLCKASTYINWEDNSVIFLLVQSMVVDLKNLLFNPSKPF SRG SQPADVDLMIDCLVSCFRISPHNNQHFKICLAQNSPSTFHYVLVNS LHRIITNSALDWWPKIDAVYCHSVELRNMFGETLHKAVQCGGAHP AIRMAPSLTFKEKVTSLKFKEKPTDLETRSYKYLLLSMVKLIHADP KLLLCNPRKQGPETQGSTAELITGLVQLVPQSHMPEIAQEAMEALL VLHQLD SIDLWNP DAPVETFW EIRYMYFYFLNSTFKFYVFLS </p>
<p>Neurofibromin 1 Variant 4</p> <p>SEQ ID NO:30</p>	<p> NWEDNSVIFLLVQSMVVDLKNLLFNPSKPF SRGSQPADVDLMIDC LVSCFRISPHNNQHFKICLAQNSPSTFHYVLVNSLHRIITNSALDWW PKIDAVYCHSVELRNMFGETLHKAVQCGGAHPAIRMAPSLTFKEK VTSLKFKEKPTDLETRSYKYLLLSMVKLIHADP KLLLCNPRKQGP TQGSTAELITGLVQLVPQSHMPEIAQEAMEALLVLHQLD SIDLWNP DAPVETFW EISSQMLFYICKKLTSHQMLSSTEILKWLREILICRNKF LLKNKQADRSSCHFLLFYGVGCDIPSSGNTSQMSMDHEELLRTPG ASLRKGKGNSSMDSAAGCSGTPPICRQAQTKLEVALYMFLWNPDT EAVLVAMSCFRHLCEEADIRCGVDEVSVHNLLPNYNTFMEFASVS </p>

	<p>NMMSTGRAALQKRVMA LLRRIEHPTAGNTEAWEDTHAKWEQAT KLILNYPKAKMEDGQAAESLHKTIVKRRMSHVSGGGSIDLSDTDS LQEWINMTGFLCALGGVCLQQRSNSGLATYSPPMGPVSRKGSMI SVMSSEGNADTPVSKFMDRLLSLMVCNHEKVGLQIRTNVKDLVG LELSPALYPMLFNKLKNTISKFFDSQGGVLLTDNTQFVEQTAIMK NLLDNHTEGSSEHLGQASIE TMMLNLVRYVRVLGNM VHAIQIKTK LCQLVEVMMARRDDL SFCQEMKFRNKMVEYLT DWVMGTSNQA ADDDVKCLTRDL DQASMEAVVSLLAGLPLQPEEGDGVELMEAKS QLFLKYFTLFMNL NDCSEVEDESAQTGGRKRGM SRRLASLRHCT VLAMSNLLNANVDSGLMH SIGLGYHKDLQTRATFMEVLT KILQQ GTEFDTLAETVLADR FERLVELVTMMGDQ GELPIAMALANVPCS QWDELARVLVTLFDSRHLLYQLLWNMF SKEVELADSMQTLFRGN SLASKIMTFCKVYGATYLQKLLDPLL RIVITSSD WQHVSFEVDPT RLEPSESLEENQRNLLQMTEKFFHAISSSEFP PQLRSVCHCLYQV VSQRFPQNSIGAVGSAMFLRFINPAIVSPYEAGILDKKPPRIERGLK LMSKILQSIANHVLF TKEEHMRPFNDFVKS NFD AARRFLDIASDC PTSDAVNHSLSFISDGNVLAHRL LWNQEKIGQYLSNRDHKAV GRRPFDKMATLLAYLGPPEHKPVADTHWSSLNLTSSKFEFMTNRH QVHEKEEFKALKTLSIFYQAGTSKAGNPIFYVARRFKTGQINGDL LIYHVLLTLKPYYAKPYEIVVDLTHTGPSNRFKTDFLSKWFVFPFG FAYDNVSAVYIYNCNSWVREYTKYHERLLTGLKGSKRLVFIDCPG KLAHIEHEQQKLPAA TLAEEDLKVFHNA LKLAHKDTKVSIVKG STAVQVTS AERTKVLGQSVFLNDIYYASEIEEICLVDENQFTLTIAN QGTPLTFMHQCECEAIVQSIHIRTRWELSQPDSIPQHTKIRPKDVPGT LLNIALLLNLGSSDPSLRSAAYNLLCALTCTFN LKIEGQSLTESGLCIP ANNTLFIVSISKT LAANEPHLLTEFLEECISGFSKSSIELKHLCLEYM TPWLSNLVRFC KHND DAKRQRTAILDKLITMTINEKQMYPSIQA KIWGLSGQITDLLDVVLDSFIKTSATGGLGSIKAEVMADTAVALAS GNVKLVSSK VIGRMCKIIDKTCLSP TPTLEQHLMWDDIAILARYML MLSFNNSLDVA AHLPYLFHVVTFLVATGPLSLRASTHGLVINIHS CTCSQLHFSEETKQVLRSLTEFSLPKFYLLFGISKVKSAAVIAFRGS YRDRSFSPGSYERETFALTSLETVTEALLEIMEACMRDIPTCKWLD QWTELAQRFAFQYNPSLQPRALVVF GCISKRVSHGQIKQIIRILSKA LESCLKGPD TYNSQV LIEATVIALTKLQPLL NKDSPLHKALFWVAV AVLQLDEVNLYSAGTALLEQNLHTLDSLRFNDK SPEEVFMAIRNP LEWHCKQMDHFVGLNFNSNFNFALVGHLLKGYRHPSPAIVARTV RILHTLLTLV NKHRNCDKFEVNTQSVAYLAALLTVSEEVSRCSLK HRKSLLLTDISMENVPMDTYPIHHGDP SYRTLKETQPVWSSPKGSEG YLAATYPTVGQTS PRARKSMSLDMGQPSQANTKKLLGTRKSFDHL ISDTKAPKRQEMESGITTPPKMRRVAETDYEMETQRSSSQQHPHL RKVS VSESNVLLDEEVLTD PKIQALLTVLATLVKYTTDEFDQRIL YEYLAEASVVPKVPV VHNLLDSKINTLLSLCQDPNLLNPIHGIVQ SVVYHEESP PQYQTSYLSQSGFNGLWRFAGPFSKQTQIPDYAELIV KFLDALIDTYLP GIDEETSEESLLTPTSPYPPALQSLSITANLNSNS MTSLATSQHSASLPCKSAVFMQLFPHQ GIDKENVELSPTTGHCN SGRTRHGSASQVQKQRSAGSFKRNSIKKIV</p>
<p>Neurofibromin 1 Variant 5 SEQ ID NO:31</p>	<p>MAAHRPVEWVQAVVSRFDEQLPIKTGQQNTHTKVSTEHNKECLIN ISKYKFSLVISGLTTILKNVNNMRIFGEAAEKNLYLSQLILD TLEKC LAGQPKDTMRLDETM LVKQLLPEICHFLHTCREGNQHAAELRNSA SGVLFSLSCNNFN AVFSRISTRLQELTVCS EDNVDVHDIELLQYINV DCAKLKRLKETA FKFKALKKVAQLAVINSLEKAFWNWVENYPD EFTKLYQIPQTDMAECAEKLFDLVDGFAESTKRKA AVWPLQIILLI LCPEIIQDISKDVVDENNMNKKLFLDSLRLKALAGHGGSRLTESAA IACVKLCKASTYINWEDNSVIFLLVQSMVVDLKNLLFNPSKPF SRG SQPADVDLMIDCLVSCFRISPHNNQHFKICLAQNSPSTFHYVLVNS</p>

	LHRIITNSALDWWPKIDAVYCHSVELRNMFGETLHKAVQGCGAHP AIRMAPSLTFKEKVTSLKFKEKPTDLETRSYKYLLLSMVKLIHADP KLLLCNPRKQGPETQGSTAELITGLVQLVPQSHMPEIAQEAMEVVRG K
Neurofibromin 1 Variant 6 SEQ ID NO:32	MHQCEAIVQSIHIRTWELSQPDSIPOHTKIRPKDVPGTLLNIAL NLGSSDPSLRSAAYNLLCALTCTFNLKIEGQLETSGLCIPANNTLFI VSISKTLAANEPHLTLEFLEECISGFSKSSIELKHLCLEYMTWPWSNL VRFCKHNDDAKRQRVTAIDLKLTMTINEKQMYPSIQAKIWGSLG QITDLLDVVLDSFIKTSATGGLGSIKAEVMADTAVALASGNVKLV SK
Neurofibromin 1 Variant 7 SEQ ID NO:33	MKRCWSNSCCQKSAIFFTPVVKETSMQLNFGILPLGFYFLSAATTS MQLSVAFLPETAFKFKALKKVAQLAVINSLEKAFWNWVENYPDE FTKLYQIPQTDMAECAEKLFDLVDGFAESTKRKAHVWPLQIILLIL CPEIIQDISKDVVDENNMMNKVRRAKLFPLYLDVKQFILLKVCITLGL LFKQSIGNHLNDHFRFLCLMDLEETYSYIILFGRGKIIPGNEQRFKII P
Neurofibromin 1 Variant 8 SEQ ID NO:34	XIHGIVQSVVYHEESPQYQTSYLQSFNGFLWRFAGPFSKQTQIP DYAELIVKFLDALIDTYLPGIDEETSEESLLTPTSPYPPALQSQLSITA NLNLSNSMTSLATSQHSPGQ
Glyceraldehyde-3 phosphate dehydrogenase Variant 2 SEQ ID NO:35	MVYMFQYDSTHGKFGHTVKAENGKLVINGNPITIFQERDPSKIKW GDAGAEYVVESTGVFTTMEKAGAHLQGGAKRVIISAPSADAPMFV MGVNHEKYDNSLKIISNASCTTNCLAPLAKVIHDNFGIVEGLMTTV HAITATQKTVDGPSGKLWRDGRGALQNIIPASTGAAKAVGKVIPEL NGKLTGMAFRVPTANVSVDLTCRLEKPAKYDDIKKVVKQASEG PLKILGYTEHQVVSDFNSDTHSSTFDAGAGIALNDHFVKLISWY DNEFGYSNRVVDLMAHMASKE
Glyceraldehyde-3 phosphate dehydrogenase Variant 3 SEQ ID NO:36	MGKVKVGVNGFGRIGRLVTRAAFNSGKVDIVAINDPFIDLNYMVY MFQYDSTHGKFGHTVKAENGKLVINGNPITIFQERDPSKIKWGD AGAEYVVESTGVFTTMEKAGAHLQGGAKRVIISAPSADAPMFV MGVNHEKYDNSLKIISNASCTTNCLAPLAKVIHDNFGIVEGLMTTV HAITATQKTVDGPSGKLWRDGRGALQNIIPASTGAAKAVGKVIPEL NGKLTGMAFRVPTANVSVDLTCRLEKPAKYDDIKKVVKQASEG PLKILGYTEHQVVSDFNSDTHSSTFDAGAGIALNDHFVKLISWY DNEFGYSNRVVDLMAHMASKE
Glyceraldehyde-3 phosphate dehydrogenase Variant 4 SEQ ID NO:37	MGKVKVGVNGFGRIGRLVTRAAFNSGKVDIVAINDPFIDLNYMVY MFQYDSTHGKFGHTVKAENGKLVINGNPITIFQERDPSKIKWGD AGAEYVVESTGVFTTMEKAGAHLQGGAKRVIISAPSADAPMFV MGVNHEKYDNSLKIISNASCTTNCLAPLAKVIHDNFGIVEGLMTTV HAITATQKTVDGPSGKLWRDGRGALQNIIPASTGAAKAVGKVIPEL NGKLTGMAFRVPTANVSVDLTCRLEKPAKYDDIKKVVKQASEG PLKILGYTEHQVVSDFNSDTHSSTFDAGAGIALNDHFVKLISWY DNEFGYSNRVVDLMAHMASKE
Glyceraldehyde-3 phosphate dehydrogenase Variant 5 SEQ ID NO:38	MEEMRDPKIKWGDAGAEYVVESTGVFTTMEKAGAHLQGGAKR VIISAPSADAPMFVGMVNHEKYDNSLKIISNASCTTNCLAPLAKVIH DNFGIVEGLMTTVHAITATQKTVDGPSGKLWRDGRGALQNIIPAST GAAKAVGKVIPELNGKLTGMAFRVPTANVSVDLTCRLEKPAKY DDIKKVVKQASEGPLKILGYTEHQVVSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSNRVVDLMAHMASKE

<p>Glyceraldehyde-3 phosphate dehydrogenase Variant 6</p> <p>SEQ ID NO:39</p>	<p>MVYMFQYDSTHGKFHGTVKAENGLVINGNPITIFQERDPSKIKWGDAGAEYVVESTGVFTTMEKAGAHLLQGGAKRVIISAPSADAPMFVMGVNHEKYDNSLKIISNASCTTNCLAPLAKVIHDNFGIVEGLMTTVHAITATQKTVDGPSGKLWRDGRGALQNIIPASTGAAKAVGKVIPELNGKLTGMAFRVPTANVSVVDLTCRLEKPAKYDDIKKVVVKQASEGPKLGILGYTEHQVVSDDFNSDTHSSTFDAGAGIALNDHFVVKLISWYDNEFGYSNRVVDLMAHMASKE</p>
<p>Fibronectin Type III Domain Containing protein 1 Variant 2</p> <p>SEQ ID NO:40</p>	<p>XPRHVKLLSTKMGLKVTWDPKDATSRPVEHYNIAYGKSLKSLKYIKVNAETYSFLIEDVEPGVVYFVLLTAENHSGVSRPVYRAESPFGGEWIEIDGFPIKGPFPNETVTEKEVPNKPLRVVRSSDDRSLVSAWKAPRLSGAKSPRRSRGFLLGYGESGRKMNYVPLTRDERTHEIKKLASESVYVVSLSQMNSQGRSQPVYRAALTKRKISEEDELDPDDISVRVMSSQSVLVSWVDPVLEKQKKVVASRQYTVRYREKGELARWDYKQIANRRVLIENLIPDTVYEFAVRISQGERDGKWSTRSVFQRTPEASAPTAPENLNVWPVNGKPTVVAASWDALPETEGKVKASKADVEQNTE DNGKPEKPEPSSSPRAPASSQHPSVPASPOGRNAKDLDDLKNNILANGGAPRKQQLRAKKAEELDLQSTEITGEEELGSRSDSPMSPLDQDQKRTLRRPSSRHGHSVVPAGRTAVRARMPPALPRREGVDKPGFSLATQPRPGAPPSASASAPAHASTQGTSHRPSLPASLNDNDLVDSEDERAVGSLHPKGAFAPQRPALSPSRQSPSSVLRDRSSVHPGAKPASPARRTPHSGAAEEDSSASAPPSRLSPPHGGSSRLPTQPHLSSPLSKGGKDGEDAPATNSNAPSRSTMSSSVSHLSSRTQVSEGAEASDGSESHGDGREDGGRQAEATAQTLRARPASGHFHLRLHKPFAANGSRPSRFSIGRGPRLLQSSSPQSTVPSRAHPRVP SHSDSHPKLSSGIHGDEEDEKPLPATVVNDHVPSSSRQPISRGWEDLRRSPQRGASLHRKEPIPENPKSTGADTHPQGKYSSLASKAQDVQQSTDADTEGHSPKAQPGSTDRHASPAPPAARSQQHPSVPRRMTPGRAPQQQPPPPVATSQHHPGPQRSRDAGRSPSQPRLSLTQAGRPRPTSQGRSHSSSDPYTASSRGMPLTALQNQDEDAQGSYDDDDSTEVEAQDVRAPAHAAARAKEAAASLPKHQQVESPTGAGAGGDHRSQRGHAASPARPSRPGGPQSRARVPSRAAPGKSEPPSKRPLSSKSQQSVSAEDDEEDAGFFKGKKEDLSSSVPKWPPSSSTPRGGKDADGSLAKEEREPAIALAPRGGS LAPVKRPLPPPPGSSPRASHVPSRLPPRSAATVSPVAGTHPWPQYTTTRAPPGHFSTTPLLRLQRMMHARFRNPLSRQPARPSYRQYNGRPNVEGKVLPGSNGKPNQGRIINGPQGTKWVVDLDRGLVLNAEGRYLQDSHGNPLRIKLGGDGRTIVDLEGTVPVSPDGLPLFGQGRHGTPLANAQDKPILSLGGKPLVGLVVIKKTTHPPTTTMQPTTTTTPLPTTTTTPRTTATTRRTTTRRTTTRRPTTTVRTTTRTTTTTPTPTTPIPTCPTLERHDDDG NLMSSNGIPECYAEDEFEFGLETDTAVPTEEAYVIYDEDEYEFETSRPPTTTEPSTTATTPRVIPEEGAISFPEEEFDLAGRKRFVAPRYVTYLNKDPSAPCSLTDALDHFQVDSLDEIIPNDLKKSDLPQPAPRNTVVAVEGCHSFVVDWDKATPGDVVTGYLVYSASYEDFIRNKWSTQASSVTHLPIENLKPNTTRYFKVQAQNP HGYGPISPSVSFVTESDNPLLVRPPGGEPWIWPAFKHDPSYTDCHGRQYVKRTWYRK FVGVL CN SLRYKIYLSDNLKDTFYSIGDSWGRGEDHCQFVDSHLDGRTGPQSYVEALPTIQGYRQYRQEPVRFNGIFGTPYYYVGVWYECGVSIPGKW</p>
<p>Eukaryotic initiation factor 4A-I Variant 2</p> <p>SEQ ID NO:41</p>	<p>MSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSESLLRGIIYAYGF EKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQIELDLKATQALVLA PTRELAQQIQKVVMALGDYMGASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIKMFVLDEADEMLSRGFKDQIYDIFQKLSNTQVLLSATMPSDVLEVTCKFM RDPILRYLKKELTLEGIROFYINVEREEWKLDLTLCDLYETLITITOA</p>

	VIFINTRRKVDWLTEKMHARDFTVSAMHGDMQKQERDVIMREFR SGSSRVLITTDLLGKLYPQNRSRWTVWP
Eukaryotic initiation factor 4A-I Variant 3 SEQ ID NO:42	MSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSSELLR GIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQ IELDLKATQALVLAAPTRELAAQIQKVVMALGDYMGASCHACIGGT NVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIKMFVLDE ADEMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLEVTKKFM RDPILVKKEELTLEGIRQFYINVEREEWKLDLTLCDLYETLTITQA VIFINTRRKVDWLTEKMHARDFTVSAMHGDMQKQERDVIMREFR SGSSRVLITTDLLNRSRWTVWP
Eukaryotic initiation factor 4A-I Variant 4 SEQ ID NO:43	MEPEGVIESNWNEIVDSFDDMNLSSELLRGIYAYGFEKPSAIQQRAI LPCIKGYDVIAQAQSGTGKTATFAISILQQIELDLKATQALVLAAPT ELAAQIQKVVMALGDYMGASCHACIGGTNVRAEVQKLQMEAPHI IVGTPGRVFDMLNRRYLSPKYIKMFVLDEADEMLSRGFKDQIYDIF QKLNSNTQVVLLSATMPSDVLEVTKKFM RDPILVKKEELTLEGI RQFYINVEREEWKLDLTLCDLYETLTIT
Eukaryotic initiation factor 4A-I Variant 5 SEQ ID NO:44	XVVMALGDYMGASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGR VFDMLNRRYLSPKYIKMFVLDEADEMLSRGFKDQIYDIFQKLNSN TQVVLLSATMPSDVLEVTKKFM RDPILVKKEELTLEGIRQFYINV EREEWKLDLTLCDLYETLTITQAVIFINTRRKVDWLTEKMHARDFT VSAMHGDMQKQERDVIMREFRSGSSRVLITTDLLGKLYPQNRSRW TVWP
Eukaryotic initiation factor 4A-I Variant 6 SEQ ID NO:45	MSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSSELLR GIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQ IELDLKATQALVLAAPTRELAAQKVVMALGDYMGASCHACIGGTN VRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIKMFVLDEA DEMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLEVTKKFM RDPILVKKEELTLEGIRQFYINVEREEWKLDLTLCDLYETLTITQAVI FINTRRKVDWLTEKMHARDFTVSAM
Eukaryotic initiation factor 4A-I Variant 7 SEQ ID NO:46	MSASQDSRSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSSELLR GIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQ IELDLKATQALVLAAPTRELAAQIQKVVMALGDYMGASCHACIGGT NVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIKMFVLDE ADEMLSRGFKDQIYDIFQKLNSNTQEELTLEGIRQFYINVEREEWK LDLTLCDLYETLTITQAVIFINTRRKVDWLTEKMHARDFTVSA
Eukaryotic initiation factor 4A-I Variant 8 SEQ ID NO:47	MEPEGVIESNWNEIVDSFDDMNLSSELLRGIYAYGFEKPSAIQQRAI LPCIKGYDVIAQAQSGTGKTATFAISILQQIELDLKAT
Eukaryotic initiation factor 4A-I Variant 9 SEQ ID NO:48	XAWAHCARGRHRPRPPTSGSRDNGPDGMEPEGVIESNWNEIVDSF DDMNLSSELLRGIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTG KTATFAISILQQIELDLKATQALVLAAPTRELAAQIQKVVMALGDY MGASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLS PKYIKMFVLDEADEMLSRGFKDQIYDIFQKL
Eukaryotic initiation factor 4A-I Variant 10 SEQ ID NO:49	MSASQDSRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSSELLRGI YAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTATFAISILQQIE LDLKATQALVLAAPTRELAAQIQKVVMALGDYMGASCHACIGGTN

	VRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIKMFVLDEADEMLS
Eukaryotic initiation factor 4A-I Variant 11 SEQ ID NO:50	MNLSESLLRGIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKT ATFAISILQQIELDLKATQALVLAAPTRELAQQIQKVVMALGDYMG ASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLS PKYIKMFVLDEADEMLSRGFKDQIYDI
Eukaryotic initiation factor 4A-I Variant 12 SEQ ID NO:51	MNLSESLLRGIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKT ATFAISILQQIELDLKATQALVLAAPTRELAQQIQKVVMALGDYMG ASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRY
Eukaryotic initiation factor 4A-I Variant 13 SEQ ID NO:52	MFVLDEADEMLSRGFKDQIYDIFQKLNSNTQVVLLSATMPSDVLE VTKKFMRDPIRILVKKEELTLEGIRQFYINVEREEWKLDTLCDLYE TLTITQAVIFINTRRKVDWLTEKMHA
Eukaryotic initiation factor 4A-I Variant 14 SEQ ID NO:53	MGRSTFLRGSRDNGPDGMEPEGVIESNWNIEVDSFDDMNLSL LRGIYAYGFEKPSAIQQRAILPCIKGYDVIAQAQSGTGKTA
L-lactate dehydrogenase chain B Variant 2 SEQ ID NO:54	MATLKEKLIAPVAEEEEATVPNNKITVVGVGQVGMACAISILGKSLA DELALVDVLEDKLGEMMDLQHGSFLQTPKIVADKDYSVTANS KIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVS NPVDILTYVTWKL SGLPKHRVIGSGCNLDSARFRYLMAEKLGIHPS SCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNSEN WKEVHKMVVESAYEVIKLGKGTNWAIGLSVADLIESMLKNLSRIH PVSTMVKGMYGIENEVFLSLPCILNARGLTSVINQKLKDDEVAQLK KSADTLWDIQDKDLKDL
L-lactate dehydrogenase chain B Variant 3 SEQ ID NO:55	MATLKEKLIAPVAEEEEATVPNNKITVVGVGQVGMACAISILGKSLA DELALVDVLEDKLGEMMDLQHGSFLQTPKIVADKDYSVTANS KIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVS NPVDILTYVTWKL SGLPKHRVIGSGCNLDSARFRYLMAEKLGIHPS SCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNSEN WKEVHKMVVESAYEVIKLGKGTNWAIGLSVADLIESMLKNLSRIH PVSTMVKGMYGIENEVFLSLPCILNARGLTSVINQKLKDDEVAQLK KSADTLWDIQDKDLKDLXLVSSRL
L-lactate dehydrogenase chain B Variant 4 SEQ ID NO:56	MATLKEKLIAPVAEEEEATVPNNKITVVGVGQVGMACAISILGKSLA DELALVDVLEDKLGEMMDLQHGSFLQTPKIVADKDYSVTANS KIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVS NPVDILTYVTWKL SGLPKHRVIGSGCNLDSARFRYLMAEKLGIHPS SCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNSEN WKEVH
L-lactate dehydrogenase chain B Variant 5 SEQ ID NO:57	MATLKEKLIAPVAEEEEATVPNNKITVVGVGQVGMACAISILGKSLA DELALVDVLEDKLGEMMDLQHGSFLQTPKIVADKDYSVTANS KIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIV
L-lactate dehydrogenase chain B Variant 6	MATLKEKLIAPVAEEEEATVPNNKITVVGVGQVGMACAISILGKSLA DELALVDVLEDKLGEMMDLQHGSFLQTPKIVADKDYSVTANS KIVVVTAGVRQQ

SEQ ID NO:58	
Nuclear heterogeneous Ribonucleoprotein A1 Variant 2 SEQ ID NO:59	MSKSESPKEPEQLRKLFIGGLSFETTDESLSHFQWGTLTDCVVM RDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAV SREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYKIEVIEIM TDRGSGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNCEVRKALS KQEMASASSSQGRSGSGNFGGGRGGGFGGNDNFGRGGNFSGRG GFGGSRGGGGYGGSGDGYNGFGNDGSNFGGGGSYNDFGNYNQ SSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSY GSGRRF
Nuclear heterogeneous Ribonucleoprotein A1 Variant 3 SEQ ID NO:60	MSKSESPKEPEQLRKLFIGGLSFETTDESLSHFQWGTLTDCVVM RDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAV SREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYKIEVIEIM TDRGSGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNCEVRKALS KQEMASASSSQGRSGSGNFGGGSYNDFGNYNQSSNFGPMKGG NFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSYGSGRRF
Nuclear heterogeneous Ribonucleoprotein A1 Variant 4 SEQ ID NO:61	MSKSESPKEPEQLRKLFIGGLSFETTDESLSHFQWGTLTDCVVM RDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAV SREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYKIEVIEIM TDRGSGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNCEVRKALS KQEMASASSSQGRSGSGNFGGGRGGGFGGNDNFGRGGNFSGRG IGDGYNGFGNDGSNFGGGGSYNDFGNYNQSSNFGPMKGGNFGG RSSGPYGGGGQYFAKPRNQGGYGGSSSSSYGSGRRF
Nuclear heterogeneous Ribonucleoprotein A1 Variant 5 SEQ ID NO:62	KIEVIEIMTDRGSGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNC EVRKALSKQEMASASSSQGRSGSGNFGGGRGGGFGGNDNFGRG GNFSGRGGFGGSRGGGGYGGSGDGYNGFGNDGSNFGGGGSYNDF GNYNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGY GSSSSSYGSGRRF
Nuclear heterogeneous Ribonucleoprotein A1 Variant 6 SEQ ID NO:63	MRDSSLVAKFLGTQDLCLFLNLALSPKEPEQLRKLFIGGLSFETTDE SLRSHFEQWGTLTDCVVMRDPNTKRSRGFGFVTYATVEEVDAAM NARPHKVDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTE EHHLRDYFEQYKIEVIEIMTDRGSGKKRGFAFVTDDHDSVDKIV IQKYHTVNGHNCEVRKALSKQEMASASSSQGRSGSGNFGGGRG GGFGG
Nuclear heterogeneous Ribonucleoprotein A1 Variant 7 SEQ ID NO:64	MRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKR AVSREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYKIEVI EIMTDRGSGKKRGFAFVTDDHDS
Nuclear heterogeneous Ribonucleoprotein A1 Variant 8 SEQ ID NO:65	MSKSESPKEPEQLRKLFIGGLSFETTDESLSHFQWGTLTDCVVM RDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAV SREDSQRPGAHLTVKKIFVGGFGGSRGGGGYGGSGDGYNGFGND GSNFGGGGSYNDFGNYNQSSN
Nuclear heterogeneous Ribonucleoprotein A1 Variant 9 SEQ ID NO:66	MSKSESPKEPEQLRKLFIGGLSFETTDESLSHFQWGTLTDCVDS QRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYKIEVIEIMTDRG SGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNCEVRKALSKQE MASASSQR

<p>Polycystic kidney disease protein 1-like 1 Variant 2</p> <p>SEQ ID NO:67</p>	<p>XSRLRASMWIDRSTRVSVHFTLYNPPTQLFTSVSLRVEILPTGSLV PSSLVESFSIFRSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMDK GVLSYWRKPRNWLELSVVGVSLTYAVSGHLVTLAGDVTNQFHR GLCRAFMDLTLMASWNQRRWLRGILLFLFTLKCIVLPQIQNTM ASCSSMMRHSPLSIFVAGLVGALMLAALSHLHRFLSMWVLPPT FTDAFPGLLFHFPRRSQKDCLLGLSKSDQRAMACYFGILLIVSATL CFGMLRGFLMTLPQKRKSFQSKSFVRLKDVTAYMWEKVLTFRL ETPKLEEAEMVENHNYLDEFANLLDELLMKINGLSDSLQPLLE KTSNNTGEARTEESPLVDISSYQAAESLTLVTQTEVQWHDGLSLQP PHPRFKQFSCLSLPSSWDYRRVPLCLANF</p>
<p>Polycystic kidney disease protein 1-like 1 Variant 3</p> <p>SEQ ID NO:68</p>	<p>XVGGPENPYLIDPENQNVTLNPGGCGTREDCVLSLGRTRTEAHT ALSRLRASMWIDRSTRVSVHFTLYNPPTQLFTSVSLRVEILPTGSL VPSSLVESFSIFRSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMD KGVLSYWRKPRNWLEVASLVSFSEK</p>
<p>Heat shock protein cognate 71 kDa Variant 2</p> <p>SEQ ID NO:69</p>	<p>MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNNAVVTVPAYFNDSQRQATKDAGTIAGNLVRLIINEPTA AAIAYGLDKKVGAEARNVLIIFDLGGGTDFDVSILTIEDGIFEVKSTAGD THLGGEDFDNRMVNHFAEFKRKHKKDISENKRAVRLRTACERA KRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVE KALRDAKLDKSIQHDIVLVGGSTRIPKIQKLLQDFNKGELNKSINP DEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPSLGIETAGGVM TVLIKRNNTIPTKQTQFTTYSDNQPGVLIQVYEGERAMTKDNNLL GKFELTGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITIT NDKGRLSKEDIERMVQEAKEYKADEKQRDKVSSKNSLESYAFN MKATVEDEKLQKINDEDKQKILDKCNEIINWLDKNQTAKEEEFE HQQKELEKVCNPIITKLYQSAGGMPGMPGPGFPGGGAPPSGGASS GPTIEEVD</p>
<p>Heat shock protein cognate 71 kDa Variant 3</p> <p>SEQ ID NO:70</p>	<p>MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNNAVVTVPAYFNDSQRQATKDAGTIAGNLVRLIINEPTA AAIAYGLDKKVGAEARNVLIIFDLGGGTDFDVSILTIEDGIFEVKSTAGD THLGGEDFDNRMVNHFAEFKRKHKKDISENKRAVRLRTACERA KRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVE KALRDAKLDKSIQHDIVLVGGSTRIPKIQKLLQDFNKGELNKSINP DEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPSLGIETAGGVM TVLIKRNNTIPTKQTQFTTYSDNQPGVLIQVYEGERAMTKDNNLL GKFELTGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITIT NDKGRLSKEDIERMVQEAKEYKADEKQRDKVSSKNSLESYAFN MKATVEDEKLQKINDEDKQKILDKCNEIINWLDKNQTAKEEEFE HQQKELEKVCNPIITKLYQSAGGMPGMPGPGFPGGGAPPSGGASS GPTIEEVD</p>
<p>Heat shock protein cognate 71 kDa Variant 4</p> <p>SEQ ID NO:71</p>	<p>MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNNAVVTVPAYFNDSQRQATKDAGTIAGNLVRLIINEPTA AAIAYGLDKKVGAEARNVLIIFDLGGGTDFDVSILTIEDGIFEVKSTAGD THLGGEDFDNRMVNHFAEFKRKHKKDISENKRAVRLRTACERA</p>

	KRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVE KALRDAKLDKSKIHDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINP DEAVAYGAAYQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMT TVLIKRNNTIPTKQTQTFTTYSNQPGLVLIQVYEGERAMTKDNNLL GKFELTGMPGMPGGFPGGGAPPSGGASSGPTIEEVD
Heat shock protein cognate 71 kDa Variant 5 SEQ ID NO:72	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDKRLIGRRFDDAVVQSDMKH WPFMVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLKGATKDAGTIAGLNLRIINEPTAAAIAYGLDKKVGAEARNVLI DLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFAE FKRKHKKDISENKRVRRLRTACERAKRTLSSSTQASIEIDSLYEG IDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSKIHDIVL VGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYGAAYQAAILSG DKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNNTIPTKQTQTFT TYSNQPGLVLIQVYEGERAMTKDNNLLGKFELTGIPAPRGVQIEV TFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEA EKYKAEDEKQRDKVSSKNSLESYAFNMKATVEDEKLQKINDED KQKILDKCNEIINWLDKNQTAKEEFEFHQKLEKVCNPIITKLYQ SAGGMPGMPGGFPGGGAPPSGGASSGPTIEEVD
Heat shock protein cognate 71 kDa Variant 6 SEQ ID NO:73	MVNHFAEFKRKHKKDISENKRVRRLRTACERAKRTLSSSTQASI EIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDK SKIHDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYGAAY QAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNNTIPT KQTQTFTTYSNQPGLVLIQVYEGERAMTKDNNLLGKFELTGIPAP RGVQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKEDI ERMVQEAKEYKAEDEKQRDKVSSKNSLESYAFNMKATVEDEKLQ KINDEDKQKILDKCNEIINWLDKNQTAKEEFEFHQKLEKVCN PIITKLYQSAGGMPGMPGGFPGGGAPPSGGASSGPTIEEVD
Heat shock protein cognate 71 kDa Variant 7 SEQ ID NO:74	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDKRLIGRRFDDAVVQSDMKH WPFMVNDAGRPKHKKDISENKRVRRLRTACERAKRTLSSSTQ ASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAK LDKSKIHDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYGA AYQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNNT IPTKQTQTFTTYSNQPGLVLIQVYEGERAMTKDNNLLGKFELTGIP PAPRGVQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSK EDIERMVQEAKEYKAEDEKQRDKVSSKNSLESYAFNMKATVEDE KLQKINDEDKQKILDKCNEIINWLDKNQTAKEEFEFHQKLEKVCN PIITKLYQSAGGMPGMPGGFPGGGAPPSGGASSGPTIEEVD
Heat shock protein cognate 71 kDa Variant 8 SEQ ID NO:75	MNPTNTVFDKRLIGRRFDDAVVQSDMKHWPFMVNDAGRPKV QVEYKGETKSFYPEEVSSMVLTKMKEIAEAYLGKTVTNVAVVTPA YFNDSQRQATKDAGTIAGLNLRIINEPTAAAIAYGLDKKVGAE ARNVLIIDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMV NHFAEFKRKHKKDISENKRVRRLRTACERAKRTLSSSTQASIEID SLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSKI HDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYG
Heat shock protein cognate 71 kDa Variant 9 SEQ ID NO:76	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDKRLIGRRFDDAVVQSDMKH WPFMVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNVAVVTPAYFNDSQRQATKDAGTIAGLNLRIINEPTA AAIAYGLDK

Heat shock protein cognate 71 kDa Variant 10 SEQ ID NO:77	MTVLIKRNTTIPTKQTQTFTTYSNQPGLVLIQVYEGERAMTKDNNL LGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITI TNDKGRLSKEDIERMVQEAKEYKADEKQRDKVSSKNSLESYAFN MKATVEDEKLQGKINDEKQKILDKCNEIINWLDKNQTAEKEEFE HQQKELEKVCNPIITKLYQSAGGMPGGMPGGFPGGGAPP
Heat shock protein cognate 71 kDa Variant 11 SEQ ID NO:78	MTKDNLLGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKST GKENKITITNDKGRLSKEDIERMVQEAKEYKADEKQRDKVSSKN SLESYAFNMKATVEDEKLQGKINDEKQKILDKCNEIINWLDKNQ TAEKEEFEHQKE
Heat shock protein cognate 71 kDa Variant 12 SEQ ID NO:79	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNLRL
Heat shock protein cognate 71 kDa Variant 13 SEQ ID NO:80	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAE
Heat shock protein cognate 71 kDa Variant 14 SEQ ID NO:81	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNLRLRIINEPTA AAIAY
Heat shock protein cognate 71 kDa Variant 15 SEQ ID NO:82	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFETKSFYPEEVSSMVLTKMKEIA EAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNLRLRIINEPT AAAIAYGLDKKVGAEARNVLIIFDLGGGTDFVSI
Heat shock protein cognate 71 kDa Variant 16 SEQ ID NO:83	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNLRLRIINEPTA
Heat shock protein cognate 71 kDa Variant 17 SEQ ID NO:84	MSKGPAVGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFT DTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKH WPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEA YLGK
Ankyrin-3 Variant 2 SEQ ID NO:85	MASSASSPAGTEDSAPAQGGFGSDYSRSSRKSDANASYLRAARA GHLEKALDYIKNGVDINICNQNGLNALHLASKEGHVEVVSELLQR EANVDAATKKGNTALHIASLAGQAEVVKVLVTNGANVNAQSQN GFTPLYMAAQENHLEVVKFLLDNGASQSLATEDGFTPLAVALQQG HDQVVSLLLENDTKGKVRPALHIAARKDDTKAAALLQNDNNA DVESKSGFTPLHIAAHYGNINVATLLNRAAAVDFTARNDITPLHV ASKRGNANMVKLLLDRGAKIDAKTRDGLTPLHCGARSQHEQVVE MLLDRAAPILSKTKNGLSPLHMATQGDHLNCVQLLQHNVPVDD VTNDYLTALHVAACHCGHYKVAKVLLDKKANPNKALNGFTPLHI ACKKNRIKVMELLKKGASIQAVTESGLTPIHVAAFMGHVNIQS LMIHGHASPNTTNVRGETALHMAARSGQAEVVRYLVQDGAQVEAK AKDDQTPHISARLGKADIVQQLLQGGASPNAATTSGYTPLHLSAR EGHEDVAAFLLDHGASLSITTKKGFTPLHVAAYGKLEVANLLQ

	<p>KSASPDAAAGKSGLTPLHVA AHYDNQKVALLLLDQGASPHAAAKN GYTPLHIAAKKNQMDIATTLLEYGADANAVTRQGIASVHLAAQEG HVDMSVLLLGRNANVNLSNKSGLTPLHLAAQEDRVNVAEVLVNQ GAHVDAQTKMGYTPLHVGCHYGNIKIVNFLQHS AKVNAKTNG YTPLHQAAQQGHTHIINVLLQNNASPNELTVNGNTALGIARRLGYI SVVDTLKIVTEETMTTTTTEKHKMNVPETMNEVLDMSDDEVK ANAPEMLSDGEYISDVEEGEDAMTGD TD KYLGPQDLKELGDDSLP AEGYMGFSLGARSASLSRFS SDRSYTLNRSSYARDSMMIEELLVPS KEQHLTFTREFDSDSLRHYSWAADTLDNVNLVSSPIHSGFLVSFV DARGGSMRGRHHGMRIIPPRKCTAPTRITCRLVKRHKLANPPPM VEGEGLASRLVEMGPAGAQLGPVIVEIPHFGSMRGKERELIVLRS ENGETWKEHQFDSKNEDL TELLNGMDEELDSPEELGKKRICRIITK DFPQYFVVSRIKQESNQIGPEGGILSSTTVPLVQASFPEGALTKRIR VGLQAQPVPEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPP PSGEGVSNKYKGDTPNLRLLCSITGGTSPAQWEDITGTTPLTFIKD CVSFTTNVSARFWLADCHQVLETVGLATQLYRELICVPYMAKFVV FAKMNDPVESSLRCFCMTDDKVDKTLEQQENFEEVARSKDIEVLE GKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRPLFSIKIRDTSQEP CGRLSFLKEPKTTKGLPQTAVCNLNLTPAHKKIEKTD RRSFASL ALRKRYSYLTPGMSPQSPCERTDIRMAIVADHLGLSWTELARELN FSVDEINQIRVENPNLSISQSFMLLKKWVTRDGKNATTDALTSVLT KINRIDIVTLLEGPIFDYGNISGTRSFADENN VFHDPVDGYPSLQVE LETPTGLHYTPPTPFQDDYFSDISSIESPLRTPSRLSDGLVPSQGNIE HSADGPPVTAEDASLED SKLEDSVPLTEMPEAVDVDESQLENVC LSWQNETSSGNLESCAQARRVTGGLDRLDSPDQCRDSITSYLK GEAGKFEANGSHTETPEAKTKSYFPESQNDVGKQSTKETLKP KIH GSGHVEEPASPLAAYQKSLEETSKLIEETKPCVPVSMKKMSRTSPA DGKPRLSLHEEEGSSGSEQKQGE GFKVKTKEIRHVEKKS HS</p>
<p>Ankyrin-3 Variant 3 SEQ ID NO:86</p>	<p>MSEEPKEKNAKPAHRKRKGKSDANASYLRAARAGHLEKALDYI KNGVDINICNQGLNALHLASKEGHVEVSELLQREANVDAATK KGNTALHIASLAGQAEVVKVLVTNGANVNAQSQNGFTPLYMAAQ ENHLEVVKFLLDNGASQSLATEDGFTPLAVALQQGHDQVVSLLLE NDTKGKVRPALHIAARKDDTKAAALLQNDNNADVESKSGFTPL HIAAHYGNINVATLLLNRAAAVDFTARNDITPLHVASKRGANMV KLLLDRGAKIDAKTRDGLTPLHCGARSGHEQVVEMLLDRAAPILS KTKNGLSPLHMATQGDHLNCVQLLLQHNVPVDDVTNDYLTALHV AAHCGHYKVAKVLLDKKANPNKALNGFTPLHIAACKKNRIKVM LLKHGASIQAVTESGLTPIHVA AFMGHVNIVSOLMHGASPNTT NVRGETALHMAARSGQAEVVRYLVQDGAQVEAKAKDDQTPLHIS ARLGKADIVQQLLQQGASPNAATTSGYTPLHLSAREGHEDVAAFL LDHGASLSITTKKGFTPLHVA AKY GKLEVANLLLQKSASPDAAAGK SGLTPLHVA AHYDNQKVALLLLDQGASPHAAAKNGYTPLHIAAK KNQMDIATTLLEYGADANAVTRQGIASVHLAAQEGHVDMSVLLL GRNANVNLSNKSGLTPLHLAAQEDRVNVAEVLVNQGAHVDAQT KMGYTPLHVGCHYGNIKIVNFLQHS AKVNAKTNGYTPLHQAA QQGHTHIINVLLQNNASPNELTVNGNTALGIARRLGYISVVDTLKI VTEETMTTTTTEKHKMNVPETMNEVLDMSDDEVK ANAPEMLS DGEYISDVEEGNRCTWYKIPKVQEFTVKSEAMTGD TD KYLGPQD LKELGDDSLPAEGYMGFSLGARSASLSRFS SDRSYTLNRSSYARDS MMIEELLVPSKEQHLTFTREFDSDSLRHYSWAADTLDNVNLVSSPI HSGFLVSFMDARGGSMRGRHHGMRIIPPRKCTAPTRITCRLVK RHKLANPPPMVEGEGLASRLVEMGPAGAQLGPVIVEIPHFGSMR GKERELIVLRS ENGETWKEHQFDSKNEDL TELLNGMDEELDSPEEL GKKRICRIITKDFPQYFVVSRIKQESNQIGPEGGILSSTTVPLVQAS FPEGALTKRIRVGLQAQPVPEIVKKILGNKATFSPIVTVEPRRRKF</p>

	<p>HKPITMTIPVPPPSGEGVSNGYKGDTPNLRLLCSITGGTSPAQWED ITGTPLTFIKDCVSFTTNVSARFWLADCHQVLETVGLATQLYRELI CVPYMAKFVVFAMNDPVESLRCFCMTDDKVDKTLEQQENFEE VARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLP FSIKIRDTSQEPCGRLSFLKEPKTTKGLPQTAVCNLNITLPAHKKIEK TDRRQSFASLALRKRYSYLTEPGMSPQSPCERDIRMAIVADHLGL SWTELARELNFSVDEINQIRVENPNLSISQSFMLLKKWVTRDGKNA TTDALTSVLTkinridivTLLEGPIFDYGNISGTRSFADENNVFHD PDV DGYPSLQVELETPTGLHYTPPTPFQDDYFSDISSIESPLRTPSRLSD GLVPSQGNIEHSADGPPVTAEDASLEDSKLEDSVPLTEMPEAVDV DESQLENVCLSWQNETSSGNLESCAQARRVTGGLLDRLDDSPDQC RDSITSYLKGEAGKFEANGSHTEITPEAKTKSYFPESQNDVGKQST KETLKPkiHSGHVEEPASPLAAYQKSLEETSKLIEETKPCVPVSM KKMSRTSPADGKPRLSLHEEEGSSGSEQKQEGGFKVKTKEIRHV EKKSHS</p>
<p>Ankyrin-3 Variant 4</p> <p>SEQ ID NO:87</p>	<p>MALPQSEDAMTGDTDKYLGPQDLKELGDDSLPAEGYMGFSLGAR SASLRSFSSDRSYTLNRSSYARDSMMIEELLVPSKEQHLTFTRFDS DSLRYHWAADTLDNVNLVSSPIHSGFLVSFMDVARGGSMRGSR HHGMRIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRLVE MGPAGAQFLGPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFD SKNEDLTELLNGMDEELDSPEELGKKRICRIITKDFPQYFAVVSRIK QESNQIGPEGGILSSTTVPLVQASFPAGALTKRIRVGLQAQVPDEI VKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPSGEGVSNGYK GDTPNLRLLCSITGGTSPAQWEDITGTPLTFIKDCVSFTTNVSAR FWLADCHQVLETVGLATQLYRELICVPYMAKFVVFAMNDPVES SLRCFCMTDDKVDKTLEQQENFEEVARSKDIEVLEGKPIYVDCY GNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQEPCGRLSFLKEP KTTKGLPQTAVCNLNITLPAHKKIEKTDRRQSFASLALRKRYSYLT EPGMSPQSPCERDIRMAIVADHLGLSWTELARELNFSVDEINQIR VENPNLSISQSFMLLKKWVTRDGKNATDALTSVLTkinridivTL LEGPIFDYGNISGTRSFADENNVFHDVDPDGYPSLQVELETPTGLHY TPPTPFQDDYFSDISSIESPLRTPSRLSDGLVPSQGNIEHSADGPPV VTAEDASLEDSKLEDSVPLTEMPEAVDVDESQLENVCLSWQNETS SGNLESCAQARRVTGGLLDRLDDSPDQCRDSITSYLKGEAGKFEA NGSHTEITPEAKTKSYFPESQNDVGKQSTKETLKPkiHSGHVEEP ASPLAAYQKSLEETSKLIEETKPCVPVSMKKMSRTSPADGKPRLSL HEEEGSSGSEQKQEGGFKVKTKEIRHVEKKSHS</p>
<p>Ankyrin-3 Variant 5</p> <p>SEQ ID NO:88</p>	<p>XFLVSFMDVARGGSMRGSRHHGMRIIPPRKCTAPTRITCRLVKRH KLANPPPMVEGEGLASRLVEMGPAGAQFLGPVIVEIPHFGSMRGK ERELIVLRSENGETWKEHQFDSKNEDLTELLNGMDEELDSPEELGK KRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASFP EGALTKRIRVGLQAQVPDEIVKKILGNKATFSPIVTVEPRRRKFHKP ITMTIPVPPPSGEGVSNGYKGDTPNLRLLCSITGGTSPAQWEDITG TTPLTFIKDCVSFTTNVSARFWLADCHQVLETVGLATQLYRELICV PYMAKFVVFAMNDPVESLRCFCMTDDKVDKTLEQQENFEEV VARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSI KIRDTSQEPCGRLSFLKEPKTTKGLPQTAVCNLNITLPAHKKIEKT DRRQSFASLALRKRYSYLTEPGMKTVERSTGATRSLPTTYSYKPF FST TRPYQSWTTAPITVGPAGKSGFTLSSSSSNTPSASPLKSIWSVSTPS PIKSTLGASTTSSVKSISDVASPIRSFRTMSSPIKTVVSQSPYNIQVSS GTLARAPAVTEATPLKGLASNSTFSSRTSPVTTAGSLLERSITMTP PASPKSNINMYSSSLPFKSIITSAAPLISSPLKSVVSPVKSAVDVISSA KITMASSLSPPVKQMPGHAVALVNGSISPLKYPSSSTLINGCKATA TLQEKISSATNSVSSVSAATDTVEKVFSTTTAMPFSPLSRYVSAAP</p>

	SAFQSLRTPSASALYTSLGSSISATTSSVTSSITVPVYSVVNVLP LKKLPDSNSFTKSAAALLSPIKLT TTETHPQPHFSRTSSPVKSSFLA PSALKLSTPSSSLSSSQEILKDVAEMKEDLMRMTAILQTDVPEEKPFQ PELPKEGRIDDEEPFKIVEKVKEDLVKVSEILKKDVCVDNKGSPKSP KSDKGHSPEDDWIEFSSEEIREARQQAASQSPSLPERVQVKAKAA SEKDYNLT KVIDYLTNDIGSSSLTNLKYKFEDAKKDGEERQKRVL KPAIALQEHKLMPPASMRSTSTSEKELCKMADSFSGTDTILESPDD FSQHDQDKSPLSDSGFETRSEKTPSAPQSAESTGPKPLFHEVPIPPVI TETRTEVVHVIRSYDPSAGDVPQTQPEEPVSPKPSPTFMELEPKPTT SSIKEKVKAFQMKASSEEDDHNRVLSKGMRVKEETHITTTTTTRMVY HSPPGGEGASERIEETMSVHDIMKAFQSGRDPKELAGLFEHKSAY SPDVHKSAAETSAQHAEDNQMKPKLERIIEVHIEKGPQSPCERTDI RMAIVADHLGLSWTELARELNFSVDEINQIRVENPNLSISQSFMLL KKWVTRDGKNATTDALTSVLT KINRIDIVTLLEGPIFDYGNISGTRS FADENNVFHDVPDVGWQNETSSGNLESCAQARRVTGGLDRLDDS PDQCRDSITSYLKGEAGKFEANGSHTEITPEAKTKSYFPESQNDVG KQSTKETLKP KIHGSGHVEEPASPLAAYQKSLEETSKLIIETKPCV PVSMKKMSRTSPADGKPRLSLHEEEGSSGSEQKQGEFGKVKTKKE IRHVEKKSHS
Ankyrin-3 Variant 6 SEQ ID NO:89	XPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFDSKNEDLTEL LNGMDEELDSPEELGKKRICRIITKDFPQYFAVVSRIKQESNQIGPE GGILSSTTVPLVQASFPÉGALTKRIRVGLQAQVPVDEIVKKILGNKA TFSPIVTVEPRRRKFHKPITMTIPVPPPSGEGVSNYKGDTTNLR LCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSARFWLADCHQ VLETVGLATQLYRELICVPYMAKFVVFAMNDPVESSLRCFCMTD DKVDKTLEQQENFEEVARSKDIEVLEGKPIYVDCYGNLAPLTKGG QQLVFNFYSFKENRLPFSIKIRDTSQEPCGRLSFLKEPKTTKGLPQT AVCNLNITLPAHKKETESDQDDEIEKTD RRQSFASLALRPQSPCERT DIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNLSISQSFML LKKWVTRDGKNATTDALTSVLT KINRIDIVTLLEGPIFDYGNISGTR SFADENNVFHDVPDVGYPQLQVELETPTGLHYTPPTPFQDDYFSDI SSIESPLRTPSRLSDGLVPSQGNIEHSADGPPVVT AEDASLEDSKLE DSVPLTEMPEAVDVDESQLENVCLSEYPQYLGNLAGSPKDVKPAE PRKLGVSSEQQEKGKSGPDEEMMEEKLSLFEDIQLEEGVESEEMT EEKVQAILKRVQQAELMSSITGWQNETSSGNLESCAQARRVTG LLDRLDDSPDQCRDSITSYLKGEAGKFEANGSHTEITPEAKTKSYFP ESQNDVGKQSTKETLKP KIHGSGHVEEPASPLAAYQKSLEETSKLII EETKPCVPVSMKKMSRTSPADGKPRLSLHEEEGSSGSEQDLKDS ESDSSEEERRVTTRVIRRRRIIKGEEAKNIPGESVTEEQFTDEEGNLI TRKITRKVLRRVIPQERKRDDVQGEFGKVKTKKEIRHVEKKSHS
Ankyrin-3 Variant 7 SEQ ID NO:90	PKTTKGLPQTAVCNLNITLPAHKKETESDQDDEIEKTD RRQSFASL ALRKRYSYLTEPGMSPQSPCERTDIRMAIVADHLGLSWTELARELN FSVDEINQIRVENPNLSISQSFMLLKKWVTRDGKNATTDALTSVLT KINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDVPDVGYPQLQVE LETPTGLHYTPPTPFQDDYFSDISSIESPLRTPSRLSDGLVPSQGNIE HSADGPPVVT AEDASLEDSKLEDSVPLTEMPEAVDVDESQLENVC LSWQNETSSGNLESCAQARRVTGGLDRLDDSPDQCRDSITSYLK GEAGKFEANGSHTEITPEAKTKSYFPESQNDVGKQSTKETLKP KIH GSGHVEEPASPLAAYQKSLEETSKLIIETKPCVPVSMKKMSRTSPA DGKPRLSLHEEEGSSGSEQKQGEFGKVKTKKEIRHVEKKSHS
Ankyrin-3 Variant 8	XLARELNFSVDEINQIRVENPNLSISQSFMLLKKWVTRDGKNATTD ALTSVLT KINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDVPDG NRI

SEQ ID NO:91	
Ankyrin-3 Variant 9 SEQ ID NO:92	XGPDEDKPPSKSSSEKTPDKTDQKSGAQFFTLEGRHPDRSVFPDT YFSYKVDEEFATPFKTVATKGLDFDPWSNNRGDDEVFDSKSREDE TKPFGLAVEDRSPATTPDTPARTPTDESTPTSEPNPFPFHEGKMFE MTRSGAIDMSKRDFVEERLQFFQIGPQSPCERTDIRMAIVADHLGL SWTELARELNFSVDEINQIRVENPNLSISQSFMLLKKWVTRDGKNA TTDALTSVLTkinridivTLLEGPIFDYGNISGTRSFADENNVFHDVP DGWQNETSSGNLESCAQARRVTGGLLDRLDDSPDQCRDSITSYL
Ankyrin-3 Variant 10 SEQ ID NO:93	MAVEEGESFPEQSDANASYLRAARAGHLEKALDYIKNGVDINICN QNGLNALHLASKEGHVEVVSELLQREANVDAATKKGNTALHIAS LAGQAEVVKVLVTNGANVNAAQSQNGFTPLYMAAQENHLEVVKF LLDNGASQSLATEDGFTPLAVALQQGHDQVVSLLLENDTKGKVR PALHIAARKDDTKAAALLQNDNNADVESKSGFTPLHIAAHYGN NVATLLLNRAAVDFTARNDITPLHVASKRGNANMVKLLDRGA KIDAKTR
Ankyrin-3 Variant 11 SEQ ID NO:94	MAVEEGESFPEQSDANASYLRAARAGHLEKALDYIKNGVDINICN QNGLNALHLASKEGHVEVVSELLQREANVDAATKKGNTALHIAS LAGQAEVVKVLVTNGANVNAAQSQNGFTPLYMAAQENHLEVVKF LLDNGASQSLATEDGFTPLAVALQQGHDQVVSLLLENDTKGKVR PALHIAARKDDTKAAALLQNDNNADVESKSGFTPLHIAAHYGN NVATLLLNRAAVDFTARNDITPLHVASKRGNANMVKLLDRGA KIDAKTR
Ankyrin-3 Variant 12 SEQ ID NO:95	XTVATKGLDFDPWSNNRGDDEVFDSKSREDETKPFGLAVEDRSPA TPDTPARTPTDESTPTSEPNPFPFHEGKMFMEMTRSGAIDMSKRDF VEERLQFFQIGPQSPCERTDIRMAIVADHLGLSWTELARELNFSV EINQIRVENPNLSISQSFMLLKKWVTRDGKNATTDALTSVLTkinri divTLLEGPIFDYGNISGTRSFADENNVFHDVPDGYPSLQVELETPT GLHYTPPTP
Ankyrin-3 Variant 13 SEQ ID NO:96	XWQNETSSGNLESCAQARRVTGGLLDRLDDSPDQCRDSITSYKLG EAGKFEANGSHTTEITPEAKTKSYFPESQNDVGKQSTKETLKPkiHG SGHVEEPASPLAAYQKSLEETSKLIIETKPCVPVSMKKMSRTSPAD GKPRLSLHEEEGSSGSEQKGEGFKVKTKKEIRHVEKKSHS
Ankyrin-3 Variant 14 SEQ ID NO:97	MNVPETMNEVLDMSDDEGNRCTWYKIPKVQEFTVKSEDAMTGD TDKYLGPQDLKELGDDSLPAEGYMGFSLGARSARYFVAVFHS
Ankyrin-3 Variant 15 SEQ ID NO:98	MTGDTDKYLGPDLDKELGDDSLPAEGYMGFSLGARSASLRSFSSD RSYTLNRSSYARDSMMIEELLVPSKEQHLTFTREFDSDSLRHYSWA ADTLDNVNLVSSPIHSGFLVSMVDARGGSMRGRHHGMRIIPPR KCTAPTRITCRLVKRHKLANPPPMVEGEGLASRLVEMGPAGAQL GPVIVEIPHFGSM
Ankyrin-3 Variant 16 SEQ ID NO:99	SPDQCRDSITSYKGEAGKFEANGSHTTEITPEAKTKSYFPESQNDV GKQSTKETLKPkiHGSGHVEEPASPLAAYQKSLEETSKLIIETKPC VPVSMKKMSRTSPADGKPRLSLHEEEGSSGSEQKVKSPGAAPTRM TACCYKQEGGFKVKTKKEIRHVEKKSHS
Ankyrin-3 Variant 17	XLARELNFSVDEINQIRVENPNLSISQSFMLLKKWVTRDGKNATTD ALTSVLTkinridivTLLEGPIFDYGNISGTRSFADENNVFHDVPDVS

SEQ ID NO:100	PNVLSSIGYPSLQVELETPTGLHYTPPTPFQDDYFSDISSIESPLRTP SRLSDGLVPSQGNIEHSADGPPVVTAEADASLEDSKLEDSVPLTEMP EAVDVDESQLENVCLSWQNETSSGNLES
Ankyrin-3 Variant 18 SEQ ID NO:101	XEDAMTGDTDKYLGPQDLKELGDDSLPAEGYMGFSLGARSASP SLRSFSSDRSYTLNRSSYARDSMMIEELLVPSKEQHLTFTREFDSDS LRHYSWAADTLDNVNLVSSPIHSGYSSPLPQYDSRFLVSFMDAR GGSMRGRSRHHGMRIIPPRKCTAPTRITCRLVKRHKLANPPPMVEG EGLASRLVEMGPAGAQL
Ankyrin-3 Variant 19 SEQ ID NO:102	XSSPIHSGFLVSFMDARGGSMRGRSRHHGMRIIPPRKCTAPTRITC RLVKRHKLANPPPMVEGEGLASRLVEMGPAGAQLGKLHLPTNPP PVNEGESLVSRLQLGPGQTKFIGPVIVEIPHFGSMRGRKERELIVLRS ENGETWKEHQFDSKNEDLTELNGMDEELDSPEELGKKRICRIITK DFPQYFVVVS
Ankyrin-3 Variant 20 SEQ ID NO:103	MTGDDTDKYLGPQDLKELGDDSLPAEGYMGFSLGARSASLRSFSSD RSYTLNRSSYARDSMMIEELLVPSKEQ
Ankyrin-3 Variant 21 SEQ ID NO:104	XIEKTDRRQSFASLALRKRYSYLTPGMSQPSPCERTDIRMAIVAD HLGLSWTELARELNFVDEINQIRVENPNLSISQSFMLLKKWVTRD GKNATTDALTSVLTKINRIDIIVTLLEGPIFDYGNISGTRSFADENNV FHDVDDGPPVVTAEADASLEDSKLEDSVPLTEMPEAVDVDESQLE NVC
Ankyrin-3 Variant 22 SEQ ID NO:105	XSPLAAYQKSLEETSKLIIETKPCVPVSMKKMSRTSPADGKPRLSL HEEEGSSGSEQVKSPGAAPTRMTACCYKDLKDESDSSSSEEERR VTTRVIRRRLLIKGEEAKNIPGESVTEEQFTDEEGNLITRKITRKVLR RIVIPQERKRDDVQGEQGVKTKKEIRHVEKKSHS
Ankyrin-3 Variant 23 SEQ ID NO:106	MTGDDTDKYLGPQDLKELGDDSLPAEGYMGFSLGARSASLRSFSSD RSYTLNRSSYARDSMMIEELLVPSKEQHLTFTREFDSDSLRHYSWA ADTLDNVNLVSSPIHSGFLVSFMDARGGSMRGRSRHHGMRIIPPR KCTAPTRITCRLVKRHKLANPP
Ankyrin-3 Variant 24 SEQ ID NO:107	MTGDDTDKYLGPQDLKELGDDSLPAEGYMGFSLGARSASHAASTV AKELTDKTGRTNLSHIFQN
Rho GTPase-activating protein 32 Variant 2 SEQ ID NO:108	MKSRLPTKQKLKQRGILKERVFGCDLGEHLLNSGFVVPVQLQSCTA FIERYGIVDGIYRLSGVASNIQRLRHEFDSEHVPDLTKEPYVQDIHS VGSCLKLYFRELNPPLTYQLYEKFSDAVSAATDEERLIKIHVDVIQQ LPPPHYRTLEFLMRHLSLLADYCSITNMHAKNLAIVWAPNLLRSK QIESACFSGTA AFMEVRIQSVVVEFILNHVDVLFSGRISMAMQEGA ASLSRPKSLLVSSPSTKLLTLEEAQARTQAQVNSPIVTENKYIEVGE GPAALQGKFHTIIEFPLERKRPQNKMKKSPVGSWSRFFNLGKSSSV SKRKLQRNESEPSEMKAMALKGGRAEGLRSASKEESLTSLHVD GDSKLFRRRPRSSDALSAFNGEMLGNRCNSYDNLPHDNESEEE GGLLHIPALMSPHSAEDVDLSPPDIGVASLDFDPMFQCSPPKAESE CLESGASFLDSPGYSKDKPSANKKDAETGSSQCQTPGSTASSEPV PLQEKLSFFFTLDLSPTEDKSSKPSSFTEKVVYAFSPKIGRKLKSKSPS MSISEPISVTLPPRVSEVIGTVSNTTAQNASSTWDKCV EERDATNR SPTQIVKMKTNETVAQEAYESEVQPLDQVAEEVELPGKEDQSVS

	<p>SSQSKAVASGQTQTGAVTHDPPQDSVPVSSVSLIPPPPPKKNVARM LALALAESAQQASTQSLKRPGTSQAGYTNYGDIAVATTEDNLSSS YSAVALDKAYFQTDRPAEQFHLQNNAPGNCDHPLPETTATGDP SNTTESGEQHHQVDLTGNQPHQAYLSGDPEKARITSVPLDSEKSD HVSFPEDQSGKNSMPTVSFLDQDQSPPRFYSGDQPPSYLGASVDKL HHPLEFADKSPTPPNLP SDKIYPPSGSPEENTSTATMTYMTTTPATA QMSTKEASWDVAEQPTTADFAAATLQRTHTNRPLPPPSQRS QPPVVGQVQAATNIGLNNSHKVQGVVPVPERPPEPRAMDDP ISDSGAAAAQCPMATAVQPGLPEKVRD GARVPLLHLRAESVPAHP CGFPAPLPPTRMMESEKMAIAIHSSSADATSSSNYHSFVTASSTSVD DALPLPLPVPQPKHASQKTVYSSFARPDVTTEPFGPDNCLHFNMT NCQYRPQSVPPHHNKLEQH QVYGARSEPPASMGRLRYNTYVAPGR NASGHHSKPCSRVEYVSSLSSSVRNTCYPEDIPPYPTIRRVQSLHAP PSSMIRSVPIRTEVPPDDEPAYCPRPLYQYKPYQSSQARSYDHYVTQ LQPYFENG RVHYRSPYSSSSSSSYSPDGALCDVDAYGTVQLRPL HRLPNRDFAFYNPRLQGKSLYSYAGLAPRPRANVTGYFSPNDHN VSMPPAADVKHTYTSWDLEDMEKYRMSIRRESRARQKVKG PVMSQYDNMTPAVQDDLGGIYVIHLRSKSDPGKTGLLSVAEGKESRH AAKAISPEGEDRFYRRHPEAEMDRAHHHGGHGSTQPEKPSLPQKQ SSLRSRKL PDMGCSLPEHRAHQEASHRQFCESKNGPPYPQAGAGQL DYGSKGIPDTSEPVSYHNSGVKYAASGQESLRLNHKEVRLSKEME RPWVRQPSAPEKHSRDCYKEEEHLTQSI VPPPKPERSHSLKLHHTQ NVERDPSVLYQYQPHGKRQSSVTVVSQYDNLEDYHSLPQHQRGV FGGGMGTYVPPGFPH PQSRTYATALGQGAFLPAELSLQHPETQIH AE</p>
<p>Rho GTPase-activating protein 32 Variant 3</p> <p>SEQ ID NO:109</p>	<p>MKS RPTKQKLKQRGILKERVFGCDLGEHLLNSGFVQPVLQSCTA FIERYGIVDGIYRLSGVASNIQRLRHEFDSEHV PDLTKEPYVQDIHS VGSLCKLYFRELNP LLLTYQLYEKFSDAVSAATDEERLIKIHDIQ LPPHYRTLEFLMRHLSLLADYCSITNMHAKNLAIVWAPNLLRSK QIESACFSGTA AFMEVRIQSVVVEFILNHVDVLFSGRISMAMQEGA ASLSRPKSLLVSSPSTKLLTLEEAQARTQAQVNSPIVTENKYIEVGE GPAALQGKFHTIIEFPLERKRPQNKMKKSPVGSWSRFFNLGKSSSV SKRKLQRNESEPSEM KAMALKGGAEGTLRSKSEESLTSLHA VD GDSKLFRRPRRPRSSDALSAFNGEMLGNRCNSYDNLPHDNESEEE GGLLHIPALMSPHSAEDVDLSPPDIGVASLDFDPM SFQCSPPKA AESE CLESGASFLDSPGYSKDKPSANKKDAETGSSQCQTPGSTAS SEPV PLQEKLSPFFTLDLSPTE DKSSKPSFTEKV VYAFSPKIGRKL SKSPS MSISEPISVTLPPRVSEVIGTVSNTTAQNASSTWDKCV EERDATNR SPTQIVKMKTNETVAQEAYESEVQPLDQVAAEEVELPG KEDQSVS SSQSKAVASGQTQTGAVTHDPPQDSVPVSSVSLIPPPPP KKNVARM LALALAESAQQASTQSLKRPGTSQAGYTNYGDIAVATTED NLSSS YSAVALDKAYFQTDRPAEQFHLQNNAPGNCDHPLPETTATG DPH SNTTESGEQHHQVDLTGNQPHQAYLSGDPEKARITSVPLDSEKSD D HVSFPEDQSGKNSMPTVSFLDQDQSPPRFYSGDQPPSYLGASVDKL HHPLEFADKSPTPPNLP SDKIYPPSGSPEENTSTATMTYMTTTPATA QMSTKEASWDVAEQPTTADFAAATLQRTHTNRPLPPPSQRS QPPVVGQVQAATNIGLNNSHKVQGVVPVPERPPEPRAMDDP ASAF ISDSGAAAAQCPMATAVQPGLPEKVRD GARVPLLHLRAESVPAHP CGFPAPLPPTRMMESEKMAIAIHSSSADATSSSNYHSFVTASSTSVD DALPLPLPVPQPKHASQKTVYSSFARPDVTTEPFGPDNCLHFNMT P NCQYRPQSVPPHHNKLEQH QVYGARSEPPASMGRLRYNTYVAPGR NASGHHSKPCSRVEYVSSLSSSVRNTCYPEDIPPYPTIRRVQSLHAP PSSMIRSVPIRTEVPPDDEPAYCPRPLYQYKPYQSSQARSYDHYVTQ LQPYFENG RVHYRSPYSSSSSSSYSPDGALCDVDAYGTVQLRPL HRLPNRDFAFYNPRLQGKSLYSYAGLAPRPRANVTGYFSPNDHN</p>

	VSMPPAADVKHTYTSWDLEDMEKYRMQSIRRESRARQKVKGVPV MSQYDNMTPAVQDDLGGIYVIHLRSKSDPGKTGLLSVAEGKESRH AAKAISPEGEDRFYRRHPEAEMDRAHHHGGHGSTQPEKPSLPQKQ SSLRSRKLPMGCSLPEHRAHQEASHRQFCESKNGPPYPQGAGQL DYGSKGIPDTSEPVSYHNSGVKYAASGOESLRLNHKEVRLSKEME RPWVRQPSAPEKHSRDCYKEEEHLTQSIVPPPKPERSHSLKLHHTQ NVERDPSVLQYQPHGKRQSSVTVVSQYDNLEDYHSLPQHQRGV FGGGMGMTYVPPGFPHQSRTYATALGQGAFLPAELSLQHPETQIH AE
Rho GTPase-activating protein 32 Variant 4 SEQ ID NO:110	MARGADVPEIPGDLTLKTCGSTASMKVKHVKKLPTFGHFPKMA ECAHFHYENVEFGSIQLSLSEEQNEVMKNGCESKELVYLVQIAQ GKSWIVKRSYEDFRVLDKHLHLCIYDRRFSQLSELPRSDTLKDSPE SVTQMLMAYLSRLSAIAGNKINCPALTWMEIDNKGNNHLLVHEES SINTPAVGAAHVIKRYTARAPDELTEVGDIVSVIDMPPKVLSTWW RGKHGFQVGLFPGHCVELINQKVPQSVTNSVPKPVSKKHGKLITFL RTFMKSRPTKQKLKQRGILKERVFGCDLGEHLLNSGFVEPQVLQS CTAFIERYGIVDGIYRLSGVASNIQRLRHEFDSEHVPDLTKEPYVQD IHSVGLCKLYFRELPNPLTTYQLYEKFSDAVSAATDEERLIKHIDV IQQLPPPHYRTLEFLMRHLSLLADYCSITNMHAKNLAIVWAPNLLR SKQIESACFSGTAAFMENVRIQSVVVEFILNHVDVLFSGRISMAMQE GAASLSRPKSLLVSSPSTKLLTLEEAQARTQAQVNSPIVTENKYIEV GEGPAALQGGKFTHTIEFPLERKRPQNKMKKSPVGSWSRFFNLGKSS SVSKRKLQRNESEPSEMAMALKGGAEGTLRSKSEESLTSLHA VDGDSKLFRRPRSSDALSAFNGEMLGNRCNSYDNLPHDNE EEEGLLHIPALMSPHSAEDVDLSPPDIGVASLDFDPMFQCSPPKA ESECLESFASFLDSPGYSKDKPSANKKDAETGSSQCQTGPSTASSE PVSPLEKLSPPFTLDLSPTEKSSKPSSTFEKVYAFSPKIGRKLKSK SPSMSISEPISVTLPVRVSEVIGTVSNTTAQNASSSTWDKCEVERDA TNRSPQIVKMKTNETVAQEAYESEVQPLDQVAAEEVELPGKEDQ SVSSSQSKAVASGQTQTGTVCPPFFL
Rho GTPase-activating protein 32 Variant 5 SEQ ID NO:111	MKSSVHSEEDDFVPELHRNVHPRERPDWEETLSAMARGADVPEIP GDLTLKTCGSTASMKVKHVKKSTTPGLMGCDNIHRLPFTKGHFPK MAECAHFHYENVEFGSIQLSLSEEQNEVMKNGCESKELVYLVQIA CQGKSWIVKRSYEDFRVLDKHLHLCIYDRRFSQLSELPRSDTL
Cytoskeletal Keratin 78 type II Variant 2 SEQ ID NO:112	MEGHEASPAQVGGDRGKVRFLQEQNKVLETKWHLLQQQGLSG SQQGLEPVFEACLDQLRKQLEQLQGERGALDAELKACRDQEEYK SKYEEEAHRRATLENDFVVLKKDVGDFLSKMELEGKLEALREYL YFLKHLNEEELGQLQTQASDTSVVLSMDNNRYLDFSSIITEVRARY EEIARSSKAEAEALYQTKYQELQVSAQLHGDRMQETKVQISQLHQ EIQRLOSTENLKKQNASLQAAITDAEQRGELALKDAQAKVDELE AALRMAKQNLARLLCEYQELTSTKLSLDVEIATYRRLLEGEECRM SGECTSQVTISSVGGSAVMSGGVGGGLGSTCGLGSGKSGSPGSCCTS IVTGGSNILGSGKDPVLDSCSVSGSSAGSSCHTILKKTVESSLKTSIT Y
Cytoskeletal Keratin 78 type II Variant 3 SEQ ID NO:113	XDVEIATYRRLLEGEECSLGGQRCHVWRSWWRLGEHLWTR
Collagen type VI, alpha 3 Variant 2	MRKHRHLPLVAVFCLFLSGFPTTHAQQQQAQDSADIIFLIDGSNN TGSVNFAVILDFLVNLEKLPITQQIRVGVVQFSDEPRMTMFLSDTY

SEQ ID NO:114	STKAQVLGAVKALGFAGGELANIGLALDFVVENHFTRAGGSRVEE GVPQVLVLISAGPSSDEIRYGVVALKQASVFSFGLGAQAASRAELQ HIATDDNLVFTVPEFRSFGDLQEKLLPYIVGVAQRHIVLKPPTIVTQ VIEVNRDIVFLVDGSSALGLANFNAIKVIQRIEIGQDLIQV AVAQYADTVRPEFYFNTHPTKREVITAVRKMPLDGSALYTGSAL DFVRNNLFTSSAGYRAAEGIPKLLVLITGGKSLDEISQPAQELKRSSI MAFAIGNKGADQAELEEIFDSSLVFIPAEFRAAPLQGMPLGLLAP LRTLSTPEVHSNKRDIIIFLLDGSANVGKTNFPYVRDFVMNLVNSL DIGNDNIRVGLVQFSDTPVTEFSLNTYQTKSDILGHLRQLQLQGGG GLNTGSALSYYVYANHFEAGGSRIREHVPQLLLLLTAGQSEDSYLQ AANALTRAGILTFCV GASQANKAELEQIAFNPSLVYLMDDFSSSLP LPQQLIQPLTTYVSGGVEEVPLAQPESKRDILFLDGSANLVGQFPV VRDFLYKIIDELNVKPEGTRIAVAQYSDDVKVESRFDEHQSKPEILN LVKRMKIKTGKALNLGYALDYAQRVIFVKSAGSRIEDGVLQFLVL LVAGRSSDRVDGPASNLKQSGVVPFIFQAKNADPAELEQIVLSPAFI LAAESLPKIGDLHPQIVNLLKSVHNGAPAPVSGEKDVVFLLDGSEG VRSGFPLLKEFVQRVVESLDVGQDRVRVAVVQYSDRTRPEFYLNS YMNKQDVVNVRQLTLLGGPTNTGALEFVLRNIVSSAGSRIT EGVPQLLIVLTADRSGDDVRNPSVVVKRGGAVPIGIGINADITEM QTISFIPDFAVAIPTFRQLGTVQQVISERVTLTREELSRLQPVLPPL PSPGVGGKRDVVFLIDGSQSAGPEFYVRTLIERLVYDLVGFDTT RVAVIQFSDDPKVEFLLNAHSSKDEVQNAVQRLRPKGGRQINVG ALEYVSRNIFKRPLGSRIEEGVPQFLVLISGKSDDEVDDPAVELKQ FGVAPFTIARNADQEELVKISLSPEYVFSVSTFRELPSLEKLLTPIT TLTSEQIKLLASTRYPPPAVESDAADIVFLIDSEGVPRDQFAHIRD FVSRIVRRLNIGPSKVRVGVVQFSNDVFPEFYLKTYRSQAPVLDAI RRLRLRGGSPNLTKALEFVARNLTVKSGSRIEDGVPQHLVLVL GGKSQDDVSRFAQVIRSSGIVSLGVGDRNIDRTELQTTNDPRLVFT VREFRELPNIEERIMNSFGPSAATPAPPVDTPPPSRPEKKKADIVFL LDGSINFRDSSFQEVLRVSEIVDTVYEDGDSIQVGLVQYNSDPTD EFFLKDFSTKRQIIDAINKVVYKGGRHANTKVGLEHLRVNHFVPEA GSRLDQRPQIAFVITGGKSVEDAQDVSLALTQRGVKVFVAVGVN IDSEEVGKIASNSATAFRVGNVQELSELSEVLETLHDAMHETLCP GVTDAKACNLVDVILGFDGSRDQNVFVAQKGFESKVDAILNRISQ MHRVSCSGGRSPTVRVSVVANTPSGPVEAFDFDEYQPEMLEKFRN MRSQHPYVLTEDTLKVYLNKFRQSSPDSVKVVIHFTDGDADGLAD LHRASENLRQEGVRALILVGLERVVNLRLMHLEFGRGFMYDRPL RLNLLDLDYELAEQLDNIAEKACCGVPCKCSGQRGDRGPIGSIGPK GIPGEDGYRGYPGDEGGPGERGPPGVNGTQGFQGCPCQGRGVKGS GFPGKEGEVGEIGLDGLDGEDGDKGLPGSSGEKGNPGRRGDKGPR GEKGERGDVGIRGDPGNPGQDSQERGPKGETGDLGPMGVPGRDG VPGGPGETGKNGGFGRRGPPGAKGNKGGPGQPGFEQEQTGRAQ GPAGPAGPPGLIGEQQISGPRGSGGAAGAPGERGRTGPLGRKGEPG EPGPKGGIGNRGPRGETGDDGRDGVGSEGRRGKKGERGFPGYPGP KGNPGEPLNGTTGPKGIRGRRGNSGPPGIVGQKGDPGYPGPAGP KGNRGDSIDQCALIQSIKDKCPCYGPLECPVFPTLAFALDTSEG VNDQTFGRMRDVVLSIVNDLTIAESNCPRGARVAVVTYNNEVTTEI RFADSKRKSVDLKIKNLQVALTSKQQSLETAMSFVARNTFKRVR NGFLMRKVAVFFSNTPTASPLREAVLKLSDAGITPLFLTRQEDR QLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDICNIDP SCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQFNEMKK YIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNASMPVK VEFSLTDYGSKEKLVDFLSRGMQLQGTALGSAIEYTIENVFESA PNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGYFFVVLGIGR KVNIKEVYTFASEPNDVFFKLVDKSTELNNEPLMRFGRLPSFVSSE NAFYLSPIRKQCDWFGQDQPTKNLVKFGHKQVNVNPNVTSSPTS
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	NPVTTTKPVTITTKPVTITTKPVTITTKPVTIINQPSVKPAAAKPAPA KPVAAKPVATKMATVRPPVAVKPATAAKPVAAPAAVRPPAAAA AKPVATKPEVPRPQAAKPAATKPATTKPMVKMSREVQVFEITENS AKLHWERAEPGPYFYDLTVTSAHDQSLVLKQNLTVTDRVIGLL AGQTYHVAVVCYLRSQVRATYHGSFSTKKSQPPPPQPARSASSSTI NLMVSTEPLALTETDICKLPKDEGTCRDFILKWWYDPNTKSCARF WYGGCGGNENKFGSQKECEKVCAPVLAKPGVISVMGT
Collagen type VI, alpha 3 Variant 3 SEQ ID NO:115	MRKHRHLPLVAVFCLFLSGFPTTHAQQQQAQDSADIIFLIDGSNN TGSVNFVILDFLVNLEKLPITGQIRVGVVQFSDEPRTMFSLDTY STKAQVLGAVKALGFAGGELANIGLALDFVVENHFTRAGGSRVEE GVPQVLVLISAGPSSDEIRYGVVALKQASVFSFGLGAQASARLEQ HIATDDNLVFTVPEFRSFGDLQEKLIPYIVGVAQRHIVLKPPTIVTQ VIEVNRDIVFLVDGSSALGLANFNAIKDFIAKVIQRLEIGQDLIQV AVAQYADTVRPEFYFNTHPTKREVITAVRKMPLDGSALYTGSA DFVRNNLFTSSAGYRAAEGIPKLLVLITGGKSLDEISQPAQELKRSSI MAFAIGNKGADQAELEEIAFDSSLVFIPAEFRAAPLQGMPLGLLAP LRTLSTGTPVHNSNRDIIFLLDGSANVGKTNFPYVRDFVMNLVNSL DIGNDNIRVGLVQFSDTPVTEFLNTYQTKSDILGHLRQLQLQGGG GLNTGSALSYVYANHFTEAGGSRIREHVPQLLLLLTAGQSEDSYLQ AANALTRAGILTFVCVGASQANKAELEQIAFNPSLVYLMDDFSSLP LPQQLIQPLTTYVSGGVVEVPLAQPESKRDILFLFDGSANLVGQFPV VRDFLYKIIDELNVKPEGTRIAVAQYSDDVKVESRFDEHQSKPEILN LVKRMKIKTGKALNLGYALDYAQRVYFVKSAGSRIEDGVLQFLVL LVAGRSSDRVDGPASNLKQSGVVPFIFQAKNADPAEIQVLSPAFI LAAESLPKIGDLHPQIVNLLKSVHNGAPAPVSGEKDVVFLLDGSEG VRSGFPLLKEFVQRVVESLDVGQDRVRVAVVQYSDRTRPEFYLS YMNKQDVVNNAVRLTLLGGPTPNTGALEFVLNRLVSSAGSRIT EGVPQLLIVLTADRSGDDVRNPSVVVKRGGAVPIGIGIGNADITEM QTISFIPDFAVAIPTFRQLGTVQQVISERVTLTRELSRLQPVLP PSPGVGGKRDVVFLIDGSQSAGPEFYVRTLIERLVDYLDVGFDTT RVAVIQFSDDPKVEFLLNAHSSKDEVQNAVQRLRPKGGRQINVG ALEYVSRNIFKRPLGSRIEAGVPQFLVLISGKSDDEVDDPAVELKQ FGVAPFTIARNADQEELVKISLSPEYVFSVSTFRELPSLEQKLLTPIT TLTSEQIKLLASTRYPPPAVESDAADIVFLIDSSEGVPRPDGFAH FVSRIVRRLNIGPSKVRVGVVQFSNDVFPEFYLKTYRSQAPVLDAI RRLRLRGGSPLNTGKALEFVARNLFVKSAGSRIEDGVPQHLVLVL GGKSQDDVSRFAQVIRSSGIVSLGVGDRNIDRTELQTTINDPRLVFT VREFRELPNIEERIMNSFGPSAATPAPPGVDTPPPSRPEKKKADIVFL LDGSINFRDSSFQEVLRVSEIVDTVYEDGDSIQVGLVQYNSDPTD EFFLKDFSTKRQIIDAINKVVYKGGRHANTKVGLEHLRVNHFVPEA GSRLDQRPQIAFVITGGKSVEDAQDVSLALTQRGVKVFVAVGV IDSEEVGKIASNSATAFRVGNVQELSELSEQVLETLHDAMHETLCP GVTDAAKACNLDVILGFDGSRDQNVFVAQKGFESKVDAILNRISQ MHRVSCSGGRSPTVRVSVVANTPSGPVEAFDFEYQPEMLEKFRN MRSQHPYVLTEDTLKVYLNKFRQSSPDSVKVVIHFTDGDGDLAD LHRASENLREQGVRALILVGLERVVNLERLMHLEFGRGFMYDRPL RLNLLDLDYELAEQLDNIAEKACCGVPCKCSGQGRGDRGPIGSIGPK GIPGEDGYRGYPGDEGGPGERGPPGVNGTQGFQCGPQGRGVKGS GFPGEKGEVGEIGLDGLDGEDGDKGLPGSSGEKGNPGRRGDKGPR GEKGERGDVGIRGDPGNPGQDSQERGPKGETGDLGPMGVPRGDG VPGGPGETGKNGGFRRGPPGAKGNKGGPGQPGFEQEQTGAQ GPAGPAGPPGLIGEQQISGPRGSGGAAGAPGERGRTGPLGRKGEPG EPGPKGGIGNRGPGETGDDGRDGVGSEGRGKKGGERGFPGYPGP KGNPGEPLNGTTGPKGIRGRRGNSGPPGIVGQKGDPPYGPAGP KGNRGDSIDQCALIQSIKDKCPCCYGPLECPVFTELAFAALDTSEGV

	<p>NQDTFGRMRDVVLSIVNDLTIAESNCPRGARVAVVTYNNEVTTEI RFADSKRKSVLDDKIKNLQVALTSKQOSLETAMSFVARNTFKRVR NGFLMRKVAVFFSNTPTTRASPQLREAVLKLSDAGITPLFLTRQEDR QLINALQINNTAVGHALVLPAGRDLTDLFENVLTCHVCLDICNIDP SCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQFNEMKK YIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNASMPVK VEFSLTDYGSKEKLVDFLSRGMTOQLQGTRALGSAIEYTIENVFESA PNPRDLKIVVLMMLTGEVPEQQLEEAQRVILQAKCKGYFFVVLGIGR KVNIEVYTFASEPNDVFFKLVDKSTELNEEPLMRFGRLLPSFVSSE NAFYLSPIRKQCDWFQGDQPTKNLVKFGHKQVNVPNNTSSPTS NPVTTTKPVTTTKPVTTTKPVTTTKPVTTIINQPSVKPAAAKPAPA KPVAAPVATKMATVRPPVAVKPATAAKPVAAPVAVRPPAAAA AKPVATKPEVPRPQAAKPAATKPAATKPMVKMSREVQVFEITENS AKLHWERAEPGPYFYDLTVTSAHDQSLVLKQNLTVTDRVIGLL AGQTYHVAVVCYLRSQVRATYHGSFSTKKSQPPPPQPARSASSSTI NLMVSTEPLALTETDICKLPKDEGTCRDFILKWYYDPNTKSCARF WYGGCGGNENKFGSQKECEKVCAPVLAKPGVISVMGT</p>
<p>Collagen type VI, alpha 3 Variant 4</p> <p>SEQ ID NO:116</p>	<p>MRKHRHLPLVAVFCLFLSGFPTTHAQQQQAVIEVNKRDIVFLVDG SSALGLANFNAIKDFIAKVIQRLQIGQDLIQVAVAQYADTVRPEFYF NTHPTKREVITAVRKMPLDGSALYTGSALDFVRNNLTSSAGYR AAEGIPKLLVLITGGKSLDEISQPAQELKRSSIMAFAGNKGADQAE LEEIAFDSSLVFPAEFRAAPLQGMPLGLLAPLRLTSGTPEESKRDL FLFDGSANLVGQFPVVRDFLYKIIDELNVKPEGTRIAVAQYSDDVK VESRFDEHQSKPEILNLVKRMKIKTGKALNLGYALDYAQRIFYKS AGSRIEDGVLQFLVLLVAGRSSDRVDGPASNLKQSGVVPFIFQAKN ADPAELEQIVLSPAFILAAESLPKIGDLHPQIVNLLKSVHNGAPAPV SGEKDVVFLLDGSEGVRSFGPLLKEFVQVRVVESLDVGQDRVRVAV VQYSDRTRPEFYLSYMNKQDVVNAVVRQLTLLGGPTPNTGAAL FVLRNILVSSAGSRITEGVPQLLIVLTADRSGDDVRNPSVVVKRGG AVPIGIGIGNADITEMQITISFIPDFAVAIPTRQLGTQVQVYSERV TREELSRQLQPVLPSPGVGGKRDVFLIDGSQSAGPEFYVVRTLI ERLVDYLDVGFDTTRVAVIQFSDDPKVEFLLNAHSSKDEVQNAVQ RLRPKGGRRQINVGNALEYVSRNIFKRPLGSRIEAGVPQFLVLISGK SDDEVDDPAVELKQFGVAPFTIARNADQELVKISLSPEYVFSVSTF RELPSLEQKLLTPITTLTSEIQIKLLASTRYPPPAVESDAADIVFLIDS SEGVPRPDGFADIRDFVSRIVRRLNIGPSKVRVGVVQFSNDVFPEFY KTYRSQAPVLDAIRRLRLRGGSPLNTGKALEFVARNLFVKSAGSRI EDGVPQHLVLVLGGKSQDDVSRFAQVIRSSGIVSLGVGDRNIDRTE LQTITNDPRLVFTVREFRELPNIEERIMNSFGPSAATPAPPVDTPPP SRPEKKKADIVFLLDGSINFRRDSFQEVLRVSEIVDTVYEDGDSIQ VGLVQYNSDPTDEFFLKDFSTKRQIIDAINKVVKGGRRHANTKVG LEHLRVNHVFPEAGSRDLQRPQIAFVITGGKSVEDAQDVSLALTQ RGVKVFAVGVRNIDSEEVGKIASNSATAFRVGNVQELSELSEQVLE TLHDAMHETLCPGVTDAAKACNLDVILGFDGSRDQNVFVAQKGF ESKVDAILNRISQMHRVSCSGGRSPTVRVSVVANTPSGPVEAFDFD EYQPEMLEKFRNMRSQHPYVLTEDTLKVYLNKFRQSSPDSVKVVI HFTDGDADGDLADLHRASENLRQEGVRALILVGLERVVNLERLMH LEFGRGFMYDRPLRLNLLDLDYELAEQLDNIAEKACCGVPCKCSG QRGDRGPIGSIGPKGIPGEDGYRGYPGDEGGPGERGPPGVNGTQGF QGCPGQRGVKGSRGFPGEKGEVGEIGLDGLDGEDGDKGLPGSSGE KGNPGRRGDKGPRGEKGERGDVGIRDPGNPGQDSQERGPGET GDLGPMGVPRDGVPGGPGETGKNGGFGRRGPPGAKGNKGGPG QPGFEGEQGTRGAQGPAGPAGPPGLIGEQQISGPRGSGGAAGAPGE RGRTGPLGRKGEPGEPGPKGGIGNRGPRGETGDDGRDGVGSEGR GKKGERGFPGYPGPKGNPGEPLNGTTGPKGIRGRRGNSGPPGIVG</p>

	<p>QKGDPGYPGPAGPKGNRGDSIDQCALIQSIKDKCPCCYGPLECPVF PTELAFALDTSEGVNQDTFGRMRDVVLSIVNDLTIAESNCPRGARV AVVTYNNEVTTEIRFADSKRKSVLDDKIKNLQVALTSKQQSLETA MSFVARNTFKRVRNGFLMRKVAVFFSNTPTTRASPQLREAVLKLSD AGITPLFLTRQEDRQLINALQINNTAVGHALVLPAGRDLTDFLENV LTCHVCLDICNIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSA ETTTLFQFNEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPS ESVDNASMPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGS AIEYTIENVFESAPNPRDLKIVVLMILTGEVPEQQLEEAQRVILQAKC KGYFFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLM RFGRLPSFVSSENAFYLSPIRQCDWFGQDQPTKNLVKFGHKQ VNVPNNTSSPTSNPVTITTKPVITTKPVITTKPVITTKPVITINQ PSVKPAAAKPAPAKPVAAKPVATKMATVRPPVAVKPATAAKPVA AKPAAVRPPAAAAAKPVATKPEVPRPQAAPAAATKPAATKPMVK MSREVQVFEITENSAKLHWERAEPGPYFYDLTVTSAHDQSLVLK QNLTVTDRVIGGLLAGQTYHVAVVCYLRSSQVRATYHGSFSTKKSQ PPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEGTCRDFILKW YYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPVLAKPGVI SVMGT</p>
<p>Collagen type VI, alpha 3 Variant 5</p> <p>SEQ ID NO:117</p>	<p>MRKHRHLPLVAVFCLFLSGFPTTHAQQQQAQDSADIIFLIDGSNN TGSVNFAVILDFLVNLLLEKLPITGQIRVGVVQFSDEPRTMFSLDTY STKAQVLGAVKALGFAGGELANIGLALDFVVENHFTRAGGSRVEE GVPQVLVLISAGPSSDEIRYGVVALKQASVFSFGLGAQASRAALQ HIATDDNLVFTVPEFRSFGDLQEKLLPYIVGVAQRHIVLSPRTIVTQ VIEVNRDIVFLVDGSSALGLANFNAIKDFIAKVIQRLEIGQDLIQV AVAQYADTVRPEFYFNTHPTKREVITAVRKMPLDGSALYTGSA DFVRNNLFTSSAGYRAAEGIPKLLVLITGGKSLDEISQPAQELKRSSI MAFAIGNKGADQAELEIAFDSSLVFIPAEFRAAPLQGMPLGLLAP LRTLSTPEVHSNKRDIIFLLDGSANVGKTNFPYVRDFVMNLVNSL DIGNDNIRVGLVQFSPTVTEFSLNTYQTKSDILGHLRQLQLQGGS GLNTGSALSYYVANHFEAGGSRIREHVPQLLLLLTAGQSEDSYLQ AANALTRAGILTFVCVGSQANKAELEQIAFNPSLVYLMDDFSSLP LPQQLIQPLTTYVSGGVVEVPLAQPESKRDILFLDGSANLVGQFPV VRDFLYKIIDELNVKPEGTRIAVAQYSDDVKVESRFDEHQSKPEILN LVKRMKIKTGKALNLGYALDYAQRVIFVKSAGSRIEDGVLQFLVL LVAGRSSDRVDGPASNLKQSGVVPFIFQAKNADPAELEQIVLSPAFI LAAESLPKIGDLHPQIVNLLKSVHNGAPAPVSGEKDVVFLLDGSEG VRSGFPLLKEFVQRVVESLDVGQDRVRVAVVQYSDRTRPEFYLNS YMNKQDVVNAVRLTLLGGPTPNTGALEFVLRNVLVSSAGSRIT EGVPQLLIVLTADRSGDDVRNPSVVVKRGGAVPVIGIGIGNADITEM QTISFIPDFAVAIPTFRQLGTVQQVISERVTQLTREELSRLQPVLQPL PSPGVGGRDVFLLIDGSQSAGPEFYVRTLIERLVYLDVGFDDTT RVAVIQFSDDPKVEFLLNAHSSKDEVQNAVQRLRPKGGGRQINVG ALEYVSRNIFKRPLGSRIEAGVPQFLVLISGKSDDEVDDPAVELKQ FGVAPFTIARNADQEELVKISLSPEYVFSVSTFRELPSLEQKLLTPIT TLTSEQIQKLLASTRYPPPGEMGASEVLLGAFSI</p>
<p>Collagen type VI, alpha 3 Variant 6</p> <p>SEQ ID NO:118</p>	<p>MRKHRHLPLVAVFCLFLSGFPTTHAQQQQAQDSADIIFLIDGSNN SSALGLANFNAIKDFIAKVIQRLEIGQDLIQVAVVQYADTVRPEFYF NTHPTKREVITAVRKMPLDGSALYTGSA DFVRNNLFTSSAGYRAAEGIPKLLVLITGGKSLDEISQPAQELKRSS MAFAIGNKGADQAELEIAFDSSLVFIPAEFRAAPLQGMPLGLLAP LRTLSTPEVHSNKRDIIFLLDGSANVGKTNFPYVRDFVMNLVNSL DIGNDNIRVGLVQFSPTVTEFSLNTYQTKSDILGHLRQLQLQGGS GLNTGSALSYYVANHFEAGGSRIREHVPQLLLLLTAGQSEDSYLQ AANALTRAGILTFVCVGSQANKAELEQIAFNPSLVYLMDDFSSLP LPQQLIQPLTTYVSGGVVEVPLAQPESKRDILFLDGSANLVGQFPV VRDFLYKIIDELNVKPEGTRIAVAQYSDDVKVESRFDEHQSKPEILN LVKRMKIKTGKALNLGYALDYAQRVIFVKSAGSRIEDGVLQFLVL LVAGRSSDRVDGPASNLKQSGVVPFIFQAKNADPAELEQIVLSPAFI LAAESLPKIGDLHPQIVNLLKSVHNGAPAPVSGEKDVVFLLDGSEG VRSGFPLLKEFVQRVVESLDVGQDRVRVAVVQYSDRTRPEFYLNS YMNKQDVVNAVRLTLLGGPTPNTGALEFVLRNVLVSSAGSRIT EGVPQLLIVLTADRSGDDVRNPSVVVKRGGAVPVIGIGIGNADITEM QTISFIPDFAVAIPTFRQLGTVQQVISERVTQLTREELSRLQPVLQPL PSPGVGGRDVFLLIDGSQSAGPEFYVRTLIERLVYLDVGFDDTT RVAVIQFSDDPKVEFLLNAHSSKDEVQNAVQRLRPKGGGRQINVG ALEYVSRNIFKRPLGSRIEAGVPQFLVLISGKSDDEVDDPAVELKQ FGVAPFTIARNADQEELVKISLSPEYVFSVSTFRELPSLEQKLLTPIT TLTSEQIQKLLASTRYPPPGEMGASEVLLGAFSI</p>

	<p>VGASQANKAELEQIAFNPSLVYLMDDFSSLPALPQQLIQPLTTYVS GGVEEVPLAQPESKRDILFLFDGSANLVGQFPVVRDFLYKIIDELNV KPEGTRIAVAQYSDDVKVESRFDEHQSKPEILNLVKRMKIKTGKAL NLGYALDYAQRIFVKASAGSRIEDGVLQFLVLLVAGRSSDRVDGP ASNLKQSGVVPFIFQAKNADPAELEQIVLSPAFILAAESLPKIGDLH PQIVNLLKSVHNGAPAPVSGEKDVVFLLDGSEGVRSGFPLLKEFVQ RVVESLDVGQDRVRVAVVQYSDRTRPEFYLN SYMNKQDVVNAV RQLTLLGGPTPNTGA ALEFVL RNILVSSAGSRITEGVPQLLIVLTAD RSGDDVRNPSVVVKRGGAVPIGIGIGNADITEMQTISFIPDFAVAIPT FRQLGTVQQVISERVTQLTREELSRLQPVLQPLPSPGVGGKRDVVF LIDGSQSAGPEFYVRTLIERLVDYLDVGFDTRVAVIQFSDDPKV EFLNAHSSKDEVQNAVQRLRPKGGRQINVGNAL EYVSRNIFKR LGSRIEEGVPQFLVLISGKSDDEVDDPAVELKQFGVAPFTIARNAD QEELVKISLSPEYVFSVSTFRELPSEKLLTPITLTSEQIQKLLAST RYPPPGEMGASEVLLGAFSI</p>
<p>Collagen type VI, alpha 3 Variant 7</p> <p>SEQ ID NO:119</p>	<p>MRKHRHLPLVAVFCLFLSGFPTTHAQQQAVIEVNKRDIVFLVDG SSALGLANFNARDFIKVIQRLEIGQDLIQVAVAQYADTVRPEFYF NTHPTKREVITAVRKMKPLDGSALYTGSA LDFVRNNLFTSSAGYR AAEGIPKLLVLITGGKSLDEISQPAQELKRSSIMAF AIGNKGADQAE LEEIAFDSSLVFIPAEFRAAPLQGMPLGLLAPLRTL SGTPEESKRDIL FLFDGSANLVGQFPVVRDFLYKIIDELNVKPEGTRIAVAQYSDDVK VESRFDEHQSKPEILNLVKRMKIKTGKALNLGYALDYAQRIFVKAS AGSRIEDGVLQFLVLLVAGRSSDRVDGPASNLKQSGVVPFIFQAKN ADPAELEQIVLSPAFILAAESLPKIGDLHPQIVNLLKSVHNGAPAV SGEKDVVFLLDGSEGVRSGFPLLKEFVQRVVESLDVGQDRVRVAV VQYSDRTRPEFYLN SYMNKQDVVNAV RQLTLLGGPTPNTGA ALE FVL RNILVSSAGSRITEGVPQLLIVLTADRSGDDVRNPSVVVKRGG AVPIGIGIGNADITEMQTISFIPDFAVAIPTFRQLGTVQQVISERVTQL TREELSRLQPVLQPLPSPGVGGKRDVVF LIDGSQSAGPEFYVRTL ERLVDYLDVGFDTRVAVIQFSDDPKVEFLNAHSSKDEVQNAVQ RLRPKGGRQINVGNAL EYVSRNIFKRPLGSRIEEGVPQFLVLISGK SDDEVDDPAVELKQFGVAPFTIARNADQEELVKISLSPEYVFSVSTF RELPSLEKLLTPITLTSEQIQKLLASTRYPPPAVESDAADIVFLIDS SEGV RPDGFAHIRDFVSRIVRRLNIGPSKVRVG VVQFSNDVFPEFY L KTYRSQAPVLD AIRRLRLRGGSPLNTGKALEFVARNLFVKASGRI EDGVPQHLVLVLGGKSQDDVSRFAQVIRSSGIVSLGVGDRNIDRTE LQTITNDPRLVFTVREFREL PNIEERIMNSFGPSAATPAPGVDTPPP SRPEKKKADIVFLLDGSINFRDSFQEVLR FVSEIVDTVYEDGDSIQ VGLVQYNSDPTDEFFLKDFSTKRQIIDAINKVVYKGGRHANTKVG LEHLRVNH FVPEAGSRLDQRPQIAFVITGGKSVEDAQDVSLALTQ RGVKVFAVGVRNIDSEEVGKIASNSATAFRVGNVQELSELSEQVLE TLHDAMHETLCPGVTDAAKACNL DVILGFDGSRDQNVFVAQKGF ESKVDAILNRISQMHRVSCSGRSPTVRVSVVANTPSGPVEAFDFD EYQPEMLEKFRNMRSQHPYVLTEDTLKVYLNKFRQSSPDSVKVVI HFTDGADGDLADLHRASENLRQEGVRALILVGLERVNLERLMH LEFGRGFMYDRPLRLNLLDLDYELAEQLDNIAEKACCGVPCKCSG QRGDRGPIGSIGPKGIPGEDGYRGYPGDEGGPGERGPPGVNGTQGF QGCPGQRGVKGSRGFPGEKGEVGEIGLDGLDGEDGDKGLPGSSGE KGNPGRRGDKGPRGEKGERGDVGIRGDPGNPGQDSQERGPKGET GDLGPMGVPRGDGVPGGPGETGKNNGGFRRGPPGAKGNKGGPG QPGFEQEQTGAQGPAGPAGPPGLIGEQQISGPRGSGGAAGAPGE RGRTGPLGRKGEPGEPGPKGGIGNRGPRGETGDDGRDGVGSEGR GKKGERGFPGYPGPKGNPGEPLNGTTGPKGIRGRRGNSGPPGIVG QKGDPGYPGPAGPKGNRGDSIDQC ALIQSIKDKCPFHGPLECPVFP TELA FALDTSEGVNQDTFGRMRDVVLSIVNDLTIAESNCPRGARV</p>

	AVVTYNNEVTTEIRFADSKRKSVLDDKIKNLQVALTSKQQSLETA MSFVARNTFKVRNNGFLMRKVAVFFSNTPTTRASPQLREAVLKLSD AGITPLFLTRQEDRQLINALQINNTAVGHALVLPAGRDLTDFLENV LTCHVCLDICNIDPSCFGFSWRPSFRDRRAAGSDVIDMAFILD ETTTLFQFNEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPS ESVDNASMPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGS AIEYTIENVFESAPNPRDLKIVVLMMLTGEVPEQQLEEAQRVILQAKC KGYFFVVLGIGRKNIKEVYTFASEPNDVFFKLVDKSTELNNEEPLM RFGRLPSFVSSENAFYLSPIRQCDWFGDQPTKNLVKFGHKQ VNVNPNVTSSPTSNPVTITTKPVITITTKPVITITTKPVITITTKPVITINQ PSVKPAAAKPAPAKPVAAPKPVATKMATVRPPVAVKPATAAKPVA AKPAAVRPPAAAAAKPVATKPEVPRPQAAPKPAATKPAATKPMVK MSREVQVFEITENSAKLHWERAEPGPYFYDLTVTSAHDQSLVLK QNLTVTDRVIGLLAGQTYHVAVVCYLRQVRATYHGSFSTKKSQ PPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEGTCRDFILKW YYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPVLAKPGVI SVMGT
Collagen type VI, alpha 3 Variant 8 SEQ ID NO:120	MRKHRHLPLVAVFCLFLSGFPTTHAQQQADVKNGAAADIIFLVD SSWTIGEEHFQLVREFLYDVVKSLAVGENDHFHALVQFNGNPHT FLLNTYRTKQEVLSHISNMSYIGGTNQTGKLEYIMQSHLTAAAGS RAGDGVPPVIVVLTDGHSKDGLALPSAELKSADVNVFAIGVEDAD EGALKEIASEPLNMHMFLENFTSLHDIVGNLVSCVHSSVSPERAG DTETLKDITAQDSADIIFLIDGSNNTGSVNFVILDFLVNLEKLP TQIRVGVVQFSDEPRMTFSLDITYSTKAQVLGAVKALGFAGGELA NIGLALDFVVENHFTRAGGSRVEEGVPQVLVLISAGPSSDEIRYGV VALKQASVFSFGLGAQAASRAELQHIAATDDNLVFTVPEFRSFGDLQ EKLLPYIVGVAQRHIVLKPPTIVTQVIEVNKRDIVFLVDGSSALGLA NFNAIRDFIAKVIQRLEIGQDLIQVAVAQYADTVRPEFYFNTHPTKR EVITAVRKMPLDGSALYTGSALDFVRNNLFTSSAGYRAAEGIPKL LVLITGGKSLDEISQPAQELKRSSIMAFIGNKGADQAELEEIAFDS SLVFIPAEFRAAPLQGMPLPGLLAPLRTLSTGTPEESKRDILFLFDGSA NLVGQFPVVRDFLYKIIDELNVKPEGTRIAVAQYSDDVKVESRFDE HQSKEILNLVKRMKI
Collagen type VI, alpha 3 Variant 9 SEQ ID NO:121	PIGTQQIRVGVVQFSDEPRMTFSLDITYSTKAQVLGAVKALGFAGG ELANIGLALDFVVENHFTRAGGSRVEEGVPQVLVLISAGPSSDEIRY GVVALKQASVFSFGLGAQAASRAELQHIAATDDNLVFTVPEFRSFG DLQEKLLPYIVGVAQRHIVLKPPTIVTQEYGLNENW
Proteasome subunit beta type-5 Variant 2 SEQ ID NO:122	MALASVLERPLPVNQRGFFGLGGRADLLDLGPGSLSDGLSLAAPG WGVPEEPGIEMLHGTTTLAFKFRHGVIVAADSRATAGAYIASQTV KKVIEINPYLLGTMAGGAADCSFWERLLARQCRIYELRNKERISVA AASKLLANMVYQYKGMGLSMGTMICGWDKRGVPSEVLCLKPKS FGMYLFCGCAERIGNMARPLLRGQ
Proteasome subunit beta type-5 Variant 3 SEQ ID NO:123	MAGGAADCSFWERLLARQCRIYELRNKERISVAAASKLLANMVY QYKGMGLSMGTMICGWDKRGPLYVVDSEGNRISGATFSVSGSGS VYAYGVMDRGYSYDLEVEQAYDLARRAIYQATYRDAYS GGAVN LYHVREDGWIRVSSDNVADLHEKYSGSTP
Proteasome subunit beta type-5 Variant 4 SEQ ID NO:124	MALASVLERPLPVNQRGFFGLGGRADLLDLGPGSLSDGLSLAAPG WGVPEEPGIEMLHGTTTLAFKASTTWTVKGTGFQGPSSL

Proteasome subunit beta type-5 Variant 5 SEQ ID NO:125	XGIEMLHGTTTTLAFKFRHGVIVAADSRATAGAYIASQTVKKVIEIN PYLLGTMAGGAADCSFWERLLARQCRIYELRNKERISVAAASKLL ANMVYQYKGMGLSMGMTMICGWDKRGPG
Heterogeneous nuclear ribonucleoproteins A2/B1 Variant 2 SEQ ID NO:126	MEREKEQFRKLFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPA SKRSRGFGFVTFSSMAEVDAAAMAARPHSIDGRVVEPKRAVAREES GKPGAHVTVKKLFGGKEDTEEHHLRDYFEEYGKIDTIEIITDRQS GKKRGFGFVTFDDHDPVDKIVLQKYHTINGHNAEVRKALSRQEM QEVQSSRSRGGGNFGFGDSRGGGGNFGPGPSNFRGGSDGYGSGR GFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGG GYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMKSGNFGGS RNMGGPYGGGNYGPGGSGGSGGYGGRSRY
Heterogeneous nuclear ribonucleoproteins A2/B1 Variant 3 SEQ ID NO:127	MEREKEQFRKLFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPA SKRSRGFGFVTFSSMAEVDAAAMAARPHSIDGRVVEPKRAVAREES GKPGAHVTVKKLFGGKEDTEEHHLRDYFEEYGKIDTIEIITDRQS GKKRGFGFVTFDDHDPVDKIVLQKYHTINGHNAEVRKALSRQEM QEVQSSRSRGGGNFGFGDSRGGGGNFGPGPSNFRGGSDGYGSGR GFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGG GYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMKSGNFGGS RNMGGPYGGGNYGPGGSGGSGGYGGRSRY
Heterogeneous nuclear ribonucleoproteins A2/B1 Variant 4 SEQ ID NO:128	MEKTLETVPLERKKREKEQFRKLFIGGLSFETTEESLRNYYEQWGK LTDCVVMRDPASKRSRGFGFVTFSSMAEVDAAAMAARPHSIDGRV VEPKRAVAREESGKPGAHVTVKKLFGGKEDTEEHHLRDYFEEY GKIDTIEIITDRQSGKKRGFGFVTFDDHDPVDKIVLQKYHTINGHNA EVRKALSRQEMQEDLEVAILEVAPVMEEEEEDMVVEDLDMATRV GATEVVMTTMEEIIMEVEITMILEIITSNLLTTVQ
Beta enolase Variant 2 SEQ ID NO:129	MAMQKIFAREILDSRGNTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRYLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPYLRHI ADLAGNPDLILPVPFNVINGGSHAGNKLAMQEFMILPVGASSFKE AMRIGAEVYHHLKGVIKAKYGKDATNVGDEGGFAPNILENNEAL ELLKTAIQAAAGYPDKVVIGMDVAASEFYRNGKYDLDFKSPDDPAR HITGEKLGELYKSFKNYPVVSIEDPFDQDDWATWTSFLSGVNIQIV GDDLTVTNPKRIAQAVEKKACNCLLLKVNQIGSVTESIQACKLAQS NGWGVVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKY NQLMREEALGDKAIFAGRKFERNPKAK
Beta enolase Variant 3 SEQ ID NO:130	MAMQKIFAREILDSRGNTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRYLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPYLRHI ADLAGNPDLILPVPFNVINGGSHAGNKLAMQEFMILPVGASSFKE AMRIGAEVYHHLKGVIKAKYGKDATNVGDEGGFAPNILENNEAL ELLKTAIQAAAGYPDKVVIGMDVAASEFYRNGKYDLDFKSPDDPAR HITGEKLGELYKSFKNYPVVSIEDPFDQDDWATWTSFLSGVNIQIV GDDLTVTNPKRIAQAVEKKACNCLLLKVNQIGSVTESIQACKLAQS NGWGVVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKY NQLMREEALGDKAIFAGRKFERNPKAK
Beta enolase Variant 4 SEQ ID NO:131	MAMQKIFAREILDSRGNTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRYLGKAKFGANAILGVSLAVCKAGAAEKGVPYLR HIADLAGNPDLILPVPFNVINGGSHAGNKLAMQEFMILPVGASSF KEAMRIGAEVYHHLKGVIKAKYGKDATNVGDEGGFAPNILENNE

	ALELLKTAIQAAGYDPKVVIGMDVAASEFYRNGKYDLDFKSPDDP ARHITGEKLGELYKSFKNYPVVSIEDPFDQDDWATWTSFLSGVNI QIVGDDLTVTNPKRIAQAVEKKACNCLLLKVNQIGSVTESIQACKL AQSNWGWVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERL AKYNQLMRIEEALGDKAIFAGRKFERNPKAK
Beta enolase Variant 5 SEQ ID NO:132	MAMQKIFAREILDSRGNPTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPLYRHI ADLAGNPDILPVPFNFVINGGSHAGNKLAMQEFMILPVGASSFKE AMRIGAEVYHHLKGVIAKYGKDATNVGDEGG
Beta enolase Variant 6 SEQ ID NO:133	MAMQKIFAREILDSRGNPTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPLYRHI ADLAGNPDILPVPFNFVINGGSHAGNKLAMQEFMILPVGASSFKE AMRIGAEVYHHLKGV
Beta enolase Variant 7 SEQ ID NO:134	MAMQKIFAREILDSRGNPTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPLYRHI ADLAGNPDILPVP
Beta enolase Variant 8 SEQ ID NO:135	MAMQKIFAREILDSRGNPTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPLYRHI ADLAGNPDILPVP
Beta enolase Variant 9 SEQ ID NO:136	MAMQKIFAREILDSRGNPTVEVDLHTAKGRFRAAVPSGASTGIYE ALELRDGDKGRLGKGVLKAVENINNTLGPALLQKKLSVVDQEK VDKFMIELDGTENKSKFGANAILGVSLAVCKAGAAEKGVPLYRHI ADLAGNPDILPVPFNFVIN
Beta enolase Variant 10 SEQ ID NO:137	MAMQKIFAREILDSRGNPTVEVDLHTAK
Glutathione S-transferase P Variant 2 SEQ ID NO:138	MPPYTVVYFPVRGRCAALRMILLADQGQSWKEEVTVTVETWQEGS LKASCLYGQLPKFQDGLTLYQSNITLRLHGLRTLGLYKGDQEEAA LVDMVNDGVEDLRCKYISLIYTNYSFADYNLLDLLLIEVLAPGC LDAFPLLSAYVGRLSARPKLKAFLASPEYVNLPIGNGKQ
Glutathione S-transferase P Variant 3 SEQ ID NO:139	EAGKDDYVKALPGQLKPFETLLSQNQGGKTFIVGDQVSIWPHAVP SSPPSASRWTQVSPSLTTCWTCC
Glutathione S-transferase Mu 3 Variant 2 SEQ ID NO:140	MSCESSMVLGYWDIRGLAHAIRLLLEFTDTSYEEKRYTCGEAPDY DRSQWLDVKFKLDLDFPNLPYLLDGKNKITQSNAILRYIARKHNM CGETEEKIRVDIENQVMDFRITQLIRLCYSSDHEKLPQYLEELPG QLKQFSMFLGKFSWFAGEKLTFVDFLTID
Glutathione S-transferase Mu 3 Variant 3	MSCESSMVLGYWDIRGLAHAIRLLLEFTDTSYEEKRYTCGEAPDY DRSQWLDVKFKLDLDFPNLPYLLDGKNKITQSNAILRYIARKHNM CGETEEKIRVDIENQVMDFRITQLIRLCYSSDHEKLPQYLEELPG

SEQ ID NO:141	QLKQFSMFLGKFSWFAGEKLTFFVDFLTVDILDQNRIFDPKCLDEFP NLKAFMCRFGDVLHFLYKTLTAPLGPADP
Rho 23 GTPase-activating protein Variant 2 SEQ ID NO:142	MNGVAFCLVGIPPRPEPRPPQLPLGPRDGCSPRRPFPWQGPRTLLL YKSPQDGFGLRHFIVYPPEASVHCSLKEEENGGRGGGSPRYRL EPMDTIFVKNVKEDGPAHRAGLRTGDRLVKVNGESVIGKTYSQVI ALIQNSDDTLELSIMPKDEDILQLAYSQDAYLKGNPYSGEARSIE PPICYPRKTYAPPARASTRATMVPEPTSALPSDPRSPAASWSDPGLR VPPAARAHLDNSSLGMSQPRPSPGAFPHLSSEPRTTPRAFPEPGSRVP PSRLECQQUALSHWLSNQVPRRAGERRCPAMAPRARSASQDRLEEV AAPRPWPCSTSQDALSQLGQEGWHRARSDDYLSRATRSALGPG ALVSPRFERCGWASQRSSARTPACPTRDLPGPQAPPNSQGLDDL GYIGYRSYSPSFQRRGTGLHALSFRDSPFGGLPTFNLAQSPASFPPE ASEPPRVVRPEPSTRALEPPAEDRGDEVVLRQKPPTGRKVQLTPAR QMNLFQGFDESPEPEASGRGERLGRKVAPLATTEDSLASIPFIDEPTS PSIDLQAKHVPASAVVSSAMNSAPVLGTSPSSPTFTFTLGRHYSD CSSIKAGRSSYLLAITTERSKSCDDGLNTRDEGRVLRRLPNRIPS LRMLRSFFTDGSLDSWGTSEDADAPSKRHSTSDLSDATFSDIRREG WLYYKQILTCKKGKAGSGLRQWKRVYAALRARSLSLKERREPG PAAAGAAAAGAGEDEAAPVCIGSCLVDISYSETKRRHVRLTTAD FCEYLFQAEDRDDMLGWIRAIENSRAEGEDPGCANQALISKKLN DYRKVSHSSGPKADSSPKGSRGLGGLKSEFLKQSAARGLRTQDLP AGSKDDSAAPKTPWGGINIIKKNKKAAPRAFGVRLEECQPATENQ RVPLIVAACCRIVEARGLESTGIYRVPGNNVSSVLEQLNRGPGD INLQDERWQDLNVISSLLKSFFRKLPEPLFTDDKYNDFIEANRIEDA RERMRTLRLKLDLPGHYETLKFLVGHLKTIADHSEKNKMEPRN LALVFGPTLVRTSEDNMTDMVTHMPDRYKIVETLIQHSDWFFSDE EDKGERTPVGDKEPQAVPNIEYLLPNIGRTVPPGDPGSADLLEI
ARHGAP23 Variant 3 SEQ ID NO:143	MDTIFVKNVKEDGPAHRAGLRTGDRLVKVNGESVIGKTYSQVIAL IQNSDDTLELSIMPKDEDILQLAYSQDAYLKGNPYSGEARSIEPP PICYPKRTYA
ARHGAP23 Variant 4 SEQ ID NO:144	XFFSDEEDKGERTPVGDKEPQAVPNIEYLLPNIGRTVPPGDPGSDST TCSSAKSKVRMKAILKA
ARHGAP23 Variant 5 SEQ ID NO:145	XTFSDIRREGWLYYKQILTCKKGKAEDRDDMLGWIRAIENSRAEG EDPGCANQALISKKLNDYRKVSHSSGPKADSSPKGSRGLGGLKSEF LKQSAARGLRTQDLPAGSKDDSAAPKTPWGGINIIKKNKKAAPRA FGVRLEECQPATENQRVPLIVAACCRI
ARHGAP23 Variant 6 SEQ ID NO:146	IRDLPGHYETLKFLVGHLKTIADHSEKNKMEPRNLALVFGPTLVR TSEDNMTDMVTHMPDRYKIVETLIQHSDWFFSDEEDKGERILPPV VQPSRVRGPPRRSRTPGRCWRSPSSRPSTASARSGGRRGGWAA
Rho 32 or Rho GTPase-activating protein 32 (ARHGAP32) SEQ ID NO:147	METESSTLGDSDVFWLESEVIIQVTDCEEEEREKFRKMKSSVH SEEDDFVPELHRNVHPRERPDWEETLSAMARGADVPEIPGDLTLK TCGSTASMKVHKVKKLPFTKGHPKMAECAHFHYENVEFGSIQLS LSEEQNEVMKNGCESKELVYLQIACQKSWIVKRSYEDFRVLDK HLHLCIYDRRFSQSELPRSDTLKDSPESTQMLMAYLSRLSAIAG NKINCGPALTWMEIDNKGHLLVHEESSINTPAVGAAHVIKRYTA RAPDELTLVGDIVSVIDMPPKVLSTWWRGKHGFQVGLFPGHCVE

	LINQKVPSVTNSVPKPVSKKHGKLITFLRTFMKSRPTKQKLKQRG ILKERVFGCDLGEHLLNSGFVQVLQSQCTAFIERYGIVDGIYRLSG VASNIQRLRHEFDSEHVPDLTKEPYVQDIHSVGLCKLYFRELNPPL LTYQLYEKFSDAVSAATDEERLIKIHDVIQQLPPPHYRTLFLMRHL SLLADYCSITNMHAKNLAIVWAPNLLRSKQIESACFSGTAAFMEVR IQSVVVEFILNHVDVLFSGRISMAMQEGAASLSRPKSLLVSSPSTKL LTLEEAQARTQAQVNSPIVTENKYIEVGEGPAALQGKFHTIIEFPLE RKRPPQNMKKSPVGSWRSFFNLGKSSSVSKRKLQRNESEPSEMKA MALKGGRAEGTLRSAKSEESLTSLHAVDGDGSKLFRPRRPRSSDAL SASFNGEMLGNRCNSYDNLPHDNESEEEGGLLHIPALMSPHSAED VDLSPPDIGVASLDFDPMFQCSPPKAESECELESGASFLDSPGYSKD KPSANKKDAETGSSQCQTPGSTASSEPVSPLOEKLSPFFTLDSLPT DKSSKPSFTEKVVYAFSPKIGRKLKSPSMSISEPISVTLPPRVSEVI GTVSNNTAQNASSTWDKCVEERDATNRSPTQIVKMKTNETVAQE AYESEVQPLDQVAAEEVELPGKEDQSVSSSQSKAVASGQTQTGAV THDPPQDSVPVSSVSLIPPPPPKNNVARMLALALAESAAQASTQSL KRPGTSQAGYNTYGDIAVATTEDNLSSSYSAVALDKAYFQTDPA EQFHLQNNAPGNCDHPLPETTATGDPHTSNTTESGEQHHQVDTLG NQPHQAYLSGDPEKARITSVPLDSEKSDDHVSFEDQSGKNSMPTV SFLDQDQSPPRFYSQDQPPSYLGASVDKLHHPLEFADKSPTPPPLPS DKIYPPSGSPEENTSTATMTYMTTTPATAQMSTKEASWDVAEQPT TADFAAATLQRTNRTNRPLPPPSQRSAEQPPVVGQVQAATNIGLN NSHKVQGVVPVPERPPEPRAMDDPASAFISDSGAAAAQCPMATAV QPGLPEKVRDGARVPLLHLRAESVPAHPCGFPAPLPTRMMESKM IAAIHSSADATSSSNYHSFVTASSTSVDDALPLPLPVPQPKHASQK TVYSSFARPDVTTEPFGPDNCLHFNMTPNQCQYRPQSVPPHHNKLE QHQVYGARSEPPASMGLRYNTYVAPGRNASGHHKPCSRVEYVS SLSSSVRNTCYPEDIPPYPTIRRVSQSLHAPPSSMIRSVPISTEVPDD EPAYCPRPLYQYKPYQSSQARSQYHVTQLQPYFENGVRVHYRSPY SSSSSSYSPDGALCDVDAYGTVQLRPLHRLPNRDFAFYNPRLQG KSLYSYAGLAPRPRANVTGYFSPNDHNVSMPAADVKHITYTSW DLEDMEKYRMQSIRRESRARQKVKGPVMSQYDNMTPAVQDDL GIYVIHLRSKSDPGKTGLLSVAEGKESRHAAKAISPEGEDRFYRRH PEAEMDRAHHHGGHGSTQPEKPSLPQKQSSLRSRKLPMGCSLPE HRAHQEASHRQFCESKNGPPYPQGAGQLDYGSKGIPDTSEPVSYH NSGVKYAASGQESLRLNHKEVRLSKEMERPWVRQPSAPEKHSRD CYKEEEHLTQIVPPPKPERSHSLKLHHTQNVERDPSVLYQYQPHG KRQSSVTVVSQYDNLEDYHSLPQHQRGVFGGGMGTYVPPGFPH PQSRTYATALGQGAFLPAELSLQHPETQIHAE
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[0079] As used herein the terms “sequence identity” or “sequence homology,” which can be used interchangeably, refer to an exact amino acid-to-amino acid correspondence of two polypeptide sequences. Typically, techniques for determining sequence identity include determining the amino acid sequence of a polypeptide, and comparing these sequences to a second amino acid sequence. Two or more sequences can be compared by determining their “percent identity,” also referred to as “percent homology.” The percent identity to a reference sequence, which may be a sequence within a longer molecule, may be calculated as the number of exact matches between two optimally aligned sequences divided by the length of the reference sequence

and multiplied by 100. Percent identity may also be determined, for example, by comparing sequence information using the advanced BLAST computer program, including version 2.2.9, available from the National Institutes of Health. The BLAST program is based on the alignment method of Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* 87:2264-2268 (1990) and as discussed in Altschul, et al., *J. Mol. Biol.* 215:403-410 (1990); Karlin and Altschul, *Proc. Natl. Acad. Sci. USA* 90:5873-5877 (1993); and Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997). Briefly, the BLAST program defines identity as the number of identical aligned symbols (i.e., nucleotides or amino acids), divided by the total number of symbols in the shorter of the two sequences. The program may be used to determine percent identity over the entire length of the sequences being compared. Default parameters are provided to optimize searches with short query sequences, for example, with the blastp program. The program also allows use of an SEG filter to mask-off segments of the query sequences as determined by the SEG program of Wootton and Federhen, *Computers and Chemistry* 17: 149-163 (1993). Ranges of desired degrees of sequence identity are approximately 80% to 100% and integer values in between. Percent identities between a disclosed sequence and a claimed sequence can be at least about 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity. In general, an exact match indicates 100% identity over the length of the reference sequence. In some cases, reference to percent sequence identity refers to sequence identity as measured using BLAST (Basic Local Alignment Search Tool). In other cases, ClustalW can be used for multiple sequence alignment. Still other programs for comparing sequences and/or assessing sequence identity include the Needleman-Wunsch algorithm and the Smith-Waterman algorithm (see, e.g., the EMBOSS Water aligner. Optimal alignment may be assessed using any suitable parameters of a chosen algorithm, including default parameters.

[0080] In one aspect, the sequence identity is at least about 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% (complete) sequence identity (homology). In one aspect, the sequence identity is over a region of at least about 10, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000 or more amino acids, or the full length of a polypeptide.

[0081] As used herein, the term “fragment” refers at least 10 consecutive amino acids of a polypeptide that can be detected using methods known in the art. Fragment may refer to an “active” fragment which is a portion of the polypeptide required for polypeptide function. The fragment can be an “immunogenic” fragment which is a portion of the polypeptide which binds an antibody.

[0082] As used herein, a “sample” or “biological sample” is meant to refer to any “biological specimen” collected from a subject, and that is representative of the content or composition of the source of the sample, considered in its entirety. A sample can be collected and processed directly for analysis, or be stored under proper storage conditions to maintain sample quality until analyses are completed. Ideally, a stored sample remains equivalent to a freshly-collected specimen. The source of the sample can be an internal organ, vein, artery, or even a fluid. Non-limiting examples of sample include blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair. In one aspect, the sample is selected from the group consisting of blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair. In certain aspects the sample is a blood sample and the subject is human. Blood samples include whole blood, plasma and serum.

[0083] The at least one protein refers to one or more proteins. In an aspect, the at least one polypeptide comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more proteins. In one aspect the at least one protein is selected from the group consisting of Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat Shock Protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In another aspect, the at least one protein is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31,

SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147 or a fragment thereof.

[0084] . In one aspect the at least one protein is selected from the group consisting of Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat Shock Protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a combination thereof. In another aspect, the at least one protein is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7,

SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147 or a combination thereof.

[0085] The biomarkers of the present invention may be used individually or in combinations for the diagnosis of cervical cancer. Any combination of the biomarkers listed above and in Table 1 can be used for the diagnosis of cervical cancers.

[0086] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III,

Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In an additional aspect, the at least one polypeptide comprises a polypeptide having at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 and at least one polypeptide selected from a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0087] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase and neurofibromin I; Farnesyl pyrophosphate synthase and Glyceraldehyde-3 phosphate dehydrogenase; Farnesyl pyrophosphate synthase and Protein 1 containing fibronectin domain type III; Farnesyl pyrophosphate synthase and Eukaryotic initiation factor 4A-I; Farnesyl pyrophosphate synthase and L-lactate dehydrogenase chain B; Farnesyl pyrophosphate synthase and Nuclear heterogeneous Ribonucleoprotein A1; Farnesyl pyrophosphate synthase and polycystic kidney disease protein 1-like 1; Farnesyl pyrophosphate synthase and heat shock protein Cognate 71 kDa; Farnesyl pyrophosphate synthase and Ankyrin-3; Farnesyl pyrophosphate synthase and Rho 23; Farnesyl pyrophosphate synthase and Rho 23-GTPase-activating protein; Farnesyl pyrophosphate synthase and Cytoskeletal Keratin 78 type II; Farnesyl pyrophosphate synthase and collagen chain (VI) Alpha-3; Farnesyl pyrophosphate synthase and Beta subunit of proteasome type-5; Farnesyl pyrophosphate synthase and Heterogeneous nuclear ribonucleoproteins A2/B1; Farnesyl pyrophosphate synthase and Histone H2B type 1-B; Farnesyl pyrophosphate synthase and homolog of DnaJ subfamily C member 13; Farnesyl pyrophosphate synthase and Beta enolase; Farnesyl pyrophosphate synthase and Glutathione S-transferase P; Farnesyl pyrophosphate synthase and Glutathione S-transferase Mu 3; or fragments thereof.

[0088] In another aspect, the at least one polypeptide comprises SEQ ID NO:1 and SEQ ID NO:2; SEQ ID NO:1 and SEQ ID NO:3; SEQ ID NO:1 and SEQ ID NO:4; SEQ ID NO:1 and SEQ ID NO:5; SEQ ID NO:1 and SEQ ID NO:6; SEQ ID NO:1 and SEQ ID NO:7; SEQ ID NO:1 and SEQ ID NO:8; SEQ ID NO:1 and SEQ ID NO:9; SEQ ID NO:1 and SEQ ID NO:10; SEQ ID NO:1 and SEQ ID NO:11; SEQ ID NO:1 and SEQ ID NO:12; SEQ ID NO:1 and SEQ ID NO:13;

SEQ ID NO:1 and SEQ ID NO:14; SEQ ID NO:1 and SEQ ID NO:15; SEQ ID NO:1 and SEQ ID NO:16; SEQ ID NO:1 and SEQ ID NO:17; SEQ ID NO:1 and SEQ ID NO:18; SEQ ID NO:1 and SEQ ID NO:19; SEQ ID NO:1 and SEQ ID NO:20; or fragments thereof.

[0089] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, neurofibromin or a fragment thereof, and at least one additional polypeptide selected from the group consisting of Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat Shock Protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0090] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Glyceraldehyde-3 phosphate dehydrogenase or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0091] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Protein 1 containing fibronectin domain type III or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of

DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0092] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Eukaryotic initiation factor 4A-I or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, and Glutathione S-transferase Mu 3 and a fragment thereof.

[0093] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, L-lactate dehydrogenase chain B or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0094] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Nuclear heterogeneous Ribonucleoprotein A1 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B,

homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0095] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, polycystic kidney disease protein 1-like 1 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0096] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, heat shock protein Cognate 71 kDa or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0097] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Ankyrin-3 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ

subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0098] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Rho 23 GTPase-activating protein or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0099] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Cytoskeletal Keratin 78 type II or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0100] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, collagen chain (VI) Alpha-3 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ

subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0101] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Beta subunit of proteasome type-5 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0102] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Heterogeneous nuclear ribonucleoproteins A2/B1 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0103] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Histone H2B type 1-B or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, homolog of DnaJ subfamily

C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0104] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, homolog of DnaJ subfamily C member 13 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0105] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Beta enolase or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

[0106] In another aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Glutathione S-transferase P or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B

type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase Mu 3 and a fragment thereof.

[0107] In one aspect, the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof, Glutathione S-transferase Mu 3 or a fragment thereof, and at least one additional polypeptide selected from the group consisting of neurofibromin, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, polycystic kidney disease protein 1-like 1, heat shock protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, collagen chain (VI) Alpha-3, Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P and a fragment thereof.

[0108] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:2 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs:3-20 and a fragment thereof.

[0109] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:3 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2 and 4-20 and a fragment thereof.

[0110] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:4 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-3 and 5-20 and a fragment thereof.

[0111] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:5 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-4 and 6-20 and a fragment thereof.

[0112] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:6 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-5 and 7-20 and a fragment thereof.

[0113] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:7 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-6 and 8-20 and a fragment thereof.

[0114] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:8 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-7 and 9-20 and a fragment thereof.

[0115] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:9 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-8 and 10-20 and a fragment thereof.

[0116] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:10 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-9 and 11-20 and a fragment thereof.

[0117] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:11 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-10 and 12-20 and a fragment thereof.

[0118] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:12 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-11 and 13-20 and a fragment thereof.

[0119] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:13 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-12 and 14-20 and a fragment thereof.

[0120] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:14 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-13 and 15-20 and a fragment thereof.

[0121] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:15 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-14 and 16-20 and a fragment thereof.

[0122] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:16 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-15 and 17-20 and a fragment thereof.

[0123] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:17 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-16 and 18-20 and a fragment thereof.

[0124] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:18 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-17 and 19-20 and a fragment thereof.

[0125] In another aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:19 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-18 and 20 and a fragment thereof.

[0126] In one aspect, the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof, and a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:20 or a fragment thereof, and at least one additional polypeptide having at least about 70% sequence identity to a polypeptide an amino acid sequence selected from the group consisting of SEQ ID NOs:2-19 and a fragment thereof.

[0127] In a further aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay. In a specific aspect, the detecting is by lateral flow.

[0128] In one aspect, the method also includes administering a treatment to the subject. In an additional aspect, the treatment is surgery, radiation, chemotherapy, targeted therapy and/or immunotherapy.

[0129] The term "treatment" is used interchangeably herein with the term "therapeutic method" and refers to both 1) therapeutic treatments or measures that cure, slow down, lessen symptoms of, and/or halt progression of a diagnosed pathologic conditions or disorder, and 2) and prophylactic/ preventative measures. Those in need of treatment may include individuals already having a particular medical disorder as well as those who may ultimately acquire the disorder (i.e., those needing preventive measures).

[0130] The terms "therapeutically effective amount", "effective dose," "therapeutically effective dose", "effective amount," or the like refer to that amount of the subject compound that will elicit the biological or medical response of a tissue, system, animal or human that is being sought by the researcher, veterinarian, medical doctor or other clinician.

[0131] The terms "administration of" and or "administering" should be understood to mean providing a pharmaceutical composition in a therapeutically effective amount to the subject in need of treatment. Administration routes can be enteral, topical or parenteral. As such, administration routes include but are not limited to intracutaneous, subcutaneous, intravenous, intraperitoneal, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, transdermal, transtracheal, subcuticular, intraarticulare, subcapsular, subarachnoid, intraspinal and intrasternal, oral, sublingual buccal, rectal, vaginal, nasal ocular administrations, as well infusion, inhalation, and nebulization. The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical

administration. The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. Suitable unit dosage forms, include, but are not limited to powders, tablets, pills, capsules, lozenges, suppositories, patches, nasal sprays, injectables, implantable sustained-release formulations, lipid complexes, etc.

[0132] The biomarkers and polypeptides disclosed herein are useful for the diagnosis of cervical cancer. As used herein, the term “diagnosis” refers to any method of detecting or determining that a subject has cervical cancer.

[0133] In another embodiment, the present invention provides a method of diagnosing cervical cancer in a subject by detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin 1, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate protein 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-147 or a fragment thereof; and diagnosing cervical cancer based on the detection of at least one polypeptide. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof.

[0134] In one aspect, the sample is blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair. In certain aspects, the sample is a blood sample and the subject is human.

[0135] In an additional aspect, the at least one polypeptide is selected is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Cognate thermal

shock protein 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In a further aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having an amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0136] In another aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay. In a specific aspect, the detecting is by lateral flow. In one aspect, the method also includes administering a treatment to the subject. In certain aspects, the treatment is surgery, radiation, chemotherapy, targeted therapy and/or immunotherapy.

[0137] In some embodiments, diagnosing, predicting, and/or monitoring the status or outcome of a cancer may comprise determining a therapeutic regimen. Determining a therapeutic regimen may comprise administering an anti-cancer therapeutic. Alternatively, determining the treatment for the cancer may comprise modifying a therapeutic regimen. Modifying a therapeutic regimen may comprise increasing, decreasing, or terminating a therapeutic regimen.

[0138] Treatment options for cervical cancer include surgery, radiation, chemotherapy, targeted therapy, and immunotherapy.

[0139] Surgical Treatment for cervical cancer depends on the type and stage of cervical cancer. For precancerous lesion surgical interventions include ablation and excision surgery. Surgical intervention for advanced cervical cancer include hysterectomy (simple or radical) and Trachelectomy.

[0140] Radiation is used to treat cervical cancer and to treat cervical cancer recurrence. There are two types of radiation typically used for treating cervical cancer, external beam radiation and brachytherapy. External beam radiation therapy (EBRT) aims x-rays at the cancer from a machine outside the body. Treatment is much like getting a regular x-ray, but the radiation dose is stronger. When EBRT is used as the main treatment for cervical cancer, it is usually combined with chemotherapy. Brachytherapy, or internal radiation therapy, puts a source of radiation in or near

the cancer. Brachytherapy is mainly used in addition to EBRT as a part of the main treatment for cervical cancer.

[0141] Chemotherapy is also used to treat cervical cancer, wither alone or in combination with another method. Chemotherapy may include Cisplatin, Carboplatin, Paclitaxel (Taxol), Topotecan, docetaxel (Taxotere), ifosfamide (Ifex), 5-fluorouracil (5-FU), irinotecan (Camptosar), gemcitabine (Gemzar) and mitomycin. Targeted therapy for the treatment of cervical cancer includes Bevacizumab. Immunotherapy for the treatment of cervical cancer includes Pembrolizumab (PD-1 inhibitor).

[0142] In an additional embodiment, the present invention provides a method of treating cervical cancer in a subject in need thereof, the method is detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-147 or a fragment thereof; diagnosing cervical cancer based on the detection of the at least one polypeptide; and administering a treatment to the subject. In one aspect, the sample is a blood sample. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-20 or a fragment thereof.

[0143] In an additional aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of

proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In a further embodiment, the at least one polypeptides is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide with an amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0144] In another aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay or immunoassay. In a specific aspect, the detecting is by lateral flow assay. In an additional aspect, the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy. In a further aspect, the chemotherapy is Cisplatin, Carboplatin, Paclitaxel, Topotecan, docetaxel, ifosfamide, 5-fluorouracil, irinotecan, gemcitabine or mitomycin. In certain aspects, the targeted therapy is bevacizumab and the immunotherapy is pembrolizumab.

[0145] The biomarkers of the present invention can be used to predict response to treatment for cervical cancer.

[0146] In a further embodiment, the present invention provides methods of predicting a response to treatment for a subject having cervical cancer by detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having amino acid sequence selected from SEQ ID NOs: 1-147 or a fragment thereof; and predicting a response to treatment based on the detection of the at least one polypeptide. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:1-20 or a fragment thereof.

[0147] In one aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In another aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0148] In an additional aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow or immunoassay. In a further aspect, the detecting is by lateral flow assay. In certain aspects, the treatment is surgery, radiation, chemotherapy, targeted therapy and immunotherapy.

[0149] The biomarkers of the present application are useful for determining the stage of cervical cancer. Cervical cancer can be classified on different scales. The Papanicolaou system classifies the lesions in degrees of severity, from grade I that corresponds to normal cytology, to grade V that corresponds to invasive squamous cancer of the cervix. The Richart classification system classifies the results of a cytology into: Negative, Reactive or not classifiable squamous atypical, HPV infection, Cervical intraepithelial neoplasia (CIN) grades I, II and III, carcinoma in situ and invasive squamous cancer of the cervix. Finally, the Bethesda nomenclature classifies the results of a cytology as: Negative, ASCUS-ASCH, low-grade intraepithelial lesions, high-grade intraepithelial lesions and invasive squamous cancer of the cervix.

[0150] The FIGO (International Federation of Gynecology and Obstetrics) staging system is used most often for cancers of the female reproductive organs, including cervical cancer. For cervical cancer, the clinical stage is used and is based on the results of the doctor's physical exam, biopsies, imaging tests, and a few other tests that are done in some cases, such as cystoscopy and proctoscopy.

Table 2

FIGO Stage		Stage description
I		
	IA	The cancer cells have grown from the surface of the cervix into deeper tissues of the cervix. Cancer has not spread to nearby lymph nodes. Cancer has not spread to distant sites. It has not spread to distant sites.
	IA1	The area of cancer can only be seen with a microscope and is less than 3 mm (about 1/8-inch) deep. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IA2	The area of cancer can only be seen with a microscope and is between 3 mm and 5 mm (about 1/5-inch) deep. It not has not spread to nearby lymph nodes. It has not spread to distant sites.
	IB	This includes stage I cancer that has spread deeper than 5 mm (about 1/5 inch) but is still limited to the cervix. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IB1	The cancer is deeper than 5 mm (about 1/5-inch) but not more than 2 cm (about 4/5-inch) in size. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IB2	The cancer is at least 2 cm in size but not larger than 4 cm. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IB3	The cancer is at least 4 cm in size and limited to the cervix. It has not spread to nearby lymph nodes. It has not spread to distant sites.

II		The cancer has grown beyond the cervix and uterus, but hasn't spread to the walls of the pelvis or the lower part of the vagina. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IIA	The cancer has grown beyond the cervix and uterus but has not spread into the tissues next to the cervix (called the parametria). It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IIA1	The cancer is not larger than 4 cm (about 1 3/5 inches). It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IIA2	The cancer is 4 cm or larger. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IIB	The cancer has grown beyond the cervix and uterus and has spread into the tissues next to the cervix (the parametria). It has not spread to nearby lymph nodes. It has not spread to distant sites.
III		The cancer has spread to the lower part of the vagina or the walls of the pelvis. The cancer may be blocking the ureters (tubes that carry urine from the kidneys to the bladder). It might or might not have not spread to nearby lymph nodes. It has not spread to distant sites.
	IIIA	The cancer has spread to the lower part of the vagina but not the walls of the pelvis. It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IIIB	The cancer has grown into the walls of the pelvis and/or is blocking one or both ureters causing kidney problems (called hydronephrosis). It has not spread to nearby lymph nodes. It has not spread to distant sites.
	IIIC	The cancer can be any size. Imaging tests or a biopsy show the cancer has spread to nearby pelvic lymph nodes (IIIC1) or para-aortic lymph nodes (IIIC2). It has not spread to distant sites.
IV		The cancer has grown into the bladder or rectum or to far away organs like the lungs or bones.

	IVA	The cancer has spread to the bladder or rectum or it is growing out of the pelvis.
	IVB	The cancer has spread to distant organs outside the pelvic area, such as distant lymph nodes, lungs or bones.

[0151] In another embodiment, the present invention provides methods for determining the stage of cervical cancer in a subject in need thereof by detecting at least one polypeptide in a sample from the subject; wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-147 or a fragment thereof; and determining the stage of cervical cancer in the subject based on the detection of the at least one polypeptide. In one aspect, the at least one polypeptide is a polypeptide having the amino acid sequence selected from SEQ ID NOs:1-20 or a fragment thereof.

[0152] In one aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In another aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at

least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0153] In an additional aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay. In a specific aspect, the detecting is by lateral flow assay. In a further aspect, the method also includes administering a treatment to the subject. In certain aspects, the treatment is surgery, radiation, chemotherapy, targeted therapy or immunotherapy. In one aspect, the cervical cancer is stage I, stage II, stage III or stage IV.

[0154] In one embodiment, the present invention provides a kit with a sample collection unit; a lateral flow device; and instructions for using the lateral flow device.

[0155] Sample collection device is any device that can be used to collect a sample. The sample blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair.

[0156] A lateral flow device is a simple to use diagnostic device used to confirm the presence or absence of a target analyte, such as pathogens or biomarkers in a sample. The most commonly known type of lateral flow rapid test strip is the pregnancy test.

[0157] Typically lateral flow assays use a device comprises several pads (made of a series of capillary beds, capable of transporting a fluid): a sample pad to receive the liquid sample; a conjugate pad, including reactive molecules used to visualize positive control, a positive line and a test line.

[0158] For the detection of a target protein, the conjugate pad includes antibodies specific for the target protein conjugated to a detectable tag; a positive line (positive control) is generated comprising fixed anti- target protein antibodies (for example anti IgG antibodies), and a test line was generated comprising fixed anti- target protein antibodies. When the sample pad is contacted with a sample containing the target protein, the target protein reacts with the anti- target protein antibodies conjugated to a detectable tag in the conjugate pad. As the liquid flows to the test and positive lines, the target protein present in the sample, conjugated with the labeled antibodies reacted with the fixed anti-target protein antibodies on the test line, and anti- target protein antibodies conjugated to the detectable tag but not conjugated to the target protein reacts with the fixed anti-Ig antibodies on the positive line. Both reactions generate a positive reading on the test line, and on the positive line.

[0159] In one aspect, the lateral flow device detects at least one polypeptide selected from Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-147 or a fragment thereof. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:1-20 or a fragment thereof.

[0160] In an additional aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In a further aspect, the at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide selected from a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NO:2-20 or a fragment thereof.

[0161] In another aspect, the lateral flow device detects the at least one polypeptide by an immunoassay. In one aspect, the sample collection unit collects a blood sample.

[0162] In an additional embodiment, the present invention provides a use of the detection of at least one polypeptide for the diagnosis of cervical cancer in a subject in need thereof, wherein the at least one polypeptide is selected from Farnesyl pyrophosphate synthase, neurofibromin I,

Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs: 1-147 or a fragment thereof. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:1-20 or a fragment thereof.

[0163] In a further aspect, the at least one polypeptide is detected in a sample from the subject and the sample is a blood sample. In another aspect, the at least one polypeptide is Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof. In one aspect, the at least one polypeptide is a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from SEQ ID NOs:2-20 or a fragment thereof.

[0164] In another aspect, the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay. In certain aspects, the detecting is by lateral flow assay.

[0165] The following examples are provided to further illustrate the embodiments of the present invention, but are not intended to limit the scope of the invention. While they are typical of those

that might be used, other procedures, methodologies, or techniques known to those skilled in the art may alternatively be used.

EXAMPLES

EXAMPLE 1

SECRETOME ANALYSIS OF CERVICAL CANCER CELL LINES

[0166] In order to identify cervical cancer biomarkers, a secretome analysis of cervical cancer cells was performed using cervical cancer cell line HeLa (cervical adenocarcinoma, positive for HPV18), SiHa cells (grade II, squamous cell cervical carcinoma, positive for HPV16), and C-33A (cervical carcinoma, negative for HPV) and the HaCaT cell line as a negative control. These lines were selected because they represent the most frequent histological types and viral genotypes in cervical intraepithelial lesions and in CC; and were either cultured (*in vitro* secretome), or inoculated into mice (*ex vivo* secretome).

[0167] HeLa and SiHa cells were cultured in serum-free Advanced RPMI 1640 supplemented with 2 mM L-glutamine and Penicillin-Streptomycin at 1 % v / v, at 37 ° C and with 5% CO₂ until a 70-80% confluence was reached. The cells were washed three times with sterile physiological solution (0.9% NaCl (w / v)). As illustrated in Figure 2, there was no significant growth differences between the cells at day 6, when the cells reached 70% confluence.

[0168] For *in vitro* secretome analysis, the cells were then incubated in serum-free RPMI 1640 without phenol red (Gibco, Invitrogen) for 20 hours, and the medium collected and centrifuged at 1,500 g for 5 minutes. The supernatant was passed through a 0.22 µm size PVDF membrane (Millex, Millipore) and stored at -70 ° C until further use (see Figure 1).

[0169] For the *ex vivo* secretome analysis, the secreted proteins were collected from tumors collected on female Nu / Nu mice (4-6 weeks) inoculated with 10⁷ HeLa or SiHa cells. After 30, 45 and 50 days after inoculation, the tumors were collected (triplicate) and washed 3 times with 50 mL of physiological solution and then incubated for 20 hours with serum free RMPI medium without phenol red. The medium was removed and centrifuged at 1,500 x g for 5 minutes, the supernatant was passed through a 0.22 µm pore size membrane PVDF membrane (Millex, Millipore) and stored at -70 ° C until further use (see Figure 1). The secreted proteins collected *in vitro* and *ex vivo* were lyophilized and resuspended in 1 mL of ultrapure water. Protein isolation was performed by phenol extraction.

[0170] To identify the proteins secreted by the different cell lines, the proteins were separated by electrophoresis on an SDS-PAGE matrix and stained with bright Coomassie blue (see Figure 3A). Each lane containing 30 µg protein was cut into 20 lines throughout the column, the proteins contained were extracted and digested with trypsin. The generated peptides were analyzed in a nano LC-MS / MS system (Q-TOF Synapt G2 MS; Waters). The identification of peptides and proteins was performed using the MASCOT search engine through the MASCOT Distiller interface (Matrix Science). The databases consulted were Swiss-Prot and NCBI.

[0171] 1662 secretome proteins were identified (see Figure 3B). As illustrated in the Venn diagram of Figure 3C, showing the intersection between the shared proteins of the CC cell lines and their negative control, 20 proteins were shared in the 3 CC cell lines and absent in the negative control (see Table 3). These proteins were candidates for use in a rapid diagnostic test. In addition to the qualitative study, a quantitative analysis of 200 secreted proteins was performed using the label-free quantification (LFQ) technique. As shown in Figure 4A, 92 proteins were found over-expressed in the 3 CC cell lines according to their Log2 value (CC cell lines vs. HaCaT). For HeLa: 45 over-expressed proteins, SiHa: 35 over-expressed proteins, C-33A: 12 over-expressed proteins. As shown in Figures 4B, 6 secreted proteins: Glyceraldehyde-3-phosphate dehydrogenase, cognate heat shock protein 71 kDa, L-lactate dehydrogenase chain B, beta subunit of proteasome type-5 and nuclear ribonucleoproteins heterogeneous A2 / B1 were found over expressed in the 3 CC cell lines compared to its negative control. Further, and as shown in Figure 4C (which represents the Heat map of proteins expressed in cell lines, where the complete linkage hierarchical grouping shows the values in Log2 (protein expression / HSP71) on a color scale), the hierarchy analysis by cluster in the heat map revealed a similarity in protein expression between the HPV positive cell lines (SiHa and HeLa). These analyzes allowed obtaining a set of common over-expressed proteins for the HPV and CC lines.

Table 3

Gene	Protein	Name
NF1	NF1_HUMAN	Neurofibromin
GAPDH	G3P_HUMAN	Glyceraldehyde-3 phosphate dehydrogenase
FNDC1	FNDC1_HUMAN	Protein 1 containing fibronectin domain type III
EIF4A1	IF4A1_HUMAN	Eukaryotic initiation factor 4A-I
LDHB	LDHB_HUMAN	L-lactate dehydrogenase chain B
HNRNPA1	ROA1_HUMAN	Nuclear heterogeneous Ribonucleoprotein A1
PKD1L1	PK1L1_HUMAN	Polycystic kidney disease protein 1-like 1

FDPS	FPPS_HUMAN	Farnesyl pyrophosphate synthase
HSPA8	HSP7C_HUMAN	Heat Shock Protein Cognate 71 kDa
ANK3	ANK3_HUMAN	Ankirin-3
ARHGAP23	ARHG23_HUMAN	Rho 23 GTPase-activating protein
KRT78	K2C78_HUMAN	Cytoskeletal Keratin 78 type II
COL6A3	CO6A3_HUMAN	Alpha-3 collagen chain (VI)
PSMB5	PSB5_HUMAN	Beta subunit of proteasome type-5
HNRNPA2B1	ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1
HIST1H2BB	H2B1B_HUMAN	Histone H2B type 1-B
RME8	DNAJC13	homolog of DnaJ subfamily C member 13
ENO3	ENOB_HUMAN	Beta enolase
GSTP1	GSTP1_HUMAN	Glutathione S-transferase P
GSTM3	GSTM3_HUMAN	Glutathione S-transferase Mu 3

EXAMPLE 2

DETECTION OF CERVICAL TUMORS

[0172] To evaluate if the proteins identified in the *in vitro* secretome analysis could be used as biomarkers for the detection of cervical tumors, female mice were inoculated with DC cells to develop tumors, and secreted proteins were measured in the serum of the animals (see Figure 5A).

[0173] A cohort of 9 mice was generated, with 3 different cell lines and their controls established at 3 different times of the PT (tumor progression). The mice were inoculated with 10^7 cells DC tumor cell lines (either HeLa or SiHa cells), and the sera were collected 30, 45 and 50 days post inoculation. Sera were subjected to a Western blot with 20 μ g protein per sample. The tests were performed in triplicate and were presented as means ($\pm$ standard deviation). A statistical Student's t-test was performed.

[0174] As illustrated in Figure 5B, illustrating the example of the detection of one of the protein of the secretome identified in Example 1; it was found by Western blot that the farnesyl pyrophosphate synthase protein was detectable in the sera of the mice inoculated with HeLa and SiHa (sera from uninoculated mice were used as controls). The protein was found expressed in all sera of the tumor-bearing mice, as detailed in Figure 5C, the level of expression was found to increase levels over time in the sera of the mice inoculated with SiHa.

[0175] The validation of the protein Farnesyl pyrophosphate synthase as a biomarker in sera was further performed in serum obtain from patients with CC:

[0176] The serum of 10 patients with CC and 10 negative controls for CC were tested, and the expression of Farnesyl pyrophosphate synthase was assessed by western blot. As illustrated in

Figures 6A and 6B, all the patients analyzed presented Farnesyl pyrophosphate synthase expression, and no expression of Farnesyl pyrophosphate synthase was found in the sera of the controls. It was also observed that the level of expression was variable among patients (see Figure 6C). As further illustrated in Figures 7A-7C, Ankyrin-3 was also demonstrated as a promising biomarker that can be used to detect cervical cancer in the serum of patient, by presenting with a significantly higher level of expression as compared to the serum of control patients. The proteome analysis of the secretome, identified 20 proteins present in CC cells and absent in negative control; and among the 6 overexpressed proteins Farnesyl pyrophosphate synthase and Ankyrin-3, used as a proof-of-principle were used to demonstrate that its level of expression (i.e., overexpression) could be analyzed in the serum of patient, showing that these proteins may be a useful promising candidate in the identification of this disease.

EXAMPLE 3

DETECTION OF PRE-CANCEROUS CERVICAL LESIONS

[0177] To evaluate if the proteins identified in the *in vitro* secretome analysis could be used as biomarkers to detect pre-cancerous cervical lesions, the serum of patient presenting pre-cancerous cervical lesions were assessed for the detection of the biomarkers by western blot.

[0178] The serum of patients with pre-neoplastic lesions, with cervical cancer or with no lesions (control) were collected and analyzed for the expression of Ankyrin-3, Rho 23 GTPase-activating protein, Alpha-3 collagen chain (IV), Beta enolase, Farnesyl pyrophosphate synthase, Histone H2B type 1-BB, Heterogeneous nuclear ribonucleoproteins A2/B1, Heat shock protein cognate 71 kDa, Cytoskeletal Keratin 78 type II, Beta subunit of proteasome type-5 and homolog of DnaJ subfamily C member 13.

[0179] As illustrated in Figures 8A-8C, it was demonstrated that Farnesyl pyrophosphate synthase was detectable in the serum of patient having pre-cancerous cervical lesions L1 and L2, as compared to control sera. Specifically, it was found that Farnesyl pyrophosphate synthase expression was 12-times higher in the serum of patient with pre-cancerous lesions as compared to control (see Figure 8D), demonstrating that pre-cancerous lesions, as well as cancerous (see example 2) can be detected in the serum of patient, by detecting the expression of Farnesyl pyrophosphate synthase in the serum, which can be used as a biomarker for the detection of precancerous cervical lesions.

[0180] As illustrated in Figures 9A-9C, it was demonstrated that Ankyrin-3 was detectable in the serum of patient having pre-cancerous cervical lesions L1 and L2, as compared to control sera. Specifically, it was found that Ankyrin-3 expression was 10-times higher in the serum of patient with pre-cancerous lesions as compared to control (see Figure 9D), demonstrating that pre-cancerous lesions, as well as cancerous (see example 2) can be detected in the serum of patient, by detecting the expression of Ankyrin-3 in the serum, which can be used as a biomarker for the detection of precancerous cervical lesions.

[0181] Similar results were obtained when the quantification of the proteins was intended by ELISA instead of by Western blot.

EXAMPLE 4

LATERAL FLOW ASSAY FOR THE DETECTION OF CERVICAL TUMOR AND PRECANCEROUS LESIONS

[0182] For lateral flow assay, strip containing dried spot antibodies for test lines and positive lines were prepared, and samples collected from patients were tested for the detection of Farnesyl pyrophosphate synthase.

[0183] Blood samples collected from patients were either directly diluted in Chase buffer at a 1/5 dilution rate (for serum sample), or further absorbed onto blood separator pad (for whole blood sample) prior to being diluted in Chase buffer. 70 μ L of diluted sample were used for each test.

[0184] The strip was assembled by removing the membrane section of the protective cover and apply CN-95 membrane. Two pieces of protective cover were removed from sections above where the nitrocellulose was placed. A 21 mm wick pad was then applied by aligning the top of the wick pad with the top of the backing card edge, and the excess backing card below the membrane, was cut off, leaving just the membrane and wick pad. The strips were cut to 5.0 mm width using Kinematic Guillotine and package in pouch with desiccant.

[0185] The test and positive lines were then prepared on the strip by spot drying antibodies. 1.0 μ L of test line antibody was applied around 9 mm from the bottom of the nitrocellulose on 20 pre-cut test strips; and 1 μ L of control line antibody was applied around 15 mm up from the bottom of the nitrocellulose on each pre-cut and spotted test strip. The strips were tapped down on piece of paper and place in 40C oven for 1-hour. Once dried, the strips were packaged with desiccant. The antibodies were previously conjugated with gold (using colloidal gold) or biotinylated.

[0186] For the assay, each conjugate were diluted to 0.02% solids using 50mM borate, 0.5% casein, 1% tween. 8 μ L of conjugate were pipetted into glass tube, followed by 10 μ L of serum. Half of the strip was place in glass tube, with bottom of nitro submerged in the testing solution to allow conjugate/serum solution to run up strip. 50 μ L of 1x PBS, 1% tween20 were then added to glass tube to chase sample.

[0187] Using the FLI assay described herein, it was demonstrated that Farnesyl pyrophosphate synthase expression level could be determined a liquid sample collected from a patient, such as the serum, and that therefore pre-cancerous lesions of low and high grade, as well as cancerous cervical lesions could be detected using the device.

[0188] Although the invention has been described with reference to the above examples, it will be understood that modifications and variations are encompassed within the spirit and scope of the invention. Accordingly, the invention is limited only by the following claims.

What is claimed is:

1. A method comprising:
 - a) detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide comprises:
 - i) Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat Shock Protein Cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or
 - ii) a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof; and
 - b) diagnosing cervical cancer based on the detection of the at least one polypeptide.
2. The method of claim 1, wherein the sample is selected from the group consisting of blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair.
3. The method of claim 2, wherein the sample is a blood sample.
4. The method of claim 1, wherein the subject is human.
5. The method of claim 1, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

6. The method of claim 1, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs:2-20 and a fragment thereof.
7. The method of claim 1, wherein the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow or immunoassay.
8. The method of claim 1, wherein the detecting is by lateral flow assay.
9. The method of claim 1, further comprising administering a treatment to the subject.
10. The method of claim 9, wherein the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy.
11. A method of diagnosing cervical cancer in a subject comprising:
 - a) detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide comprises:
 - i) Farnesyl pyrophosphate synthase, neurofibromin 1, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate protein 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or
 - ii) a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof; and
 - b) diagnosing cervical cancer based on the detection of the at least one polypeptide, thereby diagnosing cervical cancer.
12. The method of claim 11, wherein the sample is selected from the group consisting of blood, plasma, urine, saliva, sweat, organ biopsy, cerebrospinal fluid (CSF), tear, vaginal fluid, feces, skin, and hair.
13. The method of claim 12, wherein the sample is a blood sample.

14. The method of claim 11, wherein the subject is human.
15. The method of claim 11, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Cognate thermal shock protein 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.
16. The method of claim 11, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs:2-20 and a fragment thereof.
17. The method of claim 11, wherein the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay.
18. The method of claim 11, wherein the detecting is by lateral flow assay.
19. The method of claim 11, further comprising administering a treatment to the subject.
20. The method of claim 19, wherein the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy.
21. A method of treating cervical cancer in a subject in need thereof comprising:
 - a) detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide comprises:
 - i) Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of

proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or

ii) a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof;

b) diagnosing cervical cancer based on the detection of the at least one polypeptide; and

c) administering a treatment to the subject,

thereby treating the subject.

22. The method of claim 21, wherein the sample is a blood sample.

23. The method of claim 21, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

24. The method of claim 21, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide with an amino acid sequence selected from the group consisting of SEQ ID NOs:2-20 and a fragment thereof.

25. The method of claim 21, wherein the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay.

26. The method of claim 21, wherein the detecting is by lateral flow.

27. The method of claim 21, wherein the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy.

28. The method of claim 27, where in the chemotherapy is selected from the group consisting of Cisplatin, Carboplatin, Paclitaxel, Topotecan, docetaxel, ifosfamide, 5-fluorouracil, irinotecan, gemcitabine and mitomycin.

29. The method of claim 27, wherein the targeted therapy is bevacizumab.

30. The method of claim 27, wherein the immunotherapy is pembrolizumab.

31. A method of predicting a response to treatment for a subject having cervical cancer comprising:

a) detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide comprises:

i) Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or

ii) a polypeptide with at least about 70% sequence identity to a polypeptide having amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof; and

b) predicting a response to treatment based on the detection of the at least one polypeptide.

32. The method of claim 31, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B,

homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

33. The method of claim 31, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide selected from the group consisting of a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs:2-20 and a fragment thereof.

34. The method of claim 31, wherein the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay.

35. The method of claim 31, wherein the detecting is by lateral flow assay.

36. The method of claim 31, wherein the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy.

37. A method for determining the stage of cervical cancer in a subject in need thereof, comprising:

a) detecting at least one polypeptide in a sample from a subject; wherein the at least one polypeptide comprises:

i) Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or

ii) a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof; and

b) determining the stage of cervical cancer in the subject based on the detection of the at least one polypeptide.

38. The method of claim 37, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, Heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.
39. The method of claim 37, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs:2-20 and a fragment thereof.
40. The method of claim 37, wherein the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay.
41. The method of claim 37, wherein the detecting is by lateral flow assay.
42. The method of claim 37, further comprising administering a treatment to the subject.
43. The method of claim 42, wherein the treatment is selected from the group consisting of surgery, radiation, chemotherapy, targeted therapy and immunotherapy.
44. The method of claim 37, where in the cervical cancer is stage I, stage II, stage III or stage IV.
45. A kit comprising:
a) a sample collection unit;
b) a lateral flow device; and
c) instructions for using the lateral flow device.
46. The kit of claim 45, wherein the lateral flow device detects at least one polypeptide, wherein the at least one polypeptide comprises:

a) Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or

b) a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof.

47. The kit of claim 45, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

48. The kit of claim 45, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide selected with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2-20 and a fragment thereof.

49. The kit of claim 45, wherein the lateral flow device detects the at least one polypeptide by an immunoassay.

50. The kit of claim 45, wherein the sample collection unit collects a blood sample.

51. The use of the detection of at least one polypeptide for the diagnosis of cervical cancer in a subject in need thereof, wherein the at least one polypeptide comprises:

a) Farnesyl pyrophosphate synthase, neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 or a fragment thereof; or

b) a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-20 or a fragment thereof.

52. The use of claim 51, wherein the at least one polypeptide is detected in a sample from the subject.

53. The use of claim 52, wherein the sample is a blood sample.

54. The use of claim 51, wherein the at least one polypeptide comprises Farnesyl pyrophosphate synthase or a fragment thereof and at least one polypeptide selected from the group consisting of neurofibromin I, Glyceraldehyde-3 phosphate dehydrogenase, Protein 1 containing fibronectin domain type III, Eukaryotic initiation factor 4A-I, L-lactate dehydrogenase chain B, Nuclear heterogeneous Ribonucleoprotein A1, 1-like protein 1 polycystic kidney disease, heat shock protein cognate 71 kDa, Ankyrin-3, Rho 23 GTPase-activating protein, Cytoskeletal Keratin 78 type II, Alpha-3 collagen chain (VI), Beta subunit of proteasome type-5, Heterogeneous nuclear ribonucleoproteins A2/B1, Histone H2B type 1-B, homolog of DnaJ subfamily C member 13, Beta enolase, Glutathione S-transferase P, Glutathione S-transferase Mu 3 and a fragment thereof.

55. The use of claim 51, wherein the at least one polypeptide comprises a polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence of SEQ ID NO:1 or a fragment thereof and at least one polypeptide with at least about 70% sequence identity to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs:2-20 and a fragment thereof.

56. The use of claim 52, wherein the detecting is by protein microarray, fluorescence detection, flow cytometry, microfluidic device, lateral flow assay, vertical flow assay or immunoassay.
57. The use of claim 56, wherein the detecting is by lateral flow assay.