XTEN CONJUGATE COMPOSITIONS AND METHODS OF MAKING SAME

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims priority benefit to U.S. Provisional Application Serial No. 61/634,312 filed February 27, 2012, U.S. Provisional Application Serial No. 61/690,187 filed June 18, 2012, and U.S. Provisional Application Serial No. 61/709,942 filed October 4, 2012, which applications are incorporated herein by reference.

Background of the Invention

[0002] Extending the half-life a therapeutic agent, whether being a therapeutic protein, peptide or small molecule, often requires specialized formulations or modifications to the therapeutic agent itself. Conventional modification methods such as pegylation, adding to the therapeutic agent an antibody fragment or an albumin molecule, suffer from a number of profound drawbacks. While these modified forms can be prepared on a large scale, these conventional methods are generally plagued by high cost of goods, complex process of manufacturing, and low purity of the final product. Oftentimes, it is difficult, if not impossible, to purify to homogeneity of the target entity. This is particularly true for pegylation, where the reaction itself cannot be controlled precisely to generate a homogenous population of pegylated agents that carry the same number or mass of polyethylene-glycol. Further, the metabolites of these pegylated agents can have sever side effects. For example, PEGylated proteins have been observed to cause renal tubular vacuolation in animal models (Bendele, A., Seely, J., Richey, C., Sennello, G. & Shopp, G. Short communication: renal tubular vacuolation in animals treated with polyethylene-glycol-conjugated proteins. Toxicol. Sci. 1998. 42, 152–157). Renally cleared PEGylated proteins or their metabolites may accumulate in the kidney, causing formation of PEG hydrates that interfere with normal glomerular filtration. In addition, animals and humans can be induced to make antibodies to PEG (Sroda, K. et al. Repeated injections of PEG-PE liposomes generate anti-PEG antibodies. Cell. Mol. Biol. Lett. 2005.10, 37–47).

[0003] Thus, there remains a considerable need for alternative compositions and methods useful for the production of highly pure form of therapeutic agents with extended half-life properties at a reasonable cost. .

SUMMARY OF THE INVENTION

[0004] The present invention addresses this need and provides related advantages. The compositions and methods disclosed herein not only are useful as therapeutics but are also particularly useful as research tools for preclinical and clinal development of a candidate therapeutic agent. In some asepects, the present invention addresses this need by, in part, generating extended recombinant polypeptide (XTEN) reagents that can be purified to

homogeneity with one or a few simple steps, and/or that are amenable to chemical conjugation with payload peptides, proteins and small molecules with reactive groups using a wide diversity of conjugation methods. The use of the XTEN reagents generates high-yield product of XTEN-linked agent that are superior in one or more aspects including high homogeneity, high solubility, long stability, and enhanced terminal half-life compared to unconjugated product.

[0005] The present invention relates, in part, to novel compositions comprising substantially homogeneous extended recombinant polypeptides (XTEN) useful as conjugation partners for linking to one or more payload pharmacologically- or biologically-active agents, resulting in XTEN-payload compositions. In one aspect, the invention provides XTEN engineered for covalent linking to the one or more payloads either directly or via cross-linkers, resuting in XTEN-payload composition that comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more molecules of one, two, three or more types of payloads. It is an object of the present invention to provide such engineered XTEN polypeptides for use in creating conjugates with payload agents of interest as compositions with enhanced pharmaceutical properties, including enhanced pharmacokinetic properties. The invention provides XTEN that are substantially homogeneous in length and sequence that are useful for preparing the conjugates comprising the XTEN linked to one or more payloads such that the resulting XTEN-payload conjugates have a high degree of purity. Such conjugates of high purity are useful in preparing pharmaceutical compositions for subjects having a medical condition for which the one or more payloads have utility in the prevention, treatment or amelioration of the condition.

[0006] In a first aspect, the invention provides substantially homogenous XTEN polypeptide compositions useful as conjugation partners to create XTEN-cross-linker intermediates and XTEN-payload compositions. In some embodiments, the invention provides a substantially homogenous population of polypeptides comprising an extended recombinant polypeptide (XTEN), and wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of individual polypeptide molecules in said population have identical sequence length. In one embodiment of the foregoing, the XTEN is characterized in that: the total XTEN amino acid residues is at least 36 to about 3000 amino acid residues; the sum of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P) residues constitutes more than about 90% of the total amino acid residues of the XTEN; the XTEN sequence is substantially non-repetitive such that (i) the XTEN sequence contains no three contiguous amino acids that are identical unless the amino acids are serine, (ii) at least about 80%, or about 90%, or about 95% of the XTEN sequence consists of non-overlapping sequence motifs, each of the sequence motifs comprising about 9 to about 14 amino acid residues, wherein any two contiguous amino acid residues does not occur more than twice in each of the sequence motifs; or (iii) the XTEN sequence has a subsequence score of less than 10; the XTEN sequence has greater than 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or greater than 99% random coil formation as determined by GOR algorithm; the XTEN sequence has less than 2%, or 3%, or 4%, or 5% alpha helices; the XTEN sequence has less than 2%, or 3%, or 4%, or 5% beta-sheets as determined by Chou-Fasman algorithm; and the XTEN sequence lacks a predicted T-cell epitope when analyzed by TEPITOPE algorithm, wherein the TEPITOPE algorithm prediction for epitopes within the XTEN sequence is based on a score of -8, or –9, or -10. In another embodiment of the foregoing, the XTEN comprises a sequence having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 2, Table 3, Table 4 and Tables 22-25.

[0007] In other embodiments, the substantially homogenous XTEN polypeptide compositions comprise one or more affinity tags. In one embodiment, the invention provides a substantially homogenous XTEN polypeptide composition comprising a first affinity tag wherein the first affinity tag has binding affinity for a chromatography substrate selected from the group consisting of hydrophobic interaction chromatography (HIC), cation exchange, anion exchange, immobilized metal ion affinity chromatography (IMAC), and immobilized antibody. In one embodiment of the foregoing, the first affinity tag has at least about 90%, 91%, 92%, 93%, 94%, or at least about 95% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 7. In another embodiment of the foregoing XTEN and affinity tag, the composition further comprises one or more helper sequences. In one embodiment, a helper sequence comprises a sequence having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 10. In another embodiment, the helper sequence is selected from the group consisting of: KNPEQAEEQX1EET wherein X1 is independently S or R; ANPEQAEEQX1EET wherein X1 is independently S or R; KNPEQAEEQAEEQX1EET wherein X1 is independently S or R; KX2X3EQAEEQAEEQX1EET wherein X1 is independently S or R, X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; $KX2(X3)_{10}QX1EET$ wherein X1 is independently S or R, X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; $KX2(X3)_7AEEQX1EET$ wherein X1 is independently S or R, X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; $KX2X3EQE(X3)_3AEEQREET$ wherein X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; $KX2X3EQE(X3)_3AEE(X3)_5$ wherein X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; $KKQEQEKEQAEEQ(X4X5)_2REET$ wherein X4 is independently A or S and X5 is

independently K, Q, or E; KKQEQEKEQAEEQ$(X4X5)_4$REET wherein X4 is independently A or S and X5 is independently K, Q, or E; KKQEQEKEQAEEQ$(Z)_4$REET, wherein Z is any naturally-occurring L-amino acid; KX2$(X3)_n$, wherein n is an integer from 10-40 and X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; $(X3)_n$ wherein n is an integer from10-50 and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S; KX2QEQEKEQAEEQ$(X4X5)_n$X1EET wherein n is zero or an integer from 1-10 and X1 is independently S or R, X2 is independently K or N, X4 is independently A or S, and X5 is independently K, Q, or E; KX2$(X3)_n(X4X5)_m$X1EET, wherein n is an integer from 5-20, m is zero or an integer from 1-10, X1 is independently S or R, X2 is independently K or N, X3 is independently K, N, T, Q, H, P, E, D, A, R, or S, X4 is independently A or S, and X5 is independently K, Q, or E; and KX2$(X3)_n(Z)_m$X1EET, wherein n is an integer from 5-20, m is zero or an integer from 1-10, X1 is independently S or R, X2 is independently K or N, X3 is independently K, N, T, Q, H, P, E, D, A, R, or S, and Z is any naturally-occurring L-amino acid, and any sequence homologs showing at least 80%, 90%, 95%, 98%, or 99% sequence identity of the foregoing when optimally aligned.

[0008] In other embodiments of the foregoing substantially homogenous XTEN, affinity tag, and helper sequence compositions, the composition further comprises a first cleavage sequence. Where desired, the cleavage sequence is selected from the group consisting of the sequences set forth in Table 8 and Table 9. In one embodiment of the foregoing, the composition has the configuration of formula I:

(HS)-(AT1)-(CS1)-(XTEN) I

wherein HS is the helper sequence; AT1 is the first affinity tag; CS1 is the first cleavage sequence; and XTEN is the extended recombinant polypeptide. In another embodiment of the foregoing compositions, the composition further comprises a second cleavage sequence. Where desired, the first and the second cleavage sequences are capable of being cleaved by the same protease, and wherein the composition has the configuration of formula II:

(HS)-(CS1)-(XTEN)-(CS2)-(AT1) II

wherein HS is a helper sequence; AT1 is the first affinity tag; CS1 is the first cleavage sequence; CS2 is the second cleavage sequence; and XTEN is the extended recombinant polypeptide. In another embodiment of the foregoing compositions, the first affinity tag comprises the sequence RPRPRPRPRPRPR, HHHHHH, or any affinity tag known in the art or disclosed herein.

[0009] In other embodiments of the substantially homogenous XTEN compositions, the compositions comprise a first and a second affinity tag, a first and a second cleavage sequence, and a helper sequence wherein the second affinity tag is different from the first affinity tag and has binding affinity to a different chromatography substrate than that of the first affinity tag, wherein the chromatography substrate is selected from the group consisting of HIC, cation

exchange, anion exchange, IMAC, and immobilized antibody, and wherein the first and the second cleavage sequences are capable of being cleaved by the same protease, and wherein the second affinity tag has at least about 90%, 91%, 92%, 93%, 94%, or at least about 95% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 7. In one embodiment of the foregoing composition, the composition has the configuration of formula III:

(HS)-(AT1)-(CS1)-(XTEN)-(CS2)-(AT2) III

[0010] wherein HS is the helper sequence; AT1 is the first affinity tag; CS1 is the first cleavage sequence; CS2 is the second cleavage sequence; XTEN is the extended recombinant polypeptide; and AT2 is the second affinity tag. In another embodiment of the foregoing composition, the first affinity tag comprises the sequence RPRPRPRPRPRPR and the second affinity tag comprises the sequence HHHHHH. In another embodiment of the foregoing composition, the first affinity tag comprises the sequence HHHHHH and the second affinity tag comprises the sequence RPRPRPRPRPRPR. In another embodiment of the foregoing composition, the first affinity tag comprises the sequence RPRPRPRPRPRPRPRPRPRPRPR and the second affinity tag comprises the sequence HHHHHHHH.

[0011] In another aspect, the invention provides compositions comprising a substantially homogenous population of a polypeptide obtained by a process. In some embodiments, the compositions are obtained by the process comprising: culturing a host cell that comprises a vector encoding the polypeptide in a fermentation reaction under conditions effective to express the polypeptide by a crude expression product of the host cell, wherein the encoded polypeptide comprises an XTEN, a first cleavage sequence and a first affinity tag; adsorbing the polypeptide of the crude expression product onto a first chromatography substrate under conditions effective to capture the first affinity tag onto the first chromatography substrate; eluting the polypeptide; and recovering the polypeptide. In some embodiments, at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides of the resulting population have identical sequence length. In one embodiment of the foregoing composition, the first chromatography substrate is selected from the group consisting of HIC, cation exchange, anion exchange, and IMAC. In another embodiment of the foregoing composition, the affinity tag is selected from the group consisting of the affinity tags of Table 7. In another embodiment of the foregoing composition the first chromatography substrate is cation exchange and the first affinity tag comprises the sequence RPRPRPRPRPRPR. In another embodiment of the foregoing composition, the first chromatography substrate is IMAC and the first affinity tag comprises the sequence HHHHHHHH. In one embodiment of the foregoing composition, the encoding vector encodes any of the XTEN embodiments described herein comprising at least affinity tag, at least a first cleavage sequence, a helper sequence, and optionally a second cleavage sequence. In another

embodiment of the foregoing composition, the vector further encodes a second cleavage sequence and a second affinity tag wherein the first and the second cleavage sequences are capable of being cleaved by the same protease and wherein the second affinity tag has binding affinity to a second, different chromatography substrate than the first affinity tag, and wherein the composition is obtained by the process further comprising: adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag onto the second chromatography substrate; eluting the polypeptide; and recovering the polypeptide wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides of the population have identical sequence length. In one embodiment of the foregoing, the first chromatography substrate is different from the second chromatography substrate and each of the first and the second chromatography substrate are independently selected from the group consisting of HIC, cation exchange, anion exchange, and IMAC. In another embodiment of the foregoing composition, the first chromatography substrate is cation exchange and the first affinity tag comprises the sequence RPRPRPRPRPRPR or RPRPRPRPRPRPRPRPRPRPR and the second chromatography substrate is IMAC and the first affinity tag comprises the sequence HHHHHHHH or HHHHHHHH. In another embodiment of the foregoing composition, the first chromatography substrate is IMAC and the first affinity tag comprises the sequence HHHHHHHH or HHHHHHHH and the second chromatography substrate is cation exchange and the first affinity tag comprises the sequence RPRPRPRPRPRPR or RPRPRPRPRPRPRPRPRPRPRPR. In another embodiment, the foregoing compositions comprising a first or a first and a second affinity tag are further processed by treating the composition with a protease under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the affinity tag(s); adsorbing the XTEN onto a chromatography substrate under conditions effective to capture the XTEN but not the affinity tag(s) or the protease; eluting the XTEN; and recovering the XTEN. At least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of XTEN in the resulting composition have identical sequence length. In one embodiment of the foregoing composition, the cleavage sequence(s) are capable of being cleaved by a protease selected from the group consisting of the proteases of Table 9. In another embodiment of the foregoing composition, the cleavage sequence(s) are capable of being cleaved by trypsin and the protease is trypsin. In another embodiment of the foregoing composition, the chromatography substrate is anion exchange. The anion exchange substrate can be a substrate selected from the group consisting of macrocap Q, capto Q, superQ-650M, and poros D. Alternatively, the foregoing compositions comprising one affinity tag or two affinity tags are further processed by treating the composition under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the one or two affinity tags; adsorbing the protease onto a chromatography substrate under conditions effective to capture the protease

and the affinity tags but not the XTEN; and recovering the XTEN from the eluate. In some embodiments, at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of XTEN of the resulting eluate have identical sequence length. In one embodiment of the foregoing composition, the cleavage sequence(s) are capable of being cleaved by a protease selected from the group consisting of the proteases of Table 9. In another embodiment of the foregoing composition, the cleavage sequence(s) are capable of being cleaved by trypsin and the protease utilized is trypsin. The chromatography substrate can be selected from one or more of cation exchange, HIC or IMAC.

[0012] In another aspect, the invention relates, in part, to polypeptide compositions that can be cleaved into XTEN segments of equal length and sequence. In one embodiment, the invention provides a composition comprising an XTEN sequence, wherein the XTEN sequence further comprises one or more cleavage sequences capable of being cleaved by trypsin and wherein treatment with trypsin under conditions effective to cleave all the cleavage sequences results in a preparation of XTEN fragments wherein each XTEN fragment has at least about 99% sequence identity to every other fragment in the preparation. In one embodiment of the composition, the cleavage sequence has at least 86% sequence identity to or is identical to the sequence SASRSA or SASKSA. In another embodiment of the composition, the cleavage sequence comprises the sequence RX or KX, wherein X is any L-amino acid other than proline. In one embodiment of the foregoing compositions, the XTEN composition has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the sequences selected from the group of sequences set forth in Table 6.

[0013] In another aspect, the invention relates, in part, to methods for producing XTEN fragments substantially of equal length and sequence. In one embodiment, the invention provides a method of producing a substantially homogenous population of an XTEN, the method comprising treating a population of polypeptides comprising a sequence selected from the group of sequences set forth in Table 6 with trypsin under conditions effective to cleave all of the cleavage sequence(s) resulting in a substantially homogenous XTEN population wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of individual molecules of the XTEN fragments have identical sequence length. In one embodiment of the foregoing method, the method further comprises adsorbing the XTEN fragments onto a chromatography substrate under conditions effective to capture the XTEN fragments but not the protease; eluting the XTEN fragments; and recovering the XTEN fragments wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of individual molecules of the population have identical sequence length. In one embodiment of the foregoing method, the chromatography substrate is anion exchange. The substrate can be selected from the group consisting of macrocap Q, capto Q, superQ-650M, and poros D. In another embodiment of the foregoing method, the XTEN has at least about 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a sequence selected from the group of sequences set forth in Table 6. In another embodiment of the foregoing method, the resulting XTEN fragment has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a sequence selected from the group of sequences set forth in Table 2 or 3. In another embodiment, the invention provides XTEN compositions made by the process of the foregoing method embodiments.

[0014] In another aspect, the invention relates, in part, to methods for producing XTEN at high expression yields from a host cell. In some embodiments, the invention provides a method comprising culturing a host cell that comprises a vector encoding a polypeptide comprising the XTEN and a helper sequence in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product at a concentration of more than about 2 grams/liter (g/L), or about 3 g/L, or about 4 g/L, or about 5 g/L, or about 6 g/L, or about 7 g/L of said polypeptide. In one embodiment of the foregoing method, the foregoing expression yields are achieved when the fermentation reaction reaches an optical density of at least 100, or at least 130, or at least 150 at a wavelength of 600 nm. In another embodiment, the invention provides a method for comprising culturing a host cell that comprises a vector encoding a polypeptide comprising the XTEN and a helper sequence in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product at a concentration of more than about 10 milligrams/gram of dry weight host cell (mg/g), or at least about 15 mg/g, or at least about 20 mg/g, or at least about 25 mg/g, or at least about 30 mg/g, or at least about 40 mg/g, or at least about 50 mg/g of said polypeptide. In one embodiment of the foregoing method, the foregoing high-yield expression is achieved when the fermentation reaction reaches an optical density of at least 100, or at least 130, or at least 150 at a wavelength of 600 nm. In another embodiment, the invention provides a method comprising culturing a host cell that comprises a vector encoding a polypeptide comprising the XTEN and a helper sequence in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product at a concentration of more than about 10 milligrams/gram of dry weight host cell (mg/g), or at least about 250 micromoles/L, or about 300 micromoles/L, or about 350 micromoles/L, or about 400 micromoles/L, or about 450 micromoles/L, or about 500 micromoles/L of said polypeptide. In one embodiment of the foregoing method, the foregoing expression yields are achieved when the fermentation reaction reaches an optical density of at least 100, or at least 130, or at least 150 at a wavelength of 600 nm. In one embodiment of the foregoing methods, the helper sequence of the expressed polypeptide is at the N-terminus of the polypeptide, wherein the helper sequence has at least about 90%, 91%, 92%, 93%, 94%, or 95% sequence identity or is identical to a sequence selected from the group consisting of the sequences set forth in Table 10. In another embodiment of the foregoing methods, expression

vector further encodes a first affinity tag and a cleavage sequence between the affinity tag and the XTEN, and the method further comprises recovering the crude expression product of the host cell fermentation reaction mixture; adsorbing the polypeptide of the crude expression product onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate wherein the first chromatography substrate is selected from the group consisting of HIC, cation exchange, anion exchange, and IMAC; eluting and recovering the polypeptide wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides have identical sequence length. In another embodiment of the foregoing methods, expression vector further encodes a first affinity tag and a second affinity tag different from the first tag and a cleavage sequence between each affinity tag and the XTEN, and the method further comprises recovering the crude expression product of the host cell fermentation reaction mixture; adsorbing the polypeptide onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate wherein the first chromatography substrate is selected from the group consisting of HIC, cation exchange, anion exchange, and IMAC; eluting the polypeptide; adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag of the polypeptide onto the chromatography substrate wherein the second chromatography substrate is selected from the group consisting of HIC, cation exchange, anion exchange, and IMAC; eluting the polypeptide; and recovering the polypeptide wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides have identical sequence length. In one embodiment of the foregoing methods, the methods further comprise treating the polypeptide with a protease under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the polypeptide; adsorbing the XTEN onto an anion chromatography substrate under conditions effective to capture the XTEN; eluting the XTEN; and recovering the XTEN wherein at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95% of the individual XTEN molecules have identical sequence length. In the foregoing methods, the anion exchange substrate can be selected from the group consisting of macrocap Q, capto Q, superQ-650M, and poros D. In one embodiment of the foregoing methods, the cleavage sequences are capable of being cleaved by trypsin and the protease is trypsin. In another embodiment of the foregoing methods, the method further comprises treating the polypeptide with a protease under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the polypeptide; adsorbing the protease onto a chromatography substrate under conditions effective to capture the protease and the affinity tags but not the XTEN; and recovering the XTEN in the eluate wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the XTEN have identical sequence length. In one embodiment of the foregoing method, the cleavage sequence is capable of being cleaved by trypsin and the protease utilized is trypsin. In the foregoing method to capture the

protease and the affinity tag, the chromatography substrate can be selected from one or more of HIC, cation exchange, and IMAC.

[0015] In another aspect, the invention relates, in part, to a solid support comprising immobilized thereon a population of substantially identical XTEN polypeptide molecules. In one embodiment, the invention provides a solid support comprising immobilized thereon a population of substantially identical polypeptide molecule wherein the solid support comprises a chromatography substrate, immobilized polypeptides each comprising an XTEN, a first affinity tag, and a second affinity tag wherein the first affinity tag is joined to the XTEN by a cleavage sequence at the N-terminus of the XTEN and the second affinity tag is joined to the XTEN by a cleavage sequence at the C-terminus and wherein the second affinity tag is different from the first affinity tag, wherein the chromatography substrate is capable of binding to either said first or said second affinity tag but not both, and wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the immobilized polypeptide molecules have identical sequence length. In one embodiment of the XTEN comprises a sequence having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 2, Table 3, Table 4 and Tables 22-25, the first and the second affinity tag each independently have at least about 90%, 91%, 92%, 93%, 94%, or at least about 95% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 7, and the cleavage sequence is selected from the group consisting of the sequences set forth in Table 8 and Table 9. In one embodiment of the foregoing the cleavage sequence has at least about 86% sequence identity to or is identical to the sequence SASRSA or SASKSA. In one embodiment of the foregoing the cleavage sequence comprises the sequence RX or KX, wherein X is any L-amino acid other than proline. In one embodiment of the foregoing, the solid support is selected from the group consisting of HIC chromatography resin, cation exchange chromatography resin, anion exchange chromatography resin, and IMAC chromatography resin. In one embodiment of the foregoing, the first affinity tag comprises the sequence RPRPRPRPRPRPR or RPRPRPRPRPRPRPRPRPRPRPR and the second affinity tag comprises the sequence HHHHHH or HHHHHHHH. In another embodiment of the foregoing, the first affinity tag comprises the sequence HHHHHH or HHHHHHHH and the second affinity tag comprises the sequence RPRPRPRPRPRPR or RPRPRPRPRPRPRPRPRPRPRPR.

[0016] In another aspect, the invention relates, in part, to compositions of XTEN conjugated to cross-linkers. In some embodiments, the invention provides compositions of any of the XTEN described herein that is covalently linked to one or more molecules of at least a first cross-linker, wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in

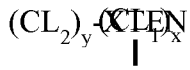
Table 13, the alkyne reactants set forth in Table 15, and the azide reactants set forth in Table 15. In one embodiment of the conjugate composition, the first cross-linker is conjugated to the at least first XTEN at a location selected from the group consisting of: an alpha-amino group of an N-terminal amino acid residue of the XTEN; an epsilon amino group of each lysine residue of the XTEN; and a thiol group of each cysteine residue of the XTEN. Where desired, the XTEN in this embodiment has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 2 and Table 3. In another embodiment of the conjugate composition, the XTEN is selected from the group consisting of AE144, AE288, AE432, AE576, AE864, Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199, and the cross-linker is conjugated to the alpha amino-group of the N-terminal amino acid of the XTEN. In another embodiment of the conjugate composition, the XTEN is selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3, and the cross-linker is conjugated to the thiol group of each cysteine residue of the XTEN. In another embodiment of the conjugate composition, the first cross-linker is selected from the group consisting of N-maleimide, iodoacetyl, pyridyl disulfide and vinyl sulfone, 3-propargyloxypropanoic acid, $(oxyethyl)_n$-acetylene where n is 1-10, dibenzylcyclooctyne (DBCO), cyclooctyne (COT), 3-azide-propionic acid, 6-azide-hexanoic acid, and $(oxyethyl)_n$-azide where n is 1-10. In the foregoing embodiments of this paragraph, the conjugate has the configuration of formula IV:

$$\begin{array}{l}(CL_1)_x \\ | \\ XTEN\end{array} \qquad \text{IV}$$

wherein independently for each occurrence CL_1 is the cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1. Where desired, the XTEN in this embodiment comprises a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula IV, CL1 is a cross-linker selected from Table 13. In other embodiments of the XTEN-crosslinker conjugate compositions, the compositions further comprise a single atom residue of a first payload conjugated to each first cross-linker wherein the

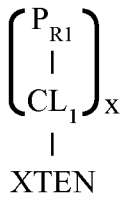
residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In one embodiment of the foregoing, the first payload of the single atom residue can be selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21. In other embodiments of the XTEN-crosslinker conjugate compositions, the compositions further comprise a payload selected from the group consisting of the payloads set forth in Tables 11 and 12 conjugated to each first cross-linker.

[0017] In other embodiments of the XTEN-crosslinker conjugate compositions, the invention provides compositions of an XTEN of the embodiments described herein covalently linked to one or more molecules of a first cross-linker and one or more molecules of a second cross-linker, wherein the first cross-linker is conjugated to either the thiol groups of each cysteine residue of the XTEN or to the epsilon amino groups of the each lysine residue of the XTEN, and the second cross-linker conjugated to alpha amino-group of the N-terminal amino acid of the XTEN wherein each cross-linker is independently selected from the group consisting of the cross-linkers set forth in Table 13, the alkyne reactants of Table 15, and the azide reactants of Table 15. In the foregoing embodiment, the composition has the configuration of formula V:



V

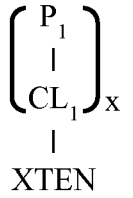
wherein independently for each occurrence; CL1 is the first cross-linker conjugated to cysteine residues of the XTEN; CL2 is the second cross-linker conjugated to XTEN at the N-terminus; x is an integer of 1 to about 10; y is an integer of 1 with the proviso that x + y is $\geq$ 2; and XTEN is either a cysteine engineered XTEN comprising x number of cysteine residues or a lysine engineered XTEN comprising x number of lysine residues. In another embodiments of the XTEN-cross-linker conjugate compositions, the compositions further comprise a single atom residue of a first payload conjugated to each of the first cross-linkers wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur and a single atom residue of a second payload conjugated to each of the second cross-linkers wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In one embodiment of the foregoing, the first payload of the single atom residue can be selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21 and the second payload of the single atom residue can be independently selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21. In some embodiments of the XTEN-cross-linker-payload residue composition, the composition has the configuration of formula VI:



VI

wherein independently for each occurrence P_{R1} is a single atom residue of a payload, wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 3, or is 2, or is 1. Where desired, the XTEN in this embodiment comprises a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula VI, the single atom residue of a payload is from a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21. In one embodiment of the conjugate of formula VI, $CL_1$is a cross-linker selected from Table 13. In one embodiment of the conjugate of formula VI, each cross-linker is linked to a cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula VI, each cross-linker is linked to a lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula VI, x is 1 and the cross-linker is linked to the N-terminal amino group of the XTEN. In another embodiment of the conjugate of formula VI, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment, the invention provides a preparation of the conjugate of formula VI in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length. In other embodiments of the XTEN-crosslinker conjugate compositions, the compositions further comprise a first payload conjugated to each of the first cross-linkers wherein the payload is selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21, and a second payload different from the first payload conjugated to the second cross-linker wherein the second payload is selected from the group consisting of payloads set forth in Tables 11, 12, 18, and 21. In one embodiment of the XTEN-crosslinker-payload conjugate composition, the composition comprises a first payload conjugated to each of the first cross-linkers wherein the payload is selected from the group consisting drug moieties of Table 21, and a second payload different from the first payload conjugated to the second cross-linker wherein the second payload is selected from the group consisting of targeting moieties of Table 21. In one embodiment of the XTEN-crosslinker-payload conjugate composition with a first and a second payload, a

single second payload is linked to the N-terminus of the XTEN by the second cross-linker conjugated by reaction of an alkyne reactant and an azide reactant selected from the group consisting of the reactants of Table 15. In some embodiments of the XTEN-cross-linker-payload composition, the composition has the configuration of formula VII:



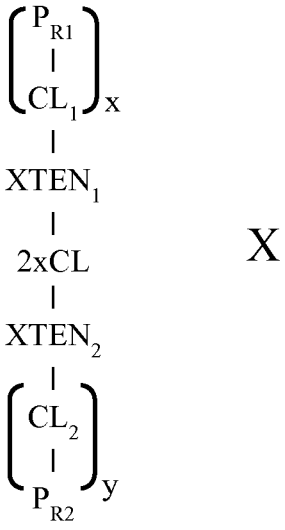
VII

wherein independently for each occurrence: P_1 is a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula VII, $CL_1$is a cross-linker selected from Table 13. In one embodiment of the conjugate of formula VII, each cross-linker is linked to a cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula VII, each cross-linker is linked to an lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula VII, x is 1 and the cross-linker is linked to the N-terminal amino group of the XTEN. In one embodiment, the conjugate of formula VII is selected from the group consisting of the conjugates set forth in Table 21. In another embodiment of the conjugate of formula VII, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. It will be understood by one of skill in the art that the compositions of the foregoing embodiments comprising the payload conjugated to an XTEN-cross-linker using the specified components represents the reaction product of the reactants and thus differs from the precise composition of the reactants. In another embodiment, the invention provides a preparation of the conjugate of formula VII in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[0018] In another aspect, the invention relates, in part, to compositions of a first and a second XTEN conjugated to each other. In some embodiments, the conjugate composition comprises a first and a second XTEN, wherein the XTEN are the same or they are different and each independently has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about

97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 3, and in which the first and the second XTEN are conjugated to each other by the N-termini of the first and the second XTEN with a cross-linker created by reaction of an alkyne reactant and an azide reactant selected from the group consisting of the reactants of Table 15, resulting in a dimeric XTEN conjugate. In one embodiment of the dimeric XTEN composition, at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the first XTEN have identical sequence length and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the second XTEN have identical sequence length. In one embodiment of the dimeric XTEN conjugate, the first XTEN has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3 and the second XTEN has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a different sequence selected from the group of sequences consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3. In another embodiment of the dimeric XTEN conjugate, the first XTEN and the second XTEN are the same and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 3. In another embodiment of the dimeric XTEN conjugate, the first XTEN and the second XTEN are the same are each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3. In another embodiment of the dimeric XTEN conjugate, the first and the second XTEN each comprises one or more cysteine residues, and further comprises a first cross-linker conjugated to each cysteine residue of the first XTEN and a second cross-linker conjugated to each cysteine residue of the second XTEN, wherein the first and the second cross-linkers are independently selected from the group consisting of the cross-linkers set forth in

Table 13. In another embodiment of the dimeric XTEN conjugate, the first and the second XTEN each comprises one or more lysine residues, and further comprises a cross-linker conjugated to each lysine residue of the first and the second XTEN of the conjugate, wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13. In another embodiment of the dimeric XTEN conjugated to cross-linkers, the conjugate further comprises a single atom residue of a first payload conjugated to each cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur, and further comprises a single atom residue of a second payload conjugated to each cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In the foregoing embodiment, the first payload of the single atom residue can be selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21, and the second payload of the single atom residue is a different payload from the first payload and can be selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21. In some embodiments of the dimeric XTEN-cross-linker-payload residue composition, the composition has the configuration of formula X

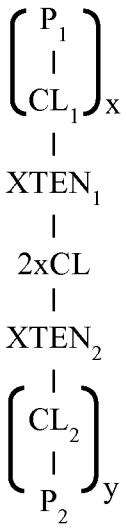


X

wherein independently for each occurrence P_{R1} is a single atom residue of a first payload wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; P_{R2} is a single atom residue of a second payload wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or 1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y is ≥ 2; 2xCL is alternatively a divalent cross-linker or the reaction product of a first and a second click chemistry reactant selected from Table 15; $XTEN_1$ is a polypeptide having at least 80%, or at least about 90%, or at least about

91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_2$ is a polypeptide having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula X, $CL_1$and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In another embodiment of the conjugate of formula X, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN. In another embodiment of the conjugate of formula X, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula X, C_2 is the reaction product of a first azide and a second alkyne click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula X, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a cysteine sulfur of $XTEN_2$. In another embodiment of the conjugate of formula X, each CL_1 is linked to a lysine epsilon amino group of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula X, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula X, $XTEN_1$ and $XTEN_2$ are identical. In another embodiment of the conjugate of formula X, $XTEN_1$ and $XTEN_2$ are different. In another embodiment, the invention provides a preparation of the conjugate of formula X in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length. In another embodiment of the dimeric XTEN conjugated to cross-linkers, the composition further comprises a first payload conjugated to each cross-linker of the first XTEN wherein the first payload is selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21, and further comprises a second payload different from the first payload wherein the second payload is conjugated to each cross-linker of the second XEN wherein the second payload is selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21. In another embodiment of the dimeric XTEN conjugated to cross-linkers, the composition further comprises a first payload conjugated to each cross-linker of the first XTEN wherein the first payload is selected from the group consisting of the targeting moieties set forth in Table 18 or Table 21 , and further comprises a second payload different from the first payload wherein the second payload is conjugated to each cross-linker of the second XTEN wherein the second payload is selected

from the group of toxins set forth in Table 18 or Table 21. In another embodiment of the dimeric XTEN conjugated to cross-linkers and a first and a second payload, the first XTEN is Seg 176 set forth in Table 3 and the second XTEN is selected from the group consisting of Seg 176 and Seg 177 set forth in Table 3. In some embodiments of the dimeric XTEN-cross-linker-payload composition, the composition has the configuration of formula XI



XI

wherein independently for each occurrence P_1 is a first payload selected from the group of payloads set forth in Tables 11, 12, 18, 19, and 21; P_2 is a second payload selected from the group of payloads set forth in Tables 11, 12, 18, 19, and 21 and that is different from P_1; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y is $\geq$ 2; 2xCL is alternatively a divalent cross-linker or the reaction product of a first and a second click chemistry reactant selected from Table 15; $XTEN_1$ is a first substantially homogeneous XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_2$ is a first substantially homogeneous having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula XI, $CL_1$and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In another embodiment of the conjugate of formula XI, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN.

In another embodiment of the conjugate of formula XI, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula XI, C_2 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula XI, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a cysteine sulfur of $XTEN_2$. In another embodiment of the conjugate of formula XI, each CL_1 is linked to a lysine epsilon amino group of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula XI, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula XI, $XTEN_1$ and $XTEN_2$ are identical. In another embodiment of the conjugate of formula XI, $XTEN_1$ and $XTEN_2$ are different. In one embodiment, the conjugate of formula XI is selected from the group consisting of the conjugates set forth in Table 21. In another embodiment, the invention provides a preparation of the conjugate of formula XI in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the respective $XTEN_1$ and $XTEN_2$ molecules of the preparation of the conjugate have identical sequence length.

[0019] In another aspect, the invention relates, in part, to compositions of a first and a second and a third XTEN conjugated to each other, resulting in trimeric conjugate compositions. In some embodiments, the conjugate compositions comprise a first and a second and a third XTEN wherein the XTEN may be the same or they may be different, and in which the first and the second and the third XTEN are conjugated to each other by the N-terminus using a trivalent cross-linker selected from the group consisting of the trivalent cross-linkers set for in Table 13 or Table 14. In one embodiment of the trimeric conjugate, the first and the second and the third XTEN are identical or are different and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in either Table 2 or Table 3. In another embodiment of the trimeric conjugate, the first and the second and the third XTEN are identical or are different and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the first XTEN have identical sequence length and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the second XTEN have identical sequence length and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the third XTEN have identical sequence length. In another embodiment of the trimeric conjugate the trivalent cross-linker is selected from the group consisting of Tris-(2-Maleimidoethyl)amine (TMEA) and amine-reactive Tris-(succimimidyl aminotricetate) (TSAT). In another embodiment of the trimeric conjugate, the first and the second and the third XTEN are

identical and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3. In another embodiment of the trimeric conjugate, the first and the second and the third XTEN are identical and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3, and the third XTEN is different from the first and the second XTEN and has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3. In another embodiment of the trimeric conjugate, each XTEN comprises at least a first cysteine residue and the conjugate further comprises a first cross-linker conjugated to each cysteine residue of the first XTEN, a second cross-linker conjugated to each cysteine residue of the second XTEN, and a third cross-linker conjugated to each cysteine residue of the third XTEN, wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13. In some embodiments of the trimeric conjugate, the composition has the configuration of formula XII:

$$\begin{array}{c}(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)\text{-}(CL2)_y \\ | \\ (XTEN_3)\text{-}(CL3)_z\end{array} \qquad \text{XII}$$

wherein independently for each occurrence; 3xCL is the trivalent cross-linker; CL1 is the first cross-linker conjugated to $XTEN_1$; CL2 is the second cross-linker conjugated to $XTEN_2$; CL3 is the third cross-linker conjugated to $XTEN_3$; x is an integer of 1 to about 10; y is an integer of 1 to about 10; z is an integer of 1 to about 10 with the proviso that $x + y + z$ is ≥ 3; $XTEN_1$ is the first XTEN; $XTEN_2$ is the second XTEN; and $XTEN_3$ is the third XTEN. In another embodiment of the trimeric conjugate, the conjugate further comprises a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and a single atom

residue of a third payload conjugated to each third cross-linker of the third XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In another embodiment of the trimeric conjugate composition, the composition further comprises a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21; a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first payload; and a third payload conjugated to each third cross-linker of the third XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first or the second payload. In one embodiment of the trimeric XTEN-payload conjugate composition, the first payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and the second and the third payloads are a drug, which may be the same or may be different and wherein the drug is selected from the group consisting of the drugs set forth in Table 11, Table 18, and Table 21. In one embodiment of the trimeric XTEN-payload conjugate composition wherein the first payload is a targeting moiety with specific binding affinity to a target and the second payload and the third payload is a drug, the targeting moiety is selected from the group consisting of LHRH and folate and the drug is selected from the group consisting of doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. In one embodiment of the trimeric XTEN-payload conjugate composition wherein the first payload is a targeting moiety with specific binding affinity to a target and the second payload and the third payload is a drug, the targeting moiety, and the drug moiety correspond to any one of conjugates 1-290 set forth in Table 21. In another embodiment of the trimeric XTEN-payload conjugate composition wherein the first payload is a targeting moiety with specific binding affinity to a target and the second payload and the third payload is a drug, the conjugate has the XTEN, the targeting moiety, and the drug moiety corresponding to conjugate 71 of Table 21. In another embodiment of the trimeric XTEN-payload conjugate composition, the composition has the configuration of formula XIII

$$P_1\text{-}(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)\text{-}(CL2)_y\text{-}P_2$$
$$|$$
$$(XTEN_3)\text{-}(CL3)_z\text{-}P_3 \qquad \text{XIII}$$

wherein independently for each occurrence 3xCL is the trivalent cross-linker is selected from the group of trivalent cross-linkers set forth in Tables 13 and 14; P_1 is conjugated to each cross-linker of the first XTEN and is selected from the group consisting of the payloads set forth in Tables

11, 12, 18 and 21, P2 is a second payload conjugated to each cross-linker of the second XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first payload, and P_3 is a third payload conjugated to each cross-linker of the third XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first or the second payload; CL_1 is the first cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL2 is a second cross-linker; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or 1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; and z is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y + z is ≥ 3; $XTEN_1$ is the first XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_2$ is the second XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_3$ is the third XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, and $XTEN_3$ are the same or are different XTEN sequences. In some embodiments, the conjugate of formula XIII further comprises a first payload wherein the payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and at least one other of the payloads is a drug wherein the drug is selected from the group consisting of the drugs set forth in Table 11, Table 19, and Table 21. In one embodiment of the foregoing, the targeting moiety is LHRH or folate and the drug is selected from doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. In another embodiment of the trimeric XTEN conjugate composition, the composition has the configuration of formula XIV:

$$(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)\text{-}(CL2)_y$$
$$|$$

$(XTEN_3)$ XIV

wherein independently for each occurrence; 3xCL is the trivalent cross-linker; CL1 is the first cross-linker conjugated to $XTEN_1$; CL2 is the second cross-linker conjugated to $XTEN_2$; x is an integer of 1 to about 10; y is an integer of 1 to about 10 with the proviso that x + y is ≥ 2; $XTEN_1$ is the first XTEN; $XTEN_2$ is the second XTEN; and $XTEN_3$ is the third XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2. In one embodiment of the trimeric XTEN conjugate composition of formula XVI, the composition further comprises a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In another embodiment of the trimeric XTEN conjugate composition of formula XVI, the composition further comprises a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21; and a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first payload. In one embodiment of the foregoing, the first payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and the second payloads is a drug selected from the group consisting of the drugs set forth in Table 6, Table 18, and Table 21. In another embodiment of the foregoing, the first payload is a targeting moiety is selected from the group consisting of LHRH and folate, and the second payload is a drug is selected from the group consisting of doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. In one embodiment of the foregoing, the first payload is a drug selected from the group consisting of the drugs of Table 11 and the proteins of Table 12 and the second payload is different from the first payload and is selected from the group consisting of the drugs of Table 11 and the proteins of Table 12. In another embodiment of the foregoing, the first payload and the second payload are identical and are selected from the group consisting of the drugs of Table 11 and the proteins of Table 12. In another embodiment of the trimeric XTEN conjugate composition, the composition has the configuration of formula XV:

$$(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)$$
$$|$$
$$(XTEN_3) \qquad \text{XV}$$

wherein independently for each occurrence; 3xCL is a trivalent cross-linker linking $XTEN_1$, $XTEN_2$, $XTEN_3$; CL1 is the first cross-linker conjugated to $XTEN_1$; x is an integer of 1 to about 10; $XTEN_1$ is the first XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 3; $XTEN_2$ is the second XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2; and $XTEN_3$ is the third XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2. In one embodiment of the trimeric XTEN conjugate composition configured as formula XVII, the composition further comprises a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In one embodiment of the trimeric XTEN conjugate composition configured as formula XVII, the composition further comprises a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21.

[0020] In another aspect, the invention relates, in part, to compositions of a first, a second, a third and a fourth XTEN conjugated to each other, resulting in tetrameric conjugate compositions. In some embodiments, the conjugate compositions comprise a first and a second and a third and a fourth XTEN wherein the XTEN are selected from the group consisting of the sequences set forth in Table 3, wherein the XTEN may be the same or they may be different, and in which the first and the second and the third and the fourth XTEN are conjugated to each other by the N-terminus using a tretravalent cross-linker wherein the tetravalent cross-linker is a tetravalent maleimide cluster. In one embodiment of the tetrameric conjugate, the first and the second and the third and the fourth XTEN are identical or are different and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in either Table 2 or Table 3. In another embodiment of the tetrameric conjugate, the first and the second and the third XTEN are identical or are different and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the first XTEN have identical sequence length and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the second XTEN have identical sequence length and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the third XTEN have identical sequence length and at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of each of the fourth XTEN have identical sequence length. In another embodiment of the tetrameric conjugate the first, the second, the third, and the fourth XTEN are the same and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least

about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3. In another embodiment of the tetrameric conjugate, the first and the second XTEN are the same and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3, and the third and the fourth XTEN are the same but are different from the first and the second XTEN and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3. In another embodiment of the tetrameric conjugate, each XTEN comprises at least a first cysteine residue and the conjugate further comprises a first cross-linker conjugated to each cysteine residue of the first XTEN, a second cross-linker conjugated to each cysteine residue of the second XTEN, a third cross-linker conjugated to each cysteine residue of the third XTEN, and a fourth cross-linker conjugated to each cysteine residue of the fourth XTEN, wherein each cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13. In some embodiments of the tetrameric conjugate compositions, the composition has the configuration of formula XVI

$$\begin{array}{c} (CL1)_v\text{-}(XTEN_1)\text{-}4xCL\text{-}(XTEN_2)\text{-}(CL2)_x \\ \qquad\qquad\quad / \quad \backslash \\ (CL3)_y\text{-}(XTEN_3) \qquad (XTEN_4)\text{-}(CL4)_z \end{array} \qquad \text{XVI}$$

wherein independently for each occurrence: 4xCL is the tetravalent cross-linker; CL1 is the first cross-linker conjugated to $XTEN_1$; CL2 is the second cross-linker conjugated to $XTEN_2$; CL3 is the third cross-linker conjugated to $XTEN_3$; CL4 is the fourth cross-linker conjugated to $XTEN_4$; v is an integer of 1 to about 10; x is an integer of 1 to about 10; y is an integer of 1 to about 10; z is an integer of 1 to about 10 with the proviso that $x + y + z$ is ≥ 4; $XTEN_1$ is the first XTEN; $XTEN_2$ is the second XTEN; $XTEN_3$ is the third XTEN; and $XTEN_3$ is the fourth XTEN. In another embodiment of the tetrameric conjugate composition, the composition further comprises a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur;

a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; a single atom residue of a third payload conjugated to each third cross-linker of the third XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and a single atom residue of a fourth payload conjugated to each fourth cross-linker of the fourth XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In another embodiment of the tetrameric conjugate composition, the composition further comprises a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21; a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21, wherein the payload is the same or is different from the first payload; a third payload conjugated to each third cross-linker of the third XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21, wherein the payload is the same or is different from the first or the second payload; and a fourth payload conjugated to each fourth cross-linker of the fourth XTEN selected from the group consisting of the payloads set forth in Tables 11, 12, 18, and 21, wherein the payload is the same or is different from the first or the second or the third payload. In one embodiment of the tetrameric XTEN-payload conjugate composition, the first payload is a targeting moiety with specific binding affinity to a target wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and at least one other of the second, third, and fourth payloads is a drug wherein the drug is selected from the group consisting of the drugs set forth in Tables 11, 18 and 21. In one embodiment of the tetrameric XTEN-payload conjugate composition, the first payload is a targeting moiety wherein the targeting moiety is selected from the group consisting of LHRH and folate, and at least one of the second, third and fourth payload is a drug selected from the group consisting of doxorubicin, paclitaxel, auristatin, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. In another embodiment of the tetrameric XTEN-payload conjugate composition, the first payload is a targeting moiety with specific binding affinity to a target wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and at least one other of the second, third, and fourth payloads is a drug wherein the drug is selected from the group consisting of the drugs set forth in Tables 11, 18 and 21, and wherein the XTEN, the targeting moiety, and the drug moiety correspond to any one of conjugates 1-290 set forth in Table 21.

[0021] In another aspect, the invention relates, in part, to compositions comprising multimeric XTEN molecules configured in a branched manner, wherein a solution of the composition has a

reduced. In one embodiment, the invention provides a composition comprising a solution that comprises a multimeric XTEN having at least three XTEN fragments linked together in a branched manner (e.g. trimeric manner) wherein the viscosity of the solution is reduced by at least 5, 6, 7, 8, 9 or 10 cP in a solution containing ≧100, 130, or 150 mg/ml of the trimeric XTEN preparation compared to a solution containing ≧100, 130, or 150 mg/ml of the corresponding linear XTEN of equal molar concentration. In another embodiment, the invention provides a composition comprising a solution that comprises a multimeric XTEN having at least four XTEN fragments linked together in a branched manner (e.g. tetrameric manner) wherein the composition has a viscosity that is less than a solution comprising a corresponding linear XTEN having the same number of amino acids and the same molar concentration, wherein the viscosity of the solution is reduced by at least 5, 6, 7, 8, 9 or 10 cP in a solution containing ≧100, 130, or 150 mg/ml of the trimeric XTEN preparation compared to a solution containing ≧100, 130, or 150 mg/ml of the corresponding linear XTEN of equal molar concentration. In another embodiment, the invention provides a composition comprising a solution that comprises a multmeric XTEN having at least five XTEN fragments linked together in a branched manner (e.g. pentameric manner) wherein the composition has a viscosity that is less than a solution comprising a corresponding linear XTEN having the same number of amino acids and the same molar concentration, wherein the viscosity of the solution is reduced by at least 5, 6, 7, 8, 9 or 10 cP in a solution containing ≧100, 130, or 150 mg/ml of the trimeric XTEN preparation compared to a solution containing ≧100, 130, or 150 mg/ml of the corresponding linear XTEN of equal molar concentration. In the foregoing embodiments of this paragraph, the individual XTEN of the multimeric configurations are selected from the group consisting of the sequences set forth in Table 2 and Table 3.

[0022] In another embodiment, the invention provides compositions of a polypeptide having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 52.

[0023] In another embodiment, the invention provides a pharmaceutical composition, comprising the conjugate of any one of the XTEN-payload conjugate embodiments described herein, and a pharmaceutically acceptable carrier. In one embodiment, the foregoing pharmaceutical composition has utility in the treatment of a condition selected from the group of conditions set forth in Table 16. In another embodiment, the foregoing pharmaceutical composition has utility for use in a pharmaceutical regimen for treatment of a subject, said regimen comprising the pharmaceutical composition. In another embodiment, the foregoing pharmaceutical regimen further comprises the step of determining the amount of pharmaceutical

composition needed to achieve a beneficial effect in a subject having a condition selected from the group of conditions set forth in Table 16. In another embodiment, the foregoing pharmaceutical regimen used for treating the subject comprises administering the pharmaceutical composition in two or more successive doses to the subject at an effective amount, wherein the administration results in at least a 10%, or 20%, or 30%, or 40%, or 50%, or 60%, or 70%, or 80%, or 90% greater improvement of at least one, two, or three parameters associated with the condition compared to an untreated subject.

[0024] In another embodiment, the invention provides a conjugate of any one of the XTEN-payload conjugate embodiments described herein for use in the preparation of a medicament for treatment of a condition selected from the group of conditions set forth in Table 16.

[0025] In some embodiments, the invention provides methods of selecting a combination of payloads linked to XTEN as a therapeutic agent, the method comprising providing a library of XTENs comprising a plurality of XTEN sequences wherein each of said XTEN sequences is conjugated to at least a first payload and at least a second payload which is different from the first payload; from said library, selecting an XTEN sequence as the therapeutic agent if it exhibits an improved in vitro or in vivo parameter as compared to that of (1) an XTEN sequence conjugated to the first payload alone; and (2) an XTEN sequence conjugated to the second payload alone. In one embodiment of the method, the first payload and second payload are therapeutically effective for ameliorating a common disease (e.g. a disease to which both the first and second payload targets). In one embodiment of the method, the first drug and second drug are therapeutically effective for treating different symptoms of a common disease. In one embodiment of the method, the common disease is selected from cancer, cancer supportive care, cardiovascular, central nervous system, endocrine disease, gastrointestinal, genitourinary, hematological, HIV infection, hormonal disease, inflammation, autoimmune disease, infectious disease, metabolic disease, musculoskeletal disease, nephrology disorders, ophthalmologic diseases, pain, and respiratory. In one embodiment of the method, the first payload and second payload mediate their therapeutic effect via a common biological pathway. In one embodiment of the method, the first payload and second payload are different drugs selected from the group consisting of the drugs set forth in Table 11, Table 18 and Table 21. In one embodiment of the method, the first payload and second payload are different biologically active proteins selected from the group consisting of the proteins set forth in Table 12, Table 18 and Table 21. In one embodiment of the method, the first payload is a drug selected from the group consisting of the drugs set forth in Table 11, Table 18 and Table 21 and the second payload is a biologically active protein selected from the group consisting of the proteins set forth in Table 12, Table 18 and Table 21.

[0026] In another embodiment, the invention provides an isolated polypeptide comprising an extended recombinant polypeptide that is linked to an affinity purification tag via a proteolytic cleavage site having a sequence selected from SASRSA or SASXSA where X is R or K.

[0027] In another embodiment, the invention provides an isolated polypeptide comprising a polypeptide comprising an XTEN that is linked at its N-terminus to a first affinity purification tag via a proteolytic cleavage site having a sequence selected from SASRSA or SASXSA where X is R or K, and at its C-terminus to a second affinity purification tag via a proteolytic cleavage site having a sequence selected from SASRSA or SASXSA where X is R or K.

[0028] In another aspect, the invention relates to a method of treating a condition in a subject with an XTEN-payload conjugate composition. In one embodiment, the invention provides a method of treating a condition in a subject comprising comprising administering an effective amount of the conjugate of any one of the XTEN-payload embodiments described herein to a subject in need thereof. In another embodiment, the invention provides a method of treating a condition in a subject comprising comprising administering an effective amount of the conjugate of the group consisting of the conjugates set forth in Table 21 to a subject in need thereof. In the foregoing embodiments of this paragraph, the condition to be treated includes, but is not limited to, the conditions set forth in Table 13. In another embodiment, the invention provides a pharmaceutical composition comprising any of the XTEN-payload conjugate embodiments described herein and a pharmaceutically acceptable carrier for use in a treatment regimen, the regimen comprising administering two or more consecutive doses of the pharmaceutical composition.

[0029] In one embodiment, the invention provides the use of a conjugate of any one of the XTEN-payload embodiments described herein for the preparation of a medicament for treatment of a condition selected from the group of conditions set forth in Table 16. In another embodiment, the invention provides a pharmaceutical composition for treatment of a condition selected from the group of conditions set forth in Table 16. comprising an effective amount of a conjugate of any one of the XTEN-payload embodiments described herein.

[0030] In another embodiment, the invention provides a composition having the structure set forth in FIG. 117.

[0031] It is specifically contemplated that the conjugate embodiments can exhibit one or more or any combination of the properties disclosed herein. In addition, any of the XTEN compositions disclosed herein can be utilized in any of the methods disclosed herein.

INCORPORATION BY REFERENCE

[0032] 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.

BRIEF DESCRIPTION OF THE DRAWINGS.

[0033] The features and advantages of the invention may be further explained by reference to the following detailed description and accompanying drawings that sets forth illustrative embodiments

[0034] FIG. 1 shows schematics of XTEN suitable for conjugation with payloads. FIG. 1A shows unmodified XTEN. FIG. 1B shows a cysteine-engineereed XTEN with an internal cysteine with a thiol side chain; below is an XTEN with an a reactive N-terminal amino group; below is an XTEN with an N-terminal cysteine with a thiol reactive group. FIG. 1C shows cysteine-engineereed XTEN with multiple internal cysteines. FIG. 1D shows shows two variations of a cysteine-engineereed XTEN with an internal cysteine with a thiol side chain;s and a reactive N-terminal amino group and, at the bottom, a shows a cysteine- and lysine-engineereed XTEN with internal cysteines and internal lysines.

[0035] FIG. 2 shows a conjugation reaction utilizing NHS-esters and their water soluble analogs sulfo-NHS-esters) reacting with a primary amino group to yield a stable amide XTEN-payload product.

[0036] FIG. 3 shows a conjugation reaction utilizing thiol groups and an N-maleimide. The maleimide group reacts specifically with sulfhydryl groups when the pH of the reaction mixture is between pH 6.5 and 7.5, forming a stable thioether linkage that is not reversible.

[0037] FIG. 4 shows a conjugation reaction utilizing haloacetyls. The most commonly used haloacetyl reagents contain an iodoacetyl group that reacts with sulfhydryl groups at physiological pH. The reaction of the iodoacetyl group with a sulfhydryl proceeds by nucleophilic substitution of iodine with a thiol producing a stable thioether linkage in the XTEN-payload.

[0038] FIG. 5 shows a conjugation reaction utilizing pyridyl disulfides. Pyridyl disulfides react with sulfhydryl groups over a broad pH range (the optimal pH is 4-5) to form disulfide bonds linking XTEN to payloads.

[0039] FIG. 6 shows a conjugation reaction utilizing zero-length cross-linkers wherein the cross-linkers are used to directly conjugate carboxyl functional groups of one molecule (such as a payload) to the primary amine of another molecule (such as an XTEN).

[0040] FIG. 7 shows different configurations of XTEN precursors that are multifunctional (or multivalent), including dedrimers. Non-limiting examples of trifunctional linkers are "Y-shaped" sulfhydryl-reactive TMEA (Tris-(2-Maleimidoethyl)amine) and amine-reactive TSAT (Tris-(succimimidyl aminotricetate). Any combination of reactive moieties can be designed using a scaffold polymer, either linear (forming a "comb" configuration) or branched (forming a "dendrimer" configuration), for multivalent display.

[0041] FIG. 8 shows a conjugation reaction utilizing the Huisgen 1,3-dipolar cycloaddition of alkynes to azides to form 1,4-disubsituted-1,2,3-triazoles, as shown.

[0042] FIG. 9 shows a conjugation reaction using thio-ene based click chemistry that may proceed by free radical reaction, termed thiol-ene reaction, or anionic reaction, termed thiol Michael addition.

[0043] FIG. 10 shows a conjugation reaction utilizing click chemistry based on reactions between hydrazides and aldehydes, resulting in the illustrated hydrazone linkage in the XTEN-payload.

[0044] FIG. 11 shows a reaction between a C-terminal acylazide and a primary amino group resulting in the formation of an amide bond.

[0045] FIG. 12 shows a conjugation reaction utilizing Native Chemical Ligation (NCL) involving a C-terminal thioester as an electrophile and N-terminal Cysteine as a nucleophile. The result of this reaction is a native amide bond at the ligation site of the XTEN-payload composition.

[0046] FIG. 13 shows a conjugation reaction utilizing expressed protein ligation (EPL) methodology. The EPL method is based on protein splicing, the process in which a protein undergoes an intramolecular rearrangement resulting in the extrusion of an internal sequence (intein) and the joining of the lateral sequences (exteins). In the method, the fused protein undergoes an N-S shift when the side chain of the first cysteine residue of the intein portion of the precursor protein nucleophilically attacks the peptide bond of the residue immediately upstream (that is, for example, the final residue of XTEN) to form a linear thioester intermediate, followed by a rearrangement to form to form an amide bond between the XTEN-cross-linker and the payload.

[0047] FIG. 14 shows a conjugation reaction utilizing traceless Staudinger ligation, like Native Chemical Ligation (NCL), resulting in a native amide bond at the ligation site

[0048] FIG. 15 shows a conjugation reaction utilizing enzymatic ligation. Transglutaminases are enzymes that catalyze the formation of an isopeptide bond between the γ-carboxamide group of glutamine of a payload peptide or protein and the ε-amino group of a lysine in a lysine-engineered XTEN (or an N-terminal amino group), thereby creating inter- or intramolecular cross-links between the XTEN and payload.

[0049] FIG. 16 shows enzymatically-created XTEN-payload compositions utilizing the sortase A transpeptidase enzyme from Staphylococcus aureus to catalyze the cleavage of a short 5-amino acid recognition sequence LPXTG between the threonine and glycine residues of Protein1 that subsequently transfers the acyl-fragment to an N-terminal oligoglycine nucleophile of Protein1. By functionalizing the Protein2 to contain an oligoglycine, the enzymatic conjugation of the two

proteins is accomplished in a site-specific fashion to result in the desired XTEN-payload composition.

[0050] FIG. 17 shows various XTEN-cross-linker precursor segments that are used as reactants to link to payloads or to other XTEN reactants. FIG. 17A is intended to show that the 1B represents the remaining reactive group of the precursors on the right. FIG. 17B shows similar reactive precurors with either multiple (left) or single (right) payload A molecules conjugated to the XTEN.

[0051] FIG. 18 shows exemplary permutations of XTEN-cross-linker precursor segments with two reactive groups of cross-linkers or reactive groups of an incorporated amino acid that are used as reactants to link to payloads or to other XTEN reactants. The 1B and 2B represent reactive groups that will, in other figures, react with a like-numbered reactive group; 1 with 1 and 2 with 2, etc.

[0052] FIG. 19 is intended to show examples of various reactants and the nomenclature for configurations illustrated elsewhere in the Drawings. FIG. 19A shows various forms of reactive XTEN segment precurors, each with a different reactive group on the N-terminus. FIG. 19B shows various cross-linkers with 2, 3 or 4 reactive groups. In the first case, the divalent cross-linker is a heterofunctional linker that reacts with two different types of reactive groups, represented by "2" and "1". In the case of the trivalent and tetravalent cross-linker, each reacts with only one type of reactive group, represented by "1". FIG. 19C illustrates the nomenclature of the reaction products of two XTEN segment precursors. In the top version, a 1A was reacted with a 1B to create a dimeric XTEN linked at the N-termini, with the residue of the cross-linker indicated by $1A_R$-$1B_R$, while the bottom version is also a dimeric XTEN linked at the N-termini, with the residue of the cross-linker indicated by $2A_R$-$2B_R$.

[0053] FIG. 20 illustrates the creation of various XTEN precursor seegments. FIG. 20A shows the steps of making an XTEN polypeptide, followed by reaction of the N-terminus with the cross-linker with 2B-1A reactive groups, with the 1A reacting with the N-terminal 1B (e.g., an alpha amino acid) to create the XTEN precursor 2 with the reactive group 2B. FIG. 20B shows the sequential addition of two cross-linkers with 2A reactive groups to 2B reactive groups of the XTEN, resulting in XTEN precuror 4, which is then reacted with a cross-linker at the N-terminus bewtween a reactive 1B and the 1A of a cross-linker, resulting in XTEN precuror 5, with reactive groups 4B and 3B. In such case, the XTEN-precurors 5 then could serve as a reactant with two different payloads or XTEN.

[0054] FIG. 21 illustrates examples of multimeric conjugates. FIG. 21A illustrates how three molecules of an XTEN with a conjugated payload A can be conjugated to a trimeric cross-linker, resulting in a trimeric XTEN-payload conjugate with three A payloads. FIG. 21B illustrates how

three molecules of a polypeptide with an A payload can be conjugated to a trimeric cross-linker, resulting in a trimeric XTEN-payload conjugate with three polypeptides with A payloads.

[0055] FIG. 22 illustrates examples of multivalent XTEN conjugates that can originate from XTEN precursors with a single cysteine. The amino group in the XTEN precursor acts as reactive group 2B and the thiol group as reactive group 1B. The XTEN precursor can be cross-linked using cross-linker that can react with group 1B. The valency of the cross-linker controls the valency of the resulting intermediate. This cross-linked intermediate can be reacted with a payload carrying a reactive group 2A that can react with the amino group forming the conjugation link 2A-BR. FIG. 22A is an XTEN precursor with single thiol group. FIG. 22B is a divalent conjugate. FIG. 22C is a trimeric conjugate. FIG. 22D is a tetrameric conjugate.

[0056] FIG. 23 illustrates examples of multivalent XTEN conjugates that can originate from XTEN precursors with a single cysteine. The amino group in the XTEN precursor acts as reactive group 1B and the thiol group as reactive group 2B. The XTEN precursor can be cross-linked using cross linker that can react with group 1B. The valency of the cross linker controls the valency of the resulting intermediate. This cross linked intermediate can be reacted with a payload carrying a reactive group 2A that can react with the thiol group forming the conjugation link 2A-BR. FIG. 23A illustrates the thiol group located close to the C-terminus of XTEN. As a result the payload is located at the distal ends of the final trimeric conjugate. FIG. 23B illustrates that the thiol group is located close to the N-terminus of XTEN. As a result the payload is located at the proximal ends of the final conjugate resulting in increased payload shielding by XTEN.

[0057] FIG. 24 illustrates an example of the creation of a "comb" configuration. FIG. 24A is a XTEN-payload precursor comprising linker reactive group 1A. The payload can be recombinantly fused to XTEN or it can be conjugated. FIG. 24B illustrates an XTEN-precursor with the comb-like cross-linkers. This can be an XTEN that carries a multiple reactive groups B. FIG. 24C shows the final product in the "comb" configuration, with five Payload A. Valency is controlled by the number of reactive groups in the Comb-like precursor.

[0058] FIG. 25 illustrates various configurations of bispecific conjugates with two payloads. FIG. 25A illustrates configurations with one molecule each of two payloads, while FIG. 25B illustrates various configurations with multiple copies of one or both payloads.

[0059] FIG. 26 illustrates various examples of conjugates with high valency. Conjugations sites of payloads can grouped (FIG. 26A) or interspersed (FIG. 26B).

[0060] FIG. 27 illustrates the preparation of bispecific conjugates from an XTEN precursor carrying both amino and thiol groups in which many chemistries can be used and the order of payload addition can vary. One can generate linker-conjugates as precursors. FIG. 27A shows the creation of a single XTEN precursor to which two different payloads are attached. FIG. 27B shows a segment approach starting from two XTEN precursor molecules. This approach allows

one to conjugate both payloads to XTEN using the same type of linker chemistry. In this case, the figure shows thiol as the group to which payloads are conjugated, and then the N-terminus of each segment is modified with a cross-linker to enable head-to-head segment conjugation, resulting in a dimeric, bispecific conjugate final product.

[0061] FIG. 28 shows examples of multivalent conjugates combining an antibody, XTEN, and a payload. Such constructs can have different valencies and provide many benefits in that the XTEN can have a cleavable linker, XTEN can provides solubility to the composition, and it can allow adjustment of the drug load per IgG, and the XTEN can be pre-conjugated with drug to simplify manufacturing. FIG. 28A illustrates two XTENs conjugated to IgG at Cys residues in the hinge region. FIG. 28B illustrates four XTEN conjugated to IgG using Cys in the hinge region. FIG. 28C illustrates XTEN conjugated outside of hinge. This can be done by inserting Cys to control conjugation site or by random conjugation to Lys side chains.

[0062] FIG. 29 shows examples of the construction of conjugates combining an antibody, XTEN, and a payload. The antibody can have one or multiple reactive groups 1B. XTEN can be conjugated to one or multiple Payloads A. In addition XTEN can carry a reactive group 1A that preferentially reacts with the reactive group 1B on the antibody. The location of reactive groups 1B in the antibody controls the number and location of XTENs that are conjugated to the antibody, resulting in the final product.

[0063] FIG. 30 shows examples of conjugates comprising a targeting moiety, XTEN, and a payload. Targeting moieties can be peptides, peptoids, or receptor ligands. FIG. 30A shows 1x(1x3) conjugate. FIG. 30B shows 1x2(1x3) conjugate. FIG. 30C shows a 3x1(1x3) conjugate.

[0064] FIG. 31 shows examples of conjugates comprising multiple different targeting moieties, XTEN, and a payload. Targeting moieties can be peptides, peptoids, receptor ligands.

[0065] FIG. 32 shows examples of conjugates comprising a targeting moiety, XTEN, and a multiple different payloads.

[0066] FIG. 33 shows examples of combinatorial XTEN conjugates. Payloads A, B, C, and D carry a reactive group 2A that reacts with reactive group 2B on the XTEN precursor. In the next step, Payloads E and F carry a reactive group 1A that reacts with reactive group 1B on XTEN, resulting in a library of different permutations of bispecific conjugates. In this case, the reactive groups 1B and 2B are thiol- and amino-groups, respectively.

[0067] FIG. 34 shows an example of the creation of a combinatorial XTEN conjugate library. Payloads A, B, C are conjugated to XTEN carrying reactive group 1A, resulting in one set of XTEN-precursor segments. Payloads E, F, and G are conjugated to XTEN carrying reactive group 1B, resulting in a second set of XTEN-precursor segments. These segments are subjected to combinatorial conjugation and then are purified from reactants. This enables the formation of combinatorial products that can be immediately subjected to *in vitro* and *in vivo* testing. In this

case, reactive groups 1A and 1B are the alpha-amino groups of XTEN with or without a bispecific cross-linker. In one example, the 1A is an azide and 1B is an alkyne or vice versa, while the payloads are attached to XTEN via thiol groups in XTEN.

[0068] FIG. 35 shows an example of the creation of a combinatorial XTEN conjugate library that optimizes the ratio between two payloads. Each library member carries a different ratio of payload A and payload E.

[0069] FIG. 36 shows an example of the creation of a combinatorial XTEN conjugate library that creates combinations of targeting moieties and payloads. The targeting moieties 1, 2, and 3 are conjugated to XTEN carrying reactive group 1A. Payloads E, F, and G are conjugated to XTEN carrying reactive group 1B. These segments are subjected to combinatorial conjugation, enabling the formation of combinatorial products where each library member comprises targeting moieties and payloads. All XTEN segments carrying payloads and conjugation groups can be purified as combinatorial products that can be immediately subjected to *in vitro* and *in vivo* testing.

[0070] FIG. 37 shows an example of an XTEN conjugate comprising targeting moieties and payloads that exert selective action on the surface of a target cell, such as a tumor cell. The particular design of the dimeric XTEN conjugate comprises LHRH and doxorubicin. This conjugate binds to the LHRH-receptor on that is over-expressed on many cancer cells. Receptor binding results in internalization followed by proteolytic break down and the intracellular liberation of doxorubicin, which is toxic to the cell.

[0071] FIG. 38 is a schematic flowchart of representative steps in the assembly, production and the evaluation of a XTEN.

[0072] FIG. 39 is a schematic flowchart of representative steps in the assembly of an XTEN polynucleotide construct encoding a fusion protein. Individual oligonucleotides **501** are annealed into sequence motifs **502** such as a 12 amino acid motif ("12-mer"), which is ligated to additional sequence motifs from a library to create a pool that encompasses the desired length of the XTEN **504**, as well as ligated to a smaller concentration of an oligo containing BbsI, and KpnI restriction sites **503.** The resulting pool of ligation products is gel-purified and the band with the desired length of XTEN is cut, resulting in an isolated XTEN gene with a stopper sequence **505**. The XTEN gene is cloned into a stuffer vector. In this case, the vector encodes an optional CBD sequence **506** and a GFP gene **508.** Digestion is then performed with BbsI/HindIII to remove **507** and **508** and place the stop codon. The resulting product is then cloned into a BsaI/HindIII digested vector, resulting in gene **500** encoding an XTEN.

[0073] FIG. 40 is a schematic flowchart of representative steps in the assembly of a gene encoding XTEN, its expression, conjugation with a payload and recovery as an XTEN-paylad, and its evaluation as a candidate product.

[0074] FIG. 41 shows generalized XTEN with either N- or C-terminal tags or N- and C-terminal sequences optimized for purification using methods illustrated in FIGS. 42.

[0075] FIG. 42 shows a generalized scheme for purification of XTEN with, in this illusrtrative embodiment, two tags in which a two-step purification method to capture first one tag and then the second can be utilized to remove truncated XTEN from fermentation, resulting in the hghly puritified target XTEN entity.

[0076] FIG. 43 shows an SDS-PAGE gel of the CBD-TEV site-XTEN_AE864 and CBD-TEV site-XTEN_AE864-GFP constructs expressed in E. coli BL21 DE3 rne-131 and E. coli BL21 DE3 cells from shake flask cultures as described in Example 10. Gel lane samples with MW markers and expressed proteins from constructs are: 1) MW marker; 2-5) lysates from 4 independent flasks expressing CBD-TEV site-XTEN_AE864-GFP fusion protein in E. coli BL21 DE3; 6-9) lysates from 4 independent flasks expressing CBD-TEV site-XTEN_AE864-GFP fusion protein in E. coli BL21 DE3 rne-131; 10-13) lysates from 4 independent flasks expressing CBD-TEV site-XTEN_AE864 fusion protein in E. coli BL21 DE3; 14-17) lysates from 4 independent flasks expressing CBD-TEV site-XTEN_AE864 fusion protein in E. coli BL21 DE3 rne-131. Full-length protein spots appear within the outline box. Bands of lower molecular weight are host-cell proteins.

[0077] FIG. 44 shows relative GFP fluorescence of the CBD-TEV site-XTEN_AE864-GFP expressed in *E. coli* BL21 DE3 rne-131 and *E. coli* BL21 DE3 cells from shake flask cultures as described in Example 10.

[0078] FIG. 45 shows an SDS-PAGE gel of the CBD-R-C-XTEN_AE864-RH8 (EC682) and CBD-R-XTEN_AE864-RH8 (EC683) constructs expressed in *E. coli* fermentations as described in Example 17. Gel lane samples with MW markers and expressed proteins from constructs are: 1) MW marker; E. coli fermentation #EC682 clarified soluble lysates time points after inoculation 2) 16 hours, 3) 24 hours, 4) 40 hours, 5) 45 hours; E. coli fermentation #EC683 clarified soluble lysates at time points after inoculation 6) 16 hours, 7) 24 hours, 8) 40 hours, 9) 45 hours; Purified CBD-R-XTEN_AE864-RH8 reference standard 10) 1 microgram, 11) 2 micrograms, and 12) 4 micrograms. For the *E. coli* fermentation clarified soluble lysates each lane represents 3 microliters of the fermenter culture. Full-length protein spots appear within the outline box. Bands of lower molecular weight are host-cell proteins.

[0079] FIG. 46 shows the trace output of Toyopearl Phenyl 650 M Hydrophobic Interaction Chromatography, as described in Example 18.

[0080] FIG. 47 shows a non-reducing 4-12% Bis-Tris SDS-PAGE analysis of Toyopearl Phenyl 650 M Hydrophobic Interaction Chromatography fractions, as indicated in the figure and as described in Example 18. The materials per lane are: Lane 1: Marker; Lane 2: Load 7.5 µl; Lane 3: Flow-through 1; Lane 4: Flow-through 2; Lane 5: Elution fraction E1; Lane 6: Elution

fraction E2; Lane 7: Elution fraction E3; Lane 8: Elution fraction E4; Lane 9: Elution fraction E5; Lane 10: Elution fraction E6; Lane 11: Elution fraction E7; Lane 12: Elution fraction E8.

[0081] FIG. 48 shows a non-reducing 4-12% Bis-Tris SDS-PAGE analysis of Toyopearl IMAC Chromatography flow through, wash (FIG. 48A) and elution fractions (FIG. 48B)(non-reducing) as described in Example 18.

[0082] FIG. 49 shows a non-reducing SDS-PAGE analysis of the trypsin-digested IMAC pool described in Example 18.

[0083] FIG. 50 shows the elution profile of the MacroCap Q Chromatography described in Example 18.

[0084] FIG. 51 shows a 4-12% Bis-Tris SDS-PAGE analysis of the MacroCap Q elution fractions, as described in Example 18. FIG. 51A, flow-through, Coomassie staining. FIG. 51B, elution fractions, Coomassie staining. FIG. 51C, elution fractions, silver staining.

[0085] FIG. 52 shows the traces from C18 RP-HPLC analysis of MacroCap Q elution fractions, as described in Example 18.

[0086] FIG. 53 shows a trace from a C18 RP-HPLC of the MacroCap Q Elution Pool, as described in Example 18.

[0087] FIG. 54 shows a non-reducing SDS-PAGE analysis of the Toyopearl Phenyl 650 M Hydrophobic Interaction Chromatography fractions, as described in Example 19.

[0088] FIG. 55 shows a non-reducing SDS-PAGE analysis of Toyopearl IMAC Chromatography fractions, as described in Example 19.

[0089] FIG. 56 shows a non-reducing 4-12% Bis-Tris SDS-PAGE/silver staining analysis of the MacroCap Q Elution fractions as described in Example 19.

[0090] FIG. 57 shows traces from C18 RP-HPLC analysis of MacroCap Q elution fractions, as described in Example 19.

[0091] FIG. 58 shows the trace from C18 RP-HPLC analysis of the MacroCap Q elution pool described in Example 19.

[0092] FIG. 59 shows an SDS-PAGE analysis of XTEN constructs with experimental tags after expression in *E.coli* as described in Example 20. Soluble lysates were loaded on the 4-12% Bis-Tris polyacrylamide gel, with amounts loaded per lane equivalent to 36 µl of cell culture suspension. The gel was stained with Coomassie Blue stain using standard methods.

[0093] FIG. 60 shows an SDS-PAGE analysis of the RP11-XTEN-His8 construct expressed in E.coli, as described in Example 20. Heat-treated soluble lysates were loaded on the 4-12% Bis-Tris polyacrylamide gel with amounts equivalent to 1 or 2 µl of cell culture suspension, respectively. The gel was stained with Coomassie Blue stain. The gel demonstrates that essentially all the expressed RP11-XTEN-His8 protein was found in the pelleted fraction.

[0094] FIG. 61 shows an SDS-PAGE analysis of the MacroCap SP purification of RP11-XTEN-His8 polypeptide described in Example 21. Fractions were analyzed by 4-12% SDS-PAGE followed by Coomassie staining.

[0095] FIG. 62 shows an SDS-PAGE analysis of the IMAC purification of the RP11-XTEN-His8 polypeptide described in Example 21. Fractions were analyzed by 4-12% SDS-PAGE followed by Coomassie staining.

[0096] FIG. 63 shows an SDS-PAGE analysis of the trypsin digestion of RP11-XTEN-His8 protein purified by two chromatographic steps (SP + IMAC) described in Example 21. Preparations were analyzed by 4-12% SDS-PAGE followed by Coomassie staining (FIG. 63A) and silver staining (FIG. 63B).

[0097] FIG. 64 shows the results of the analysis of the conjugation reaction of DBCO-Mal to the 3xThiol-XTEN as described in Example 23. FIG. 64A shows the C18 RP-HPLC analysis of the reaction mixture. A 20 µg protein sample was loaded on a Phenomenex Jupiter C18 5uM 300A 4.6mm x 150mm column. The proteins were eluted with a 5-50% gradient of acetonitrile in 0.1% trifluoroacetic acid. FIG. 64B shows the HIC purification of DBCO-XTEN reaction product. FIG. 64C shows the C18 RP-HPLC analysis of the HIC-purified DBCO-XTEN reaction product.

[0098] FIG. 65 shows results from trypsin cleavage of a double tagged precursor XTEN, as described in Example 24. FIG. 65A shows a4-12% Bis-Tris SDS-PAGE analysis of protein samples loaded at 2 µg per lane. The gel was stained with an Invitrogen SimplyBlue SafeStain. FIG. 65B shows a4-12% Bis-Tris SDS-PAGE analysis of protein samples loaded at0.5 µg per lane. The gel was stained with a Pierce Silver Stain Kit.

[0099] FIG. 66 shows results of an SDS-PAGE analysis of MacroCap Q purification of trypsin digested double tagged precursor, as described in Example 24. FIG. 66A shows a4-12% Bis-Tris SDS-PAGE analysis of protein samples loaded at 3 µg per lane. The gel was stained with Invitrogen SimplyBlue SafeStain. FIG. 66B shows a4-12% Bis-Tris SDS-PAGE analysis of protein samples loads at 0.5 µg per lane. The gel was stained with a Pierce Silver Stain Kit. FIG. 66C shows a 4-12% Bis-Tris SDS-PAGE analysis of protein samples loaded at 0.5 µg per lane. The gel was stained with a Pierce Silver Stain Kit.

[00100] FIG. 67 shows results from a C18 RP-HPLC test for residual trypsin activity. FIG. 67A is the trace output of analysis of synthetic [G2]GLP2 peptide in intact form. FIG. 67B is the trace output of analysis of synthetic [G2]GLP2 peptide digested with bovine trypsin. FIG. 67C is the trace output of analysis of XTEN_AE869_Am1,C2 spiked with [G2]GLP2 and incubated overnight at 37°C, as described in Example 24.

[00101] FIG. 68 shows preparation of GLP2-XTEN conjugate from GLP2-Cys peptide and 1xAmino-XTEN as described in Example 26. 20 µg protein samples were loaded on

Phenomenex Jupiter C18 5uM 300A 4.6mm x 150mm column. Proteins were eluted with 5-50% gradient of acetonitrile in 0.1% trifluoroacetic acid and detected by absorbance at 214 nm (left panels A-C). 100 µg protein samples were desalted using NanoSep 3K Omega centrifugal devices (Pall Corp.). Protein solutions in 50% acetonitrile, 0.5% formic acid were infused into high-resolution mass spectrometer at flow rate 10ul/min. ESI-MS spectra were acquired in 800-1600 amu range and reconstructed into zero-charge spectra using Bayesian Protein Reconstruction Software (right panels A-C). FIG. 68A: initial 1xAmino-XTEN protein. FIG. 68B: product of the reaction between 1xAmino-XTEN and sulfo-SMCC cross-linker. FIG. 68C: purified GLP2-XTEN conjugate after reaction between GLP2-Cys and N-Mal-XTEN.

[00102] FIG. 69 shows preparation of GLP2-XTEN conjugate from GLP2-Mal peptide and 1xThiol-XTEN as described in Example 27. 20 µg protein samples were loaded on Phenomenex Jupiter C18 5uM 300A 4.6mm x 150mm column. Proteins were eluted with 5-50% gradient of acetonitrile in 0.1% trifluoroacetic acid and detected by absorbance at 214 nm (left panels A, B). 100 µg protein samples were desalted using NanoSep 3K Omega centrifugal devices (Pall Corp.). Protein solutions in 50% acetonitrile, 0.5% formic acid were infused into high-resolution mass spectrometer at flow rate 10ul/min. ESI-MS spectra were acquired in 800-1600 amu range and reconstructed into zero-charge spectra using Bayesian Protein Reconstruction Software (right panels A, B). FIG. 69A: initial 1xThiol-XTEN protein. FIG. 69B: product of the reaction between GLP2-Mal and 1xThiol-XTEN.

[00103] FIG. 70 shows the results of the purification of GLP2-XTEN using preparative C4 RP-HPLC as described in Example 27. FIG. 70A shows a chromatography profile of preparative RP-HPLC. A fraction at 56-62 min was collected and evaporated under vacuum . FIG. 70B shows an analysis by C18 RP-HPLC for purified GLP2-XTEN.

[00104] FIG. 71 shows results of the conjugation of DBCO-Mal to 1xThiol-XTEN, as described in Example 28. FIG. 71A shows C18 RP-HPLC analysis of the reaction mixture. A 20 µg protein sample was loaded on Phenomenex Jupiter C18 5uM 300 A 4.6mm x 150 mm column. Proteins were eluted with a 5-50% gradient of acetonitrile in 0.1% trifluoroacetic acid. FIG. 71B shows the HIC purification of DBCO-XTEN. FIG. 71C shows the C18 RP-HPLC analysis of the HIC-purified DBCO-XTEN.

[00105] FIG. 72 shows results of analytical assays of XTEN conjugated with cross-linked FITC, as described in Example 31. FIG. 72A shows the co-migration in a gel imaged by UV light box to show the large apparent MW of FITC-containing conjugated species, also detected by SEC at OD214 (protein signal) and OD495 (FITC signal) in a SEC column, indicating successful labeling of the XTEN with minimal free dye contamination. The materials by lane (left to right, after the MW standards are: labeled FITC-CL-CBD-XTEN; labeled FITC-CL-XTEN; purified FITC-CL-XTEN; purified FITC-CL-XTEN; and purified FITC-CL-XTEN. The gel was imaged

by UV light box to show FITC apparent MW of FITC containing species. FIG. 72B shows the results of SEC analysis of FITC-conjugated XTEN, showing the overlap of the output of materials detected at OD214 and OD495, and also the apparent large molecular weight.

[00106] FIG. 73 shows results of SEC analyses of the peak elution fractions of conjugates of GFP cross-linked to XTEN and free GFP, as described in Example 32. Cross-linking was confirmed by co-migration of the OD214 protein signal and OD395 GFP signal in the SEC column.

[00107] FIG. 74 shows the results of pharmacokinetic assays of GFP-X-XTEN and FITC-X-XTEN tested in cynomolgus monkeys, as described in Example 33.

[00108] FIG. 75 shows the pharmacokinetic profile (plasma concentrations) in cynomolgus monkeys after single doses of different compositions of GFP linked to unstructured polypeptides of varying length, administered either subcutaneously or intravenously, as described in Example 33. The compositions were GFP-L288, GFP-L576, GFP-XTEN_AF576, GFP-Y576 and XTEN_AD836-GFP. Blood samples were analyzed at various times after injection and the concentration of GFP in plasma was measured by ELISA using a polyclonal antibody against GFP for capture and a biotinylated preparation of the same polyclonal antibody for detection. Results are presented as the plasma concentration versus time (h) after dosing and show, in particular, a considerable increase in half-life for the XTEN_AD836-GFP, the composition with the longest sequence length of XTEN. The construct with the shortest sequence length, the GFP-L288 had the shortest half-life.

[00109] FIG. 76 shows an SDS-PAGE gel of samples from a stability study of the fusion protein of XTEN_AE864 fused to the N-terminus of GFP. The GFP-XTEN was incubated in cynomolgus plasma and rat kidney lysate for up to 7 days at 37°C, as described in Example 55. In addition, GFP-XTEN administered to cynomolgus monkeys was also assessed. Samples were withdrawn at 0, 1 and 7 days and analyzed by SDS PAGE followed by detection using Western analysis and detection with antibodies against GFP.

[00110] FIG. 77 shows the near UV circular dichroism spectrum of Ex4-XTEN_AE864, performed as described in Example 56.

[00111] FIG. 78 shows results of a size exclusion chromatography analysis of glucagon-XTEN construct samples measured against protein standards of known molecular weight, with the graph output as absorbance versus retention volume, as described in Example 58. The glucagon-XTEN constructs are 1) glucagon-Y288; 2) glucagonY-144; 3) glucagon-Y72; and 4) glucagon-Y36. The results indicate an

[00112] FIG. 79 is a schematic of the logic flow chart of the algorithm SegScore (Example 59). In the figure the following legend applies: i, j - counters used in the control loops that run through the entire sequence; HitCount- this variable is a counter that keeps track of how many

times a subsequence encounters an identical subsequence in a block; SubSeqX - this variable holds the subsequence that is being checked for redundancy; SubSeqY - this variable holds the subsequence that the SubSeqX is checked against; BlockLen - this variable holds the user determined length of the block; SegLen - this variable holds the length of a segment. The program is hardcoded to generate scores for subsequences of lengths 3, 4, 5, 6, 7, 8, 9, and 10; Block - this variable holds a string of length BlockLen. The string is composed of letters from an input XTEN sequence and is determined by the position of the i counter; SubSeqList - this is a list that holds all of the generated subsequence scores.

[00113] FIG. 80 depicts the application of the algorithm SegScore to a hypothetical XTEN of 11 amino acids in order to determine the repetitiveness. An XTEN sequence consisting of N amino acids is divided into N-S+1 subsequences of length S (S=3 in this case). A pair-wise comparison of all subsequences is performed and the average number of identical subsequences is calculated to result, in this case, in a subsequence score of 1.89.

[00114] FIG. 81 provides the results of the assay to measure the fluorescence signal of RP11 clones pSD0107 to pSD0118), as described in Example 12. One positive control (pLCW970) and two negative controls (pBr322 and pLCW970+10 mM phosphate) were included. The GFP expression level was measured using samples from 2-3 shake flasks per construct.

[00115] FIG. 82 shows the screening results of libraries LCW1157-1159. FIG. 82A-C provides the fluorescence histograms of LCW1157-1159, showing the number of colonies identified for each fluorescence signal region, as described in Example 12. The average fluorescence reading of the negative control (black arrow) and positive pSD0116 (white arrow) are marked in the figures. FIG. 82D-F provides the correlation between the fluorescence reading in the original test and the retest of the select clones.

[00116] FIG. 83 shows results of the SDS-PAGE analysis of the top 8 expression construct products and controls under unreduced conditions, as described in Example 12. The desired full length protein end product RP11-XTEN-GFP is indicated by an arrow, and the higher band is the dimer of the protein. Lanes: 1-8: top 8 expression constructs (expression level from high to low, based on fluorescence reading of the retests), 1. LCW1159.004, 2. LCW1159.006, 3. LCW1158.004, 4. LCW1157.040, 5. LCW1158.003, 6. LCW1157.039, 7. LCW1157.025, 8. LCW1157.038; C1-C3: Controls: C1. pSD0114, C2. pSD0116, C3. pCW1146 (Negative control).

[00117] FIG. 84 shows the SDS-PAGE evaluation of the MacroCap SP capture efficiency for the top 4 expression construct products under non-reducing conditions, as described in Example 12. Lanes 1-4: load, flow through, wash and elution of LCW1159.004, 2. Lanes 5-8: load, flow through, wash and elution of LCW1159.006. Lanes 9-12: load, flow through, wash and elution of LCW1158.004. 13-16: load, flow through, wash and elution of LCW1157.040. Lanes 17-20 1-4:

load, flow through, wash and elution of negative control. Unmarked lanes are molecular weight standards.

[00118] FIG. 85 shows the summary of library LCW1163 screening results with a comparison of the fluorescence signal of the top 4 expression products and the controls in the retests, as described in Example 12. Each sample had 4 replicates, represented by 4 individual dots in the figure.

[00119] FIG. 86 shows the summary of library LCW1160 screening results, as described in Example 12. Fluorescence histogram of LCW1157-1159, showing the number of colonies identified for each fluorescence signal region; average fluorescence reading of negative control (black arrow), pSD0116 (white arrow), and LCW1159.004 (high expression candidates from screening LCW1157-1159, grey arrow) were marked in the figures.

[00120] FIG. 87 shows 4-12% SDS-PAGE/silver staining analysis of MacroCap Q fractions as described in Example 14. FIG. 87A: Batch 2, lane 1: molecular weight standard; lanes 2-5: MacroCap Q flow through fractions 1-4, respectively; lanes 6-16: MacroCap Q elution fractions 1-11, respectively. FIG. 87B: Batch 1, lane 1: molecular weight standard; lanes 2-6: MacroCap Q flow through fractions 1-5, respectively; lanes 7-16: MacroCap Q elution fractions 1-10, respectively.

[00121] FIG. 88 shows results from the analyses of intermediates and final product during the preparation of 1xDBCO,3xLHRH-XTEN, as described in Example 34.

[00122] FIG. 89 shows results of analyses of reaction mixtures from the preparation of conjugates to 1xAzide,3xMMAE-XTEN analyzed by C18-RP-HPLC and mass spectroscopy, as described in Example 35. FIG. 89A is analysis of the initial 1xAmino,3xThiol-XTEN reactant. FIG. 89B is analysis of the protein modification with MMAE-Maleimide, showing the mass increase corresponding to modifications of three cysteines with MMAE-Mal. FIG. 89C shows the analysis of the protein modification with Azide-PEG4-NHS ester, with mass increases corresponding to the single addition of the azide-PEG4 moiety.

[00123] FIG. 90 shows analyses of the reaction products in conjugates of 3xLHRH,3xMMAE-XTEN as described in Example 36. FIG. 90A: SDS-PAGE analysis of the click conjugate. 0.5 µg of proteins were loaded per lane on 12% Bis-Tris NuPAGE mini gel (Life Technologies). The gel was stained with Pierce Silver Stain Kit (Thermo Scientific, cat. # 24612). Lane1, 1xAzide,3xMMAE-XTEN; lane 2, 1xDBCO,3xLHRH-XTEN; lane 3, products of click chemistry reaction. The conjugation product band is indicated by the arrow. FIG. 90B: C4 RP-HPLC analysis of the click conjugate reactants and products- (1) 1xDBCO,3xLHRH-XTEN; (2) 1xAzide,3xMMAE-XTEN; (3) products of click chemistry reaction.

[00124] FIG. 91 shows a flow chart of the reaction during preparation of conjugates of 1xLHRH,3xMMAE-XTEN, as described in Example 37. FIG. 91A: initial 1xAmino,3xThiol-

XTEN; FIG. 91B: protein modification with 2,2'-Dipyridyl disulfide; FIG. 91C: protein modification with DBCO-sulfo-NHS; FIG. 91D: deprotection of cysteines with TCEP; FIG. 91E: Modification of three cysteines with MMAE-Mal; FIG. 91F: Conjugation of LHRH-azide to N-terminal DBCO.

[00125] FIG. 92 shows a flow chart of the reaction during preparation of conjugates of 1xMal,3xPTX-XTEN reactant, as described in Example 41. FIG. 92A: Initial 1xAmino,3xThiol-XTEN; FIG. 92B: Protein modification with PTX-Mal; FIG. 92C: Protein modification with Sulfo-SMCC.

[00126] FIG. 93 shows results of analyses of reaction mixtures from the preparation of iodoacetyl-XTEN, as described in Example 42. FIG. 93A: 1xAmino-XTEN analyzed by C18-RP-HPLC before and after incubation with 10x excess of SIA.FIG. 93B: ESI-MS analysis of 1xAmino-XTEN modified with SIA. FIG. 93C: Samples analyzed by C18 RP-HPLC- Bottom profile – HCKFWW peptide. Medium profile – IA-XTEN. Upper profile – reaction of IA-XTEN with 5x excess of HCKFWW peptide.

[00127] FIG. 94 shows the results of screening libraries LCW1171, 1172, 1203, and 1204, as described in Example 14. FIG. 94A-D: Fluorescence histogram of LCW1171, 1172, 1203, 1204, showing the number of colonies identified for each fluorescence signal region; average fluorescence reading of negative control (black arrow) and pSD0116 (white arrow) when screening LCW1171-1172 were marked in the FIGS. 94A and B; average fluorescence reading of negative control (black arrow), pSD0116 (white arrow), and CBD control (grey arrow) when screening LCW1203-1204 are marked in FIGS. 94C and D.

[00128] FIG. 95 shows the results of screening libraries LCW1208-1210, as described in Example 12. FIGS. 95A-C: Fluorescence histograms of LCW1208-1210, showing the number of colonies identified for each fluorescence signal region; average fluorescence reading of negative control (black arrow) and CBD control (grey arrow) are marked in the figures.

[00129] FIG. 96 illustrated the production of XTEN segments from a precursor that contains three repeat copies of XTEN of identical length and sequence. In FIG. 96A, the XTEN precursor comprises three identical copies of XTEN that are flanked by identical protease cleavage sites. In FIG. 96B, the XTEN precursor further comprises N- and C- terminal affinity purification tags to facilitate purification of full-length precursor molecules. Following purification of the precursor it is cleaved by protease that acts on all the incorporated cleavage sequences to release the tags from the XTEN, which is followed by purification to separate the individual units of XTEN, facilitating the high-yield production of XTENs with short and intermediate lengths from long-chain precursor molecules.

[00130] FIG. 97 illustrates different embodiments of trimeric, branched XTEN-payload conjugates in which all conjugates shown can be prepared from the identical XTEN molecules

via conjugation to its N-terminal amino group and a functional group, such as the thiol of cysteine, that is located close to the C-terminus. FIG. 97A and B illustrates conjugates having a single payload molecule, with FIG. 97A using a 4-arm cross-linker with all the XTEN conjugated in close proximity to the payload, resulting in significant shielding of payload interactions with other molecules. FIG. 97B illustrates a configuration in where the payload is conjugated to a single XTEN arm that is branched at the distal end of the configuration, resulting in reduced payload shielding compared to the configuration of FIG. 97A. FIG. 97C illustrates a conjugate with two payloads that can result in increased avidity or increased potency. FIGS. 97D and E illustrates configurations with three identical payloads to further increase potency and/or avidity. FIG. 97F illustrates a configuration with one payload A and two identical copies of payload B for high-avidity binding or interactions. FIG. 97G illustrates a configuration with 3 different payloads enabling the inclusion of three different functions into a single XTEN conjugate.

[00131] FIG. 98 illustrates a scheme for synthesis of a conjugate between a branched XTEN and a single payload molecule. Initially, the thiol group in XTEN is blocked by reaction with iodoacetamide (alternatively, one can start the synthesis using XTEN which lacks a thiol group). Next, a DBCO group is added to the alpha-amino group of XTEN, then is reacted with a tetrafunctional cross linker that comprises one iodoacetyl group and three azide groups. The resulting XTEN is next reacted with a payload that carries a free thiol group resulting in the final XTEN-payload conjugate.

[00132] FIG. 99 illustrates a scheme for synthesis of a conjugate between a branched XTEN and a single payload molecule. An intermediate is produced by reacting XTEN with a trifunctional linker comprising two azide functions and an NHS function followed by the addition of payload A to the thiol group via maleimide chemistry (the order of these two steps can be inverted). A second intermediate is produce by reacting XTEN with a cysteine with iodoacetamide to block the free thiol group followed by addition of DBCO to the alpha-amino group via NHS activation (the order of these two steps can be inverted). Subsequently, the two intermediate molecules are conjugated using a click chemistry reaction, resulting in the final XTEN-payload conjugate.

[00133] FIG. 100 illustrates a scheme for synthesis of a conjugate having a branched XTEN and two identical payload molecules. An intermediate is produced by adding a DBCO group to the alpha-amino group of an XTEN via NHS chemistry. A second intermediate is produced by blocking the free thiol group of an XTEN with iodoacetamide followed by addition of a trifunctional cross-linker (2 N-maleimide groups and a carboxyl group that is activated by NHS) to the alpha amino-group (the order of these two steps can be inverted). The two intermediates are reacted resulting in the branched conjugate, and then two payload A molecules are added via click chemistry reaction resulting in the final product XTEN-payload conjugate.

[00134] FIG. 101 illustrates a scheme for synthesis of a conjugate having a branched XTEN and three identical payload molecules. An intermediate is produced by adding a DBCO group to the alpha-amino group of an XTEN via NHS chemistry. Another intermediate is produced by conjugating payload A to the thiol group of an XTEN via a N-maleimide functional group. The three molecules are linked together via a trifunctional cross-linker comprising three azide functions, resulting in the final XTEN-payload conjugate.

[00135] FIG. 102 illustrates a scheme for synthesis of a conjugate having a branched XTEN and three identical payload molecules. An intermediate is produced by adding a DBCO group to the thiol group of an XTEN A via N-maleimide chemistry. In the next step, payload A is conjugated to the alpha amino-group of the XTEN intermediate via NHS chemistry. Three molecules of the resulting XTEN are linked via a trifunctional cross-linker comprising three azide functions, resulting in the final XTEN-payload conjugate.

[00136] FIG. 103 illustrates a scheme for synthesis of a conjugate having a branched XTEN and two Payload A and one Payload B molecules per conjugate. An intermediate is produced by adding Payload A to the thiol group of an XTEN using an N-maleimide functional group, followed by the addition of a trifunctional cross linker (two azide groups and a carboxyl group that is activated by NHS) to the alpha amino-group (the order of these two steps can be inverted). A second intermediate is produced by adding DBCO to the alpha amino-group of an XTEN via NHS activation followed by the addition of Payload B to the free thiol group of the XTEN using an N-maleimide group (the order of these two steps can be inverted). Two molecules of the second intermediate are reacted with one molecule of the first intermediate to form the final XTEN-payload conjugate.

[00137] FIG. 104 illustrates a scheme for synthesis of a conjugate having a branched XTEN and three different payloads. An intermediate is produced by adding Payload A to the thiol group on an XTEN using an N-maleimide functional group followed by the addition of a trifunctional cross linker (one azide group, one N-maleimide group and one carboxyl group that is activated by NHS) to the alpha amino-group (the order of these two steps can be inverted). A second intermediate is produced by adding Payload B to the alpha amino-group of XTEN via NHS chemistry. A third intermediate is produced by adding DBCO to the alpha amino-group of an XTEN via NHS activation followed by the addition of payload C to the free thiol group of the XTEN using an N-maleimide group (the order of these two steps can be inverted). The three intermediates are reacted with each other to form the final XTEN-payload conjugate.

[00138] FIG. 105 illustrates a scheme for synthesis of a conjugate having a dimeric or tetrameric branched XTEN and Payload A molecules. An intermediate is produced by adding DBCO to the thiol group of an XTEN using N-maleimide functional group followed by the addition Payload A to the amino group of the XTEN using NHS (the order of these two steps can be inverted).

Subsequently the intermediate is multimerized by addition of azide cross-linkers. Use of a divalent cross-linker yields the dimeric configuration, and a tetravalent cross-linker yields the tetrameric configuration of the final product.

[00139] FIG. 106 illustrates a scheme for synthesis of a conjugate having a branched XTEN and three different payloads. An intermediate is produced by adding Payload A to the thiol group of an XTEN using N-maleimide functional group, followed by the addition of a trifunctional cross linker (one azide group, one N-maleimide group and one carboxyl group that is activated by NHS) to the alpha amino-group (the order of these two steps can be inverted). A second intermediate is produced by adding Payload B to the free thiol group of an XTEN via an N-maleimide functional group. A third intermediate is produced by adding DBCO to the alpha amino-group of an XTEN via NHS activation followed by the addition of Payload C to the free thiol group using a N-maleimide group (the order of these two steps can be inverted). The three intermediates are reacted with each other to form the final XTEN-payload conjugate.

[00140] FIG. 107 shows results of analyses of reaction mixtures from the preparation of conjugates to 1xDBCO,3xFA(γ)-XTEN analyzed by C18-RP-HPLC and mass spectroscopy, as described in Example 38. FIG. 107A is analysis of the initial 1xAmino,3xThiol-XTEN reactant. FIG. 107B is analysis of the protein modification with Folate-gamma-Maleimide, showing the mass increase corresponding to modifications of three cysteines with FA(γ)-Mal. FIG. 107C shows the analysis of the protein modification with DBCO-sulfo-NHS ester, with mass increases corresponding to the single addition of the DBCO moiety.

[00141] FIG. 108 shows C4 RP-HPLC analyses of the click conjugate reactants and product 3xFA(γ),3xMMAE-XTEN, as described in Example 39. (1) 1xDBCO,3xFA(γ)-XTEN; (2) 1xAzide,3xMMAE-XTEN; (3) products of click chemistry reaction.

[00142] FIG. 109 shows analyses of final 3xFA(γ),3xMMAE-XTEN product purified by preparative RP-HPLC, as described in Example 39. FIG. 109A shows size exclusion chromatography analysis (Phenomenex BioSep-SEC-s4000 600 x 7.80mm column, 50mM Sodium Phosphate pH 6.5, 300mM NaCl buffer, flow rate 0.5ml/min, isocratic elution 70min). FIG. 109B shows RP-HPLC analysis (Phenomenex Jupiter C18 5μM 300Å 150 x 4.60mm column, Buffer A: 0.1% TFA in H2O, Buffer B: 0.1% TFA in CAN, flow rate 1ml/min, gradient 5% to 50%B in 45min). FIG. 3C shows ESI-MS analysis (QSTAR-XL, calculated MW 85,085.4 Da, experimental MW 85,091 Da).

[00143] FIG. 110 shows the results of GPCR Ca^{2+} mobilization activity of recombinant GLP2-2G-XTEN (filled squares) and conjugate GLP2-2G-XTEN (filled circles), performed as described in Example 62.

[00144] FIG. 111 shows the results of an in vitro human plasma stability of recombinant GLP2-2G-XTEN (filled squares) and conjugate GLP2-2G-XTEN (filled triangles) at various time points at 37°C, performed as described in Example 63.

[00145] FIG. 112 shows the results of the pharmacokinetic profile of recombinant GLP2-2G-XTEN (filled squares) and conjugate GLP2-2G-XTEN (filled triangles) in rats, performed as described in Example 64.

[00146] FIG. 113. FIG. 113A shows the SEC-HPLC analysis of the reaction products between Tris-[2-maleimidoethyl]amine and 1xAmino,1xThiol-XTEN432: FIG. 113A- conjugation mixture: peak 1 – trimeric XTEN, peak 2 – dimeric XTEN, peak 3 – unreacted monomeric XTEN; FIG. 113B- linear XTEN_1296 control; FIG. 113C- linear XTEN_864 control; FIG. 113D- linear XTEN_432 control.

[00147] FIG. 114. FIG. 114A shows the C18 RP-HPLC analysis of DBCO-sulfo-NHS conjugation to 1xAmino-XTEN_288, as described in Example 65. Unreacted XTEN eluted at 19 min. 1xDBCO-XTEN_288 eluted at 27 min. DBCO-sulfo-NHS reagent and product of its hydrolysis eluted at 41.5 min and 38.5 min, respectively. FIG. 114B shows C18 RP-HPLC analysis of Azido-PEG4-NHS ester conjugation to Tris(2-aminoethyl)amine. 3xAzide-PEG4-TAEA was identified by MALDI-TOF MS and ESI-MS as a product with MW of 966 Da.

[00148] FIG. 115 shows the SEC-HPLC analysis, as described in Example 66, of the reaction products between 3xAzide-PEG4-TAEA and 1xDBCO-XTEN_288: (trace A) conjugation mixture: peak 1 – trimeric XTEN, peak 2 – dimeric XTEN, peak 3 – unreacted monomeric XTEN, peak 4 – low molecular weight compounds; (trace B) linear XTEN_864 control; (trace C) linear XTEN576 control; (trace D) linear XTEN_288 control.

[00149] FIG. 116 shows results of a killing assay demonstrating selective cytotoxicity of 3xFA(γ),3xMMAE-XTEN on KB cells, as described in Example 69. The inhibitory dose response curves are shown for the groups of free MMAE (filled circles); 3xMMAE-XTEN (filled, inverted triangles) and 3xFA(γ),3xMMAE-XTEN in the presence (filled triangles) and absence (filled squares) of folic acid competitor on KB cells.

[00150] FIG. 117 shows the structure of the XTEN-payload conjugate 3xFA(γ),3xMMAE-XTEN. FIG. 117A shows the two XTEN linked by the reaction of the azide 1-azido-3,6,9,12-tetraoxapentadecan-15-oic acid, N-hydroxysuccinimide ester and the alkyne 6-(11,12-didehydrodibenzo[b,f]azocin-5(6H)-yl)-6-oxohexanoic acid, N-hydroxysuccinimide (or N-hydroxysulfosuccinimide) ester. FIG. 117B shows the X residue of Cys modified with folate-γ-aminopentyl-maleimide. FIG. 117C shows the Z residue of Cys modified with maleimidocaproyl-valine-citrulline-*p*-aminobenzyloxycarbonyl-monomethylauristatin E.

DETAILED DESCRIPTION OF THE INVENTION

[00151] Before the embodiments of the invention are described, it is to be understood that such embodiments are provided by way of example only, and that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention.

[00152] Unless otherwise defined, 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 methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention.

DEFINITIONS

[00153] In the context of the present application, the following terms have the meanings ascribed to them unless specified otherwise:

[00154] As used throughout the specification and claims, the terms "a", "an" and "the" are used in the sense that they mean "at least one", "at least a first", "one or more" or "a plurality" of the referenced components or steps, except in instances wherein an upper limit is thereafter specifically stated. Therefore, a "payload", as used herein, means "at least a first payload" but includes a plurality of payloads. The operable limits and parameters of combinations, as with the amounts of any single agent, will be known to those of ordinary skill in the art in light of the present disclosure.

[00155] The terms "polypeptide", "peptide", and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified, for example, by disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation, such as conjugation with a labeling component.

[00156] As used herein, the term "amino acid" refers to either natural and/or unnatural or synthetic amino acids, including but not limited to both the D or L optical isomers, and amino acid analogs and peptidomimetics. Standard single or three letter codes are used to designate amino acids.

[00157] A "pharmacologically active" agent includes any drug, compound, composition of matter or mixture desired to be delivered to a subject, e.g. therapeutic agents, diagnostic agents, or drug delivery agents, which provides or is expected to provide some pharmacologic, often beneficial, effect that can be demonstrated in vivo or in vitro. Such agents may include peptides, proteins, carbohydrates, nucleic acids, nucleosides, oligonucleotides, and small molecule synthetic compounds, or analogs thereof.

[00158] The term "natural L-amino acid" means the L optical isomer forms of glycine (G), proline (P), alanine (A), valine (V), leucine (L), isoleucine (I), methionine (M), cysteine (C), phenylalanine (F), tyrosine (Y), tryptophan (W), histidine (H), lysine (K), arginine (R), glutamine (Q), asparagine (N), glutamic acid (E), aspartic acid (D), serine (S), and threonine (T).

[00159] The term "non-naturally occurring," as applied to sequences and as used herein, means polypeptide or polynucleotide sequences that do not have a counterpart to, are not complementary to, or do not have a high degree of homology with a wild-type or naturally-occurring sequence found in a mammal. For example, a non-naturally occurring polypeptide or fragment may share no more than 99%, 98%, 95%, 90%, 80%, 70%, 60%, 50% or even less amino acid sequence identity as compared to a natural sequence when suitably aligned.

[00160] The terms "hydrophilic" and "hydrophobic" refer to the degree of affinity that a substance has with water. A hydrophilic substance has a strong affinity for water, tending to dissolve in, mix with, or be wetted by water, while a hydrophobic substance substantially lacks affinity for water, tending to repel and not absorb water and tending not to dissolve in or mix with or be wetted by water. Amino acids can be characterized based on their hydrophobicity. A number of scales have been developed. An example is a scale developed by Levitt, M, et al., J Mol Biol (1976) 104:59, which is listed in Hopp, TP, et al., Proc Natl Acad Sci U S A (1981) 78:3824. Examples of "hydrophilic amino acids" are arginine, lysine, threonine, alanine, asparagine, and glutamine. Of particular interest are the hydrophilic amino acids aspartate, glutamate, and serine, and glycine. Examples of "hydrophobic amino acids" are tryptophan, tyrosine, phenylalanine, methionine, leucine, isoleucine, and valine.

[00161] A "fragment" when applied to a biologically active protein, is a truncated form of a the biologically active protein that retains at least a portion of the therapeutic and/or biological activity. A "variant," when applied to a biologically active protein is a protein with sequence homology to the native biologically active protein that retains at least a portion of the therapeutic and/or biological activity of the biologically active protein. For example, a variant protein may share at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity compared with the reference biologically active protein. As used herein, the term "biologically active protein variant" includes proteins modified deliberately, as for example, by

site directed mutagenesis, synthesis of the encoding gene, insertions, or accidentally through mutations and that retain activity.

[00162] The term "sequence variant" means polypeptides that have been modified compared to their native or original sequence by one or more amino acid insertions, deletions, or substitutions. Insertions may be located at either or both termini of the protein, and/or may be positioned within internal regions of the amino acid sequence. A non-limiting example is insertion of an XTEN sequence within the sequence of the biologically-active payload protein. Another non-limiting example is substitution of an amino acid in an XTEN with a different amino acid. In deletion variants, one or more amino acid residues in a polypeptide as described herein are removed. Deletion variants, therefore, include all fragments of a payload polypeptide sequence. In substitution variants, one or more amino acid residues of a polypeptide are removed and replaced with alternative residues. In one aspect, the substitutions are conservative in nature and conservative substitutions of this type are well known in the art.

[00163] The term "moiety" means a component of a larger composition or that is intended to be incorporated into a larger composition, such as a functional group of a drug molecule or a targeting peptide joined to a larger polypeptide.

[00164] As used herein, "terminal XTEN" refers to XTEN sequences that have been fused to or in the N- or C-terminus of the payload when the payload is a peptide or polypeptide.

[00165] The term "XTEN release site" refers to a cleavage sequence in XTEN-payload that can be recognized and cleaved by a protease, effecting release of an XTEN or a portion of an XTEN from the XTEN-payload polypeptide. As used herein, "mammalian protease" means a protease that normally exists in the body fluids, cells or tissues of a mammal. XTEN release sites can be engineered to be cleaved by various mammalian proteases (a.k.a. "XTEN release proteases") such as trypsin, FXIa, FXIIa, kallikrein, FVIIIa, FVIIIa, FXa, FIIa (thrombin), Elastase-2, MMP-12, MMP13, MMP-17, MMP-20, or any protease that is present in a subject. Other equivalent proteases (endogenous or exogenous) that are capable of recognizing a defined cleavage site can be utilized. The cleavage sites can be adjusted and tailored to the protease utilized.

[00166] The term "within", when referring to a first polypeptide being linked to a second polypeptide, encompasses linking that connects the N-terminus of the first or second polypeptide to the C-terminus of the second or first polypeptide, respectively, as well as insertion of the first polypeptide into the sequence of the second polypeptide. For example, when an XTEN is linked "within" a payload polypeptide, the XTEN may be linked to the N-terminus, the C-terminus, or may be inserted between any two amino acids of the payload polypeptide.

[00167] "Activity" as applied to form(s) of a XTEN-payload composition provided herein, refers to an action or effect, including but not limited to receptor binding, antagonist activity,

agonist activity, a cellular or physiologic response, or an effect generally known in the art for the payload, whether measured by an *in vitro*, *ex vivo* or *in vivo* assay or a clinical effect.

[00168] As used herein, the term "ELISA" refers to an enzyme-linked immunosorbent assay as described herein or as otherwise known in the art.

[00169] A "host cell" includes an individual cell or cell culture which can be or has been a recipient for the subject vectors such as those described herein. Host cells include progeny of a single host cell. The progeny may not necessarily be completely identical (in morphology or in genomic of total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. A host cell includes cells transfected in vivo with a vector of this invention.

[00170] "Isolated" when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. As is apparent to those of skill in the art, a non-naturally occurring polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, does not require "isolation" to distinguish it from its naturally occurring counterpart. In addition, a "concentrated", "separated" or "diluted" polynucleotide, peptide, polypeptide, protein, antibody, or fragments thereof, is distinguishable from its naturally occurring counterpart in that the concentration or number of molecules per volume is generally greater than that of its naturally occurring counterpart. In general, a polypeptide made by recombinant means and expressed in a host cell is considered to be "isolated."

[00171] An "isolated" nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. For example, an isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal or extra-chromosomal location different from that of natural cells.

[00172] A "chimeric" protein contains at least one fusion polypeptide comprising at least one region in a different position in the sequence than that which occurs in nature. The regions may normally exist in separate proteins and are brought together in the fusion polypeptide; or they may normally exist in the same protein but are placed in a new arrangement in the fusion polypeptide. A chimeric protein may be created, for example, by chemical synthesis, or by

creating and translating a polynucleotide in which the peptide regions are encoded in the desired relationship.

[00173] "Fused," and "fusion" are used interchangeably herein, and refers to the joining together of two or more peptide or polypeptide sequences by recombinant means.

[00174] "Operably linked" means that the DNA sequences being linked are contiguous, and in reading phase or in-frame. An "in-frame fusion" refers to the joining of two or more open reading frames (ORFs) to form a continuous longer ORF, in a manner that maintains the correct reading frame of the original ORFs. For example, a promoter or enhancer is operably linked to a coding sequence for a polypeptide if it affects the transcription of the polypeptide sequence. Thus, the resulting recombinant fusion protein is a single protein containing two or more segments that correspond to polypeptides encoded by the original ORFs (which segments are not normally so joined in nature).

[00175] "Crosslinking," "conjugating," "link," "linking" and "joined to" are used interchangeably herein, and refer to the covalent joining of two different molecules by a chemical reaction. The crosslinking can occur in one or more chemical reactions, as described more fully, below.

[00176] The term "conjugation partner" as used herein, refers to the individual components that can be linked or are linked in a conjugation reaction.

[00177] The term "conjugate" is intended to refer to the heterogeneous molecule formed as a result of covalent linking of conjugation partners one to another, e.g., a biologically active payload covalently linked to a XTEN molecule or a cross-linker covalently linked to a reactive XTEN.

[00178] "Cross-linker" and "linker" and "cross-linking agent" are used interchangably and in their broadest context to mean a chemical entity used to covalently join two or more entities. For example, a cross-linker joins two, three, four or more XTEN, or joins a payload to an XTEN, as the entities are defined herein. A cross-linker includes, but is not limited to, the reaction product of small molecule zero-length, homo- or hetero-bifunctional, and multifunctional cross-linker compounds, the reaction product of two click-chemstry reactants. It will be understood by one of skill in the art that a cross-linker can refer to the covalently-bound reaction product remaining after the crosslinking of the reactants. The cross-linker can also comprise one or more reactants which have not yet reacted but which are capable to react with another entity.

[00179] In the context of polypeptides, a "linear sequence" or a "sequence" is an order of amino acids in a polypeptide in an amino to carboxyl terminus direction in which residues that neighbor each other in the sequence are contiguous in the primary structure of the polypeptide. A "partial sequence" is a linear sequence of part of a polypeptide that is known to comprise additional residues in one or both directions.

[00180] "Heterologous" means derived from a genotypically distinct entity from the rest of the entity to which it is being compared. For example, a glycine rich sequence removed from its native coding sequence and operatively linked to a coding sequence other than the native sequence is a heterologous glycine rich sequence. The term "heterologous" as applied to a polynucleotide, a polypeptide, means that the polynucleotide or polypeptide is derived from a genotypically distinct entity from that of the rest of the entity to which it is being compared.

[00181] The terms "polynucleotides", "nucleic acids", "nucleotides" and "oligonucleotides" are used interchangeably. They refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

[00182] The term "complement of a polynucleotide" denotes a polynucleotide molecule having a complementary base sequence and reverse orientation as compared to a reference sequence, such that it could hybridize with a reference sequence with complete fidelity.

[00183] "Recombinant" as applied to a polynucleotide means that the polynucleotide is the product of various combinations of recombination steps which may include cloning, restriction and/or ligation steps, and other procedures that result in expression of a recombinant protein in a host cell.

[00184] The terms "gene" and "gene fragment" are used interchangeably herein. They refer to a polynucleotide containing at least one open reading frame that is capable of encoding a particular protein after being transcribed and translated. A gene or gene fragment may be genomic or cDNA, as long as the polynucleotide contains at least one open reading frame, which may cover the entire coding region or a segment thereof. A "fusion gene" is a gene composed of at least two heterologous polynucleotides that are linked together.

[00185] "Homology" or "homologous" or "sequence identity" refers to sequence similarity or interchangeability between two or more polynucleotide sequences or between two or more polypeptide sequences. When using a program such as BestFit to determine sequence identity, similarity or homology between two different amino acid sequences, the default settings may be

used, or an appropriate scoring matrix, such as blosum45 or blosum80, may be selected to optimize identity, similarity or homology scores. Preferably, polynucleotides that are homologous are those which hybridize under stringent conditions as defined herein and have at least 70%, preferably at least 80%, more preferably at least 90%, more preferably 95%, more preferably 97%, more preferably 98%, and even more preferably 99% sequence identity compared to those sequences. Polypeptides that are homologous preferably have sequence identities that are at least 70%, preferably at least 80%, even more preferably at least 90%, even more preferably at least 95-99% identical.

[00186] "Ligation" as applied to polynucleic acidss refers to the process of forming phosphodiester bonds between two nucleic acid fragments or genes, linking them together. To ligate the DNA fragments or genes together, the ends of the DNA must be compatible with each other. In some cases, the ends will be directly compatible after endonuclease digestion. However, it may be necessary to first convert the staggered ends commonly produced after endonuclease digestion to blunt ends to make them compatible for ligation.

[00187] The terms "stringent conditions" or "stringent hybridization conditions" includes reference to conditions under which a polynucleotide will hybridize to its target sequence, to a detectably greater degree than other sequences (e.g., at least 2-fold over background). Generally, stringency of hybridization is expressed, in part, with reference to the temperature and salt concentration under which the wash step is carried out. Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short polynucleotides (e.g., 10 to 50 nucleotides) and at least about 60°C for long polynucleotides (e.g., greater than 50 nucleotides)—for example, "stringent conditions" can include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and three washes for 15 min each in 0.1×SSC/1% SDS at 60°C to 65°C. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2×SSC, with SDS being present at about 0.1%. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating Tm and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. *et al.*, "Molecular Cloning: A Laboratory Manual," 3rd edition, Cold Spring Harbor Laboratory Press, 2001. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 μg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be

used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art.

[00188] The terms "percent identity," percentage of sequence identity," and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences. Percent identity may be measured over the length of an entire defined polynucleotide sequence, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polynucleotide sequence, for instance, a fragment of at least 45, at least 60, at least 90, at least 120, at least 150, at least 210 or at least 450 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured. The percentage of sequence identity is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of matched positions (at which identical residues occur in both polypeptide sequences), dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. When sequences of different length are to be compared, the shortest sequence defines the length of the window of comparison. Conservative substitutions are not considered when calculating sequence identity.

[00189] "Percent (%) sequence identity," with respect to the polypeptide sequences identified herein, is defined as the percentage of amino acid residues in a query sequence that are identical with the amino acid residues of a second, reference polypeptide sequence or a portion thereof, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity, thereby resulting in optimal alignment. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve optimal alignment over the full length of the sequences being compared. Percent identity may be measured over the length of an entire defined polypeptide sequence, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment

length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

[00190] "Repetitiveness" used in the context of polynucleotide sequences refers to the degree of internal homology in the sequence such as, for example, the frequency of identical nucleotide sequences of a given length. Repetitiveness can, for example, be measured by analyzing the frequency of identical sequences.

[00191] A "vector" is a nucleic acid molecule, preferably self-replicating in an appropriate host, which transfers an inserted nucleic acid molecule into and/or between host cells. The term includes vectors that function primarily for insertion of DNA or RNA into a cell, replication of vectors that function primarily for the replication of DNA or RNA, and expression vectors that function for transcription and/or translation of the DNA or RNA. Also included are vectors that provide more than one of the above functions. An "expression vector" is a polynucleotide which, when introduced into an appropriate host cell, can be transcribed and translated into a polypeptide(s). An "expression system" usually connotes a suitable host cell comprised of an expression vector that can function to yield a desired expression product.

[00192] "Serum degradation resistance," as applied to a polypeptide, refers to the ability of the polypeptides to withstand degradation in blood or components thereof, which typically involves proteases in the serum or plasma. The serum degradation resistance can be measured by combining the protein with human (or mouse, rat, monkey, as appropriate) serum or plasma, typically for a range of days (e.g. 0.25, 0.5, 1, 2, 4, 8, 16 days), typically at about 37°C. The samples for these time points can be run on a Western blot assay and the protein is detected with an antibody. The antibody can be to a tag in the protein. If the protein shows a single band on the western, where the protein's size is identical to that of the injected protein, then no degradation has occurred. In this exemplary method, the time point where 50% of the protein is degraded, as judged by Western blots or equivalent techniques, is the serum degradation half-life or "serum half-life" of the protein.

[00193] The terms "$t_{1/2}$", "half-life", "terminal half-life", "elimination half-life" and "circulating half-life" are used interchangeably herein and, as used herein means the terminal half-life calculated as $\ln(2)/K_{el}$. K_{el} is the terminal elimination rate constant calculated by linear regression of the terminal linear portion of the log concentration vs. time curve. Half-life typically refers to the time required for half the quantity of an administered substance deposited in a living organism to be metabolized or eliminated by normal biological processes.

[00194] "Active clearance" means the mechanisms by which a protein is removed from the circulation other than by filtration, and which includes removal from the circulation mediated by cells, receptors, metabolism, or degradation of the protein.

[00195] "Apparent molecular weight factor" and "apparent molecular weight" are related terms referring to a measure of the relative increase or decrease in apparent molecular weight exhibited by a particular amino acid or polypeptide sequence. The apparent molecular weight is determined using size exclusion chromatography (SEC) or similar methods by comparing to globular protein standards, and is measured in "apparent kD" units. The apparent molecular weight factor is the ratio between the apparent molecular weight and the actual molecular weight; the latter predicted by adding, based on amino acid composition, the calculated molecular weight of each type of amino acid in the composition or by estimation from comparison to molecular weight standards in an SDS electrophoresis gel. Determination of both the apparent molecular weight and apparent molecular weight factor for representative proteins is described in the Examples.

[00196] The terms "hydrodynamic radius" or "Stokes radius" is the effective radius (R_h in nm) of a molecule in a solution measured by assuming that it is a body moving through the solution and resisted by the solution's viscosity. In the embodiments of the invention, the hydrodynamic radius measurements of the XTEN polypeptides correlate with the "apparent molecular weight factor" which is a more intuitive measure. The "hydrodynamic radius" of a protein affects its rate of diffusion in aqueous solution as well as its ability to migrate in gels of macromolecules. The hydrodynamic radius of a protein is determined by its molecular weight as well as by its structure, including shape and compactness. Methods for determining the hydrodynamic radius are well known in the art, such as by the use of size exclusion chromatography (SEC), as described in U.S. Patent Nos. 6,406,632 and 7,294,513. Most proteins have globular structure, which is the most compact three-dimensional structure a protein can have with the smallest hydrodynamic radius. Some proteins adopt a random and open, unstructured, or 'linear' conformation and as a result have a much larger hydrodynamic radius compared to typical globular proteins of similar molecular weight.

[00197] "Physiological conditions" refers to a set of conditions in a living host as well as *in vitro* conditions, including temperature, salt concentration, pH, that mimic those conditions of a living subject. A host of physiologically relevant conditions for use in *in vitro* assays have been established. Generally, a physiological buffer contains a physiological concentration of salt and is adjusted to a neutral pH ranging from about 6.5 to about 7.8, and preferably from about 7.0 to about 7.5. A variety of physiological buffers are listed in Sambrook et al. (2001). Physiologically relevant temperature ranges from about 25^0C to about 38^0C, and preferably from about 35^0C to about 37^0C.

[00198] A "single atom residue of a payload" means the atom of a payload that is chemically linked to XTEN after reaction with the subject XTEN or XTEN-linker compositions; typically a sulfur, an oxygen, a nitrogen, or a carbon atom. For example, an atom residue of a payload could

be a sulfur residue of a cysteine thiol reactive group in a payload, a nitrogen molecule of an amino reactive group of a peptide or polypeptide or small molecule payload, a carbon or oxygen residue or a reactive carboxyl or aldehyde group of a peptide, protein or a small molecule or synthetic, organic drug.

[00199] A "reactive group" is a chemical structure that can be coupled to a second reactive group. Examples of reactive groups are amino groups, carboxyl groups, sulfhydryl groups, hydroxyl groups, aldehyde groups, azide groups. Some reactive groups can be activated to facilitate conjugation with a second reactive group, either directly or through a cross-linker. As used herein, a reactive group can be a part of an XTEN, a cross-linker, an azide/alkyne click-chemistry reactant, or a payload so long as it has the ability to participate in a chemical reaction. Once reacted, a conjugation bond links the residues of the payload or cross-linker or XTEN reactants.

[00200] "Controlled release agent", "slow release agent", "depot formulation" and "sustained release agent" are used interchangeably to refer to an agent capable of extending the duration of release of a polypeptide of the invention relative to the duration of release when the polypeptide is administered in the absence of agent. Different embodiments of the present invention may have different release rates, resulting in different therapeutic amounts.

[00201] The term "payload" as used herein refers to any protein, peptide sequence, small molecule, drug or composition of matter that has a biological, pharmacological or therapeutic activity or beneficial effect when administered in a subject or that can be demonstrated *in vitro*. Payload also includes a molecule that can be used for imaging or *in vivo* diagnostic purposes. Examples of payloads include, but are not limited to, cytokines, enzymes, hormones, blood coagulation factors, and growth factors, chemotherapeutic agents, antiviral compounds, toxins, anti-cancer drugs, radioactive compounds, and contrast agents, as well as targeting peptides, proteins, antibodies, antibody fragments, or compounds used to bind to receptors or ligands.

[00202] The terms "antigen", "target antigen" and "immunogen" are used interchangeably herein to refer to the structure or binding determinant that an antibody fragment or an antibody fragment-based therapeutic binds to or has specificity against.

[00203] The term "antagonist", as used herein, includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native polypeptide disclosed herein. Methods for identifying antagonists of a polypeptide may comprise contacting a native polypeptide with a candidate antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the native polypeptide. In the context of the present invention, antagonists may include proteins, nucleic acids, carbohydrates, antibodies or any other molecules that decrease the effect of a biologically active protein.

[00204] A "defined medium" refers to a medium comprising nutritional and hormonal requirements necessary for the survival and/or growth of the cells in culture such that the components of the medium are known. Traditionally, the defined medium has been formulated by the addition of nutritional and growth factors necessary for growth and/or survival. Typically, the defined medium provides at least one component from one or more of the following categories: a) all essential amino acids, and usually the basic set of twenty amino acids plus cysteine; b) an energy source, usually in the form of a carbohydrate such as glucose; c) vitamins and/or other organic compounds required at low concentrations; d) free fatty acids; and e) trace elements, where trace elements are defined as inorganic compounds or naturally occurring elements that are typically required at very low concentrations, usually in the micromolar range. The defined medium may also optionally be supplemented with one or more components from any of the following categories: a) one or more mitogenic agents; b) salts and buffers as, for example, calcium, magnesium, and phosphate; c) nucleosides and bases such as, for example, adenosine and thymidine, hypoxanthine; and d) protein and tissue hydrolysates.

[00205] The term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native polypeptide disclosed herein. Suitable agonist molecules specifically include agonist antibodies or antibody fragments, fragments or amino acid sequence variants of native polypeptides, peptides, small organic molecules, etc. Methods for identifying agonists of a native polypeptide may comprise contacting a native polypeptide with a candidate agonist molecule and measuring a detectable change in one or more biological activities normally associated with the native polypeptide.

[00206] "Inhibition constant", or "Ki", are used interchangeably and mean the dissociation constant of the enzyme-inhibitor complex, or the reciprocal of the binding affinity of the inhibitor to the enzyme.

[00207] As used herein, "treat" or "treating," or "palliating" or "ameliorating" are used interchangeably and mean administering a drug or a biologic to achieve a therapeutic benefit, to cure or reduce the severity of an existing condition, or to achieve a prophylactic benefit, prevent or reduce the likelihood of onset or severity the occurrence of a condition. By therapeutic benefit is meant eradication or amelioration of the underlying condition being treated or one or more of the physiological symptoms associated with the underlying condition such that an improvement is observed in the subject, notwithstanding that the subject may still be afflicted with the underlying condition.

[00208] A "therapeutic effect" or "therapeutic benefit," as used herein, refers to a physiologic effect, including but not limited to the mitigation, amelioration, or prevention of disease in humans or other animals, or to otherwise enhance physical or mental wellbeing of humans or animals, resulting from administration of a polypeptide of the invention other than the ability to

induce the production of an antibody against an antigenic epitope possessed by the biologically active protein. For prophylactic benefit, the compositions may be administered to a subject at risk of developing a particular disease, condition or symptom of the disease (e.g., a bleed in a diagnosed hemophilia A subject), or to a subject reporting one or more of the physiological symptoms of a disease, even though a diagnosis of this disease may not have been made.

[00209] The terms "therapeutically effective amount" and "therapeutically effective dose", as used herein, refer to an amount of a drug or a biologically active protein, either alone or as a part of a polypeptide composition, that is capable of having any detectable, beneficial effect on any symptom, aspect, measured parameter or characteristics of a disease state or condition when administered in one or repeated doses to a subject. Such effect need not be absolute to be beneficial. Determination of a therapeutically effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

[00210] The term "therapeutically effective dose regimen", as used herein, refers to a schedule for consecutively administered multiple doses (i.e., at least two or more) of a biologically active protein, either alone or as a part of a polypeptide composition, wherein the doses are given in therapeutically effective amounts to result in sustained beneficial effect on any symptom, aspect, measured parameter or characteristics of a disease state or condition.

I). GENERAL TECHNIQUES

[00211] The practice of the present invention employs, unless otherwise indicated, conventional techniques of immunology, biochemistry, chemistry, molecular biology, microbiology, cell biology, genomics and recombinant DNA, which are within the skill of the art. *See* Sambrook, J. *et al.*, "Molecular Cloning: A Laboratory Manual," 3rd edition, Cold Spring Harbor Laboratory Press, 2001; "Current protocols in molecular biology", F. M. Ausubel, *et al.* eds.,1987; the series "Methods in Enzymology," Academic Press, San Diego, CA.; "PCR 2: a practical approach", M.J. MacPherson, B.D. Hames and G.R. Taylor eds., Oxford University Press, 1995; "Antibodies, a laboratory manual" Harlow, E. and Lane, D. eds., Cold Spring Harbor Laboratory,1988; "Goodman & Gilman's The Pharmacological Basis of Therapeutics," 11th Edition, McGraw-Hill, 2005; and Freshney, R.I., "Culture of Animal Cells: A Manual of Basic Technique," 4th edition, John Wiley & Sons, Somerset, NJ, 2000, the contents of which are incorporated in their entirety herein by reference.

[00212] Host cells can be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium (MEM, Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium (DMEM, Sigma) are suitable for culturing eukaryotic cells. In addition, animal cells can be grown in a defined medium that lacks serum but is supplemented with hormones, growth factors or any other factors necessary for the survival and/or growth of a particular cell type. Whereas a defined medium supporting cell survival

maintains the viability, morphology, capacity to metabolize and potentially, capacity of the cell to differentiate, a defined medium promoting cell growth provides all chemicals necessary for cell proliferation or multiplication. The general parameters governing mammalian cell survival and growth in vitro are well established in the art. Physicochemical parameters which may be controlled in different cell culture systems are, e.g., pH, pO_2, temperature, and osmolarity. The nutritional requirements of cells are usually provided in standard media formulations developed to provide an optimal environment. Nutrients can be divided into several categories: amino acids and their derivatives, carbohydrates, sugars, fatty acids, complex lipids, nucleic acid derivatives and vitamins. Apart from nutrients for maintaining cell metabolism, most cells also require one or more hormones from at least one of the following groups: steroids, prostaglandins, growth factors, pituitary hormones, and peptide hormones to proliferate in serum-free media (Sato, G. H., et al. in "Growth of Cells in Hormonally Defined Media", Cold Spring Harbor Press, N.Y., 1982). In addition to hormones, cells may require transport proteins such as transferrin (plasma iron transport protein), ceruloplasmin (a copper transport protein), and high-density lipoprotein (a lipid carrier) for survival and growth in vitro. The set of optimal hormones or transport proteins will vary for each cell type. Most of these hormones or transport proteins have been added exogenously or, in a rare case, a mutant cell line has been found which does not require a particular factor. Those skilled in the art will know of other factors required for maintaining a cell culture without undue experimentation.

[00213] Growth media for growth of prokaryotic host cells include nutrient broths (liquid nutrient medium) or LB medium (Luria Bertani). Suitable media include defined and undefined media. In general, media contains a carbon source such as glucose needed for bacterial growth, water, and salts. Media may also include a source of amino acids and nitrogen, for example beef or yeast extract (in an undefined medium) or known quantities of amino acids (in a defined medium). In some embodiments, the growth medium is LB broth, for example LB Miller broth or LB Lennox broth. LB broth comprises peptone (enzymatic digestion product of casein), yeast extract and sodium chloride. In some embodiments, a selective medium is used which comprises an antibiotic. In this medium, only the desired cells possessing resistance to the antibiotic will grow.

II). XTEN PROTEIN POLYMER AND CONJUGATE COMPOSITIONS

[00214] The present invention relates, in part, to substantially homogeneous compositions comprising extended recombinant polypeptides (XTEN). In a first aspect, the invention provides XTEN compositions that are substantially homogeneous in length. Such compositions are useful as reagent conjugation partners to create XTEN-cross-linker intermediates and XTEN-payload compositions. Additionally, it is an object of the present invention to provide methods to create

the substantially homogeneous XTEN compositions. The present invention also provides methods to create such substantially homogeneous XTEN compositions at high yield.

[00215] In a second aspect, the invention provides XTEN. For example, the XTENs capable of linking to one or more payload conjugation partners, resulting in payload-XTEN conjugates are specifically engineered to incorporate defined numbers of reactive amino acids for linking to the payloads either directly or via cross-linkers or azide/alkyne reactants. The present invention also provides methods to create such engineered XTEN polymers for use in creating conjugates with payload agents of interest as compositions with enhanced pharmaceutical properties, including enhanced pharmacokinetic and pharmacologic properties, as well as reduced toxicity.

[00216] In another aspect, the invention provides substantially homogeneous XTEN polymers comprising defined numbers of cross-linkers or azide/alkyne reactants as reactant conjugation partners in monomeric and multimeric configurations and methods of the preparation of such reactants. The XTEN derivatives comprising cross-linkers or azide/alkyne reactants are used as reactants in the conjugation of payload agents to result in XTEN-payload conjugate exhibiting the desired physical, pharmaceutical, and pharmacological properties.

[00217] In another aspect, the invention provides compositions of XTEN-payload in which one or more XTEN are chemically linked to one or more payloads, including combinations of different payloads, in defined numbers in either monomeric or multimeric configurations to provide compositions with enhanced pharmaceutical, pharmacokinetic, and pharmacologic properties. Such compositions linked to such payloads may have utility, when adminisered to a subject, in the prevention, treatment or amelioration of diseases or conditions due to a pharmacologic or biologic effect of the payload.

1. XTEN: extended recombinant polypeptides

[00218] In one aspect, the invention provides substantially homogeneous XTEN polypeptide compositions that are useful as conjugation partners to link to one or more payloads, either directly or via a cross-linker reactant resulting in an XTEN-payload conjugate.

[00219] XTEN are polypeptides with non-naturally occurring, substantially non-repetitive sequences having a low degree or no secondary or tertiary structure under physiologic conditions. XTEN typically have from about 36 to about 3000 amino acids, of which the majority or the entirety are small hydrophilic amino acids. As used herein, "XTEN" specifically excludes whole antibodies or antibody fragments (e.g. single-chain antibodies and Fc fragments). XTEN polypeptides have utility as a conjugation partners in that they serve in various roles, conferring certain desirable properties when linked to a payload. The resulting XTEN-payload conjugates have enhanced properties, such as enhanced pharmacokinetic, physicochemical, pharmacologic, and pharmaceutical properties compared to the corresponding payload not linked

to XTEN, making them useful in the treatment of certain conditions for which the payload is known in the art to be used.

[00220] The unstructured characteristic and physicochemical properties of the XTEN result, in part, from the overall amino acid composition that is disproportionately limited to 4-6 types of hydrophilic amino acids, the linking of the amino acids in a quantifiable non-repetitive design, and the length of the XTEN polypeptide. In an advantageous feature common to XTEN but uncommon to native polypeptides, the properties of XTEN disclosed herein are not tied to absolute primary amino acid sequences, as evidenced by the diversity of the exemplary sequences of Table 2 that, within varying ranges of length, possess similar properties, many of which are documented in the Examples. Accordingly, XTEN have properties more like non-proteinaceous, hydrophilic polymers than they do proteins. The XTEN of the present invention exhibit one or more of the following advantageous properties: conformational flexibility, reduced or lack of secondary structure, high degree of aqueous solubility, high degree of protease resistance, low immunogenicity, low binding to mammalian receptors, a defined degree of charge, and increased hydrodynamic (or Stokes) radii; properties that are similar to certain hydrophilic polymers (e.g., polyethylene glycol) that make them particularly useful as conjugation partners.

[00221] The XTEN component(s) of the subject conjugates are designed to behave like denatured peptide sequences under physiological conditions, despite the extended length of the polymer. "Denatured" describes the state of a peptide in solution that is characterized by a large conformational freedom of the peptide backbone. Most peptides and proteins adopt a denatured conformation in the presence of high concentrations of denaturants or at elevated temperature. Peptides in denatured conformation have, for example, characteristic circular dichroism (CD) spectra and are characterized by a lack of long-range interactions as determined by NMR. "Denatured conformation" and "unstructured conformation" are used synonymously herein. In some embodiments, the invention provides XTEN sequences that, under physiologic conditions, resemble denatured sequences that are largely devoid of secondary structure. In other cases, the XTEN sequences are substantially devoid of secondary structure under physiologic conditions. "Largely devoid," as used in this context, means that less than 50% of the XTEN amino acid residues of the XTEN sequence contribute to secondary structure as measured or determined by the means described herein. "Substantially devoid," as used in this context, means that at least about 60%, or about 70%, or about 80%, or about 90%, or about 95%, or about 97%, or at least about 99% of the XTEN amino acid residues of the XTEN sequence do not contribute to secondary structure, as measured or determined by the methods described herein.

[00222] A variety of methods and assays are known in the art for determining the physicochemical properties of the subject XTEN. Such properties include but are not limited to

secondary or tertiary structure, solubility, protein aggregation, stability, absolute and apparent molecular weight, purity and uniformity, melting properties, contamination and water content. The methods to measure such properties include analytical centrifugation, EPR, HPLC-ion exchange, HPLC-size exclusion chromatography (SEC), HPLC-reverse phase, light scattering, capillary electrophoresis, circular dichroism, differential scanning calorimetry, fluorescence, HPLC-ion exchange, HPLC-size exclusion, IR, NMR, Raman spectroscopy, refractometry, and UV/Visible spectroscopy. In particular, secondary structure can be measured spectrophotometrically, e.g., by circular dichroism spectroscopy in the "far-UV" spectral region (190-250 nm). Secondary structure elements, such as alpha-helix and beta-sheet, each give rise to a characteristic shape and magnitude of CD spectra, as does the lack of these structure elements. Secondary structure can also be predicted for a polypeptide sequence via certain computer programs or algorithms, such as the well-known Chou-Fasman algorithm (Chou, P. Y., *et al.* (1974) *Biochemistry*, 13: 222-45) and the Garnier-Osguthorpe-Robson algorithm ("Gor algorithm") (Garnier J, Gibrat JF, Robson B. (1996), GOR method for predicting protein secondary structure from amino acid sequence. Methods Enzymol 266:540-553), as described in US Patent Application Publication No. 20030228309A1. For a given sequence, the algorithms can predict whether there exists some or no secondary structure at all, expressed as the total and/or percentage of residues of the sequence that form, for example, alpha-helices or beta-sheets or the percentage of residues of the sequence predicted to result in random coil formation (which lacks secondary structure). Polypeptide sequences can be analyzed using the Chou-Fasman algorithm using sites on the world wide web at, for example, fasta.bioch.virginia.edu/fasta_www2/fasta_www.cgi?rm=misc1 and the Gor algorithm at npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_gor4.html (both accessed on September 5, 2012). Additional methods are disclosed in Arnau, *et al.*, Prot Expr and Purif (2006) 48, 1-13.

[00223] In one embodiment, the XTEN sequences used in the subject conjugates have an alpha-helix percentage ranging from 0% to less than about 5% as determined by the Chou-Fasman algorithm. In another embodiment, the XTEN sequences have a beta-sheet percentage ranging from 0% to less than about 5% as determined by the Chou-Fasman algorithm. In one embodiment, the XTEN sequences of the conjugates have an alpha-helix percentage ranging from 0% to less than about 5% and a beta-sheet percentage ranging from 0% to less than about 5% as determined by the Chou-Fasman algorithm. In one embodiment, the XTEN sequences of the conjugates have an alpha-helix percentage less than about 2% and a beta-sheet percentage less than about 2%. The XTEN sequences of the conjugate compositions have a high degree of random coil percentage, as determined by the GOR algorithm. In some embodiments, an XTEN sequence has at least about 80%, more preferably at least about 90%, more preferably at least about 91%, more preferably at least about 92%, more preferably at least about 93%, more

preferably at least about 94%, more preferably at least about 95%, more preferably at least about 96%, more preferably at least about 97%, more preferably at least about 98%, and most preferably at least about 99% random coil, as determined by the GOR algorithm. In one embodiment, the XTEN sequences of the conjugate compositions have an alpha-helix percentage ranging from 0% to less than about 5% and a beta-sheet percentage ranging from 0% to less than about 5% as determined by the Chou-Fasman algorithm and at least about 90% random coil, as determined by the GOR algorithm. In another embodiment, the XTEN sequences of the disclosed compositions have an alpha-helix percentage less than about 2% and a beta-sheet percentage less than about 2% at least about 90% random coil, as determined by the GOR algorithm. In another embodiment, the XTEN sequenes of the compositions are substantially lacking secondary structure as measured by circular dichroism.

[00224] The selection criteria for the XTEN to be linked to the payload used to create the conjugate compositions generally relate to attributes of physicochemical properties and conformational structure of the XTEN that is, in turn, used to confer enhanced pharmaceutical, pharmacologic, and pharmacokinetic properties to the compositions.

1. Non-repetitive Sequences

[00225] It is specifically contemplated that the subject XTEN sequences included in the subject conjugate composition embodiments are substantially non-repetitive. In general, repetitive amino acid sequences have a tendency to aggregate or form higher order structures, as exemplified by natural repetitive sequences such as collagens and leucine zippers. These repetitive amino acids may also tend to form contacts resulting in crystalline or pseudocrystaline structures. In contrast, the low tendency of non-repetitive sequences to aggregate enables the design of long-sequence XTENs with a relatively low frequency of charged amino acids that would otherwise be likely to aggregate if the sequences were repetitive. The non-repetitiveness of a subject XTEN can be observed by assessing one or more of the following features. In one embodiment, a substantially non-repetitive XTEN sequence has no three contiguous amino acids in the sequence that are identical amino acid types unless the amino acid is serine, in which case no more than three contiguous amino acids are serine residues. In another embodiment, as described more fully below, a substantially non-repetitive XTEN sequence in which 80-99% of the sequence is comprised of motifs of 9 to 14 amino acid residues wherein the motifs consist of 3, 4, 5 or 6 types of amino acids selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the sequence of any two contiguous amino acid residues in any one motif is not repeated more than twice in the sequence motif.

[00226] The degree of repetitiveness of a polypeptide or a gene can be measured by computer programs or algorithms or by other means known in the art. According to the current invention, algorithms to be used in calculating the degree of repetitiveness of a particular polypeptide, such

as an XTEN, are disclosed herein, and examples of sequences analyzed by algorithms are provided (*see* Examples, below). In one embodiment, the repetitiveness of a polypeptide of a predetermined length can be calculated (hereinafter "subsequence score") according to the formula given by Equation I:

$$\text{Subsequence score} = \frac{\sum_{i=1}^{m} Count_i}{m} \qquad \text{I}$$

wherein: m = (amino acid length of polypeptide) – (amino acid length of subsequence) + 1; and $Count_i$ = cumulative number of occurrences of each unique subsequence within $sequence_i$

[00227] An algorithm termed "SegScore" was developed to apply the foregoing equation to quantitate repetitiveness of polypeptides, such as an XTEN, providing the subsequence score wherein sequences of a predetermined amino acid length "n" are analyzed for repetitiveness by determining the number of times (a "count") a unique subsequence of length "s" appears in the set length, divided by the absolute number of subsequences within the predetermined length of the sequence. FIG. 79 depicts a logic flowchart of the SegScore algorithm, while FIG. 80 portrays a schematic of how a subsequence score is derived for a fictitious XTEN with 11 amino acids and a subsequence length of 3 amino acid residues. For example, a predetermined polypeptide length of 200 amino acid residues has 192 overlapping 9-amino acid subsequences and 198 3-mer subsequences, but the subsequence score of any given polypeptide will depend on the absolute number of unique subsequences and how frequently each unique subsequence (meaning a different amino acid sequence) appears in the predetermined length of the sequence.

[00228] In the context of the present invention, "subsequence score" means the sum of occurrences of each unique 3-mer frame across 200 consecutive amino acids of the cumulative XTEN polypeptide divided by the absolute number of unique 3-mer subsequences within the 200 amino acid sequence. Examples of such subsequence scores derived from 200 consecutive amino acids of repetitive and non-repetitive polypeptides are presented in Example 45. In one embodiment, the invention provides a XTEN-payload comprising one XTEN in which the XTEN has a subsequence score less than 12, more preferably less than 10, more preferably less than 9, more preferably less than 8, more preferably less than 7, more preferably less than 6, and most preferably less than 5. In another embodiment, the invention provides XTEN-cross-linker conjugates comprising an XTEN in which the XTEN have a subsequence score of less than 10, more preferably less than 9, more preferably less than 8, more preferably less than 7, more preferably less than 6, and most preferably less than 5. In another embodiment, the invention

provides XTEN-click-chemistry conjugates comprising an XTEN in which the XTEN have a subsequence score of less than 10, more preferably less than 9, more preferably less than 8, more preferably less than 7, more preferably less than 6, and most preferably less than 5. In yet another embodiment, the invention provides XTEN conjugate compositions comprising at least two linked XTEN in which each individual XTEN has a subsequence score of less than 10, or less than 9, or less than 8, or less than 7, or less than 6, or less than 5, or less. In yet another embodiment, the invention provides XTEN conjugate compositions comprising at least three linked XTEN in which each individual XTEN has a subsequence score of less than 10, or less than 9, or less than 8, or less than 7, or less than 6, or less than 5, or less. In the embodiments of the XTEN compositions described herein, an XTEN with a subsequence score of 10 or less (i.e., 9, 8, 7, etc.) is characterized as substantially non-repetitive.

[00229] In one aspect, the non-repetitive characteristic of XTEN of the present invention together with the particular types of amino acids that predominate in the XTEN, rather than the absolute primary sequence, confers one or more of the enhanced physicochemical and biological properties of the XTEN and the resulting XTEN-payload conjugates. These enhanced properties include a higher degree of expression of the XTEN protein in the host cell, greater genetic stability of the gene encoding XTEN, a greater degree of solubility, less tendency to aggregate, and enhanced pharmacokinetics of the resulting conjugate compared to payloads not conjugated to XTEN or payloads conjugated to proteins having repetitive sequences. These enhanced properties permit more efficient manufacturing, greater uniformity of the final product, lower cost of goods, and/or facilitate the formulation of XTEN-comprising pharmaceutical preparations containing extremely high protein concentrations, in some cases exceeding 100 mg/ml. In some embodiments, the XTEN polypeptide sequences of the conjugates are designed to have a low degree of internal repetitiveness in order to reduce or substantially eliminate immunogenicity when administered to a mammal. Polypeptide sequences composed of short, repeated motifs largely limited to only three amino acids, such as glycine, serine and glutamate, may result in relatively high antibody titers when administered to a mammal despite the absence of predicted T-cell epitopes in these sequences. This may be caused by the repetitive nature of polypeptides, as it has been shown that immunogens with repeated epitopes, including protein aggregates, cross-linked immunogens, and repetitive carbohydrates are highly immunogenic and can, for example, result in the cross-linking of B-cell receptors causing B-cell activation. (Johansson, J., *et al.* (2007) Vaccine, 25 :1676-82 ; Yankai, Z., *et al.* (2006) Biochem Biophys Res Commun, 345 :1365-71 ; Hsu, C. T., *et al.* (2000) Cancer Res, 60:3701-5); Bachmann MF, *et al.* Eur J Immunol. (1995) 25(12):3445-3451).

2. Exemplary Sequence Motifs

[00230] The present invention encompasses XTEN used as conjugation partners that comprise multiple units of shorter sequences, or motifs, in which the amino acid sequences of the motifs are substantially non-repetitive. The non-repetitive property can be met even using a "building block" approach using a library of sequence motifs that are multimerized to create the XTEN sequences, as shown in FIGS. 18-19. While an XTEN sequence may consist of multiple units of as few as four different types of sequence motifs, because the motifs themselves generally consist of non-repetitive amino acid sequences, the overall XTEN sequence is designed to render the sequence substantially non-repetitive.

[00231] In one embodiment, an XTEN has a substantially non-repetitive sequence of greater than about 36 to about 3000, or about 100 to about 2000, or about 144 to about 1000 amino acid residues, wherein at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 97%, or about 99% to about 100% of the XTEN sequence consists of non-overlapping sequence motifs, and wherein each of the motifs has about 9 to 36 amino acid residues. As used herein, "non-overlapping" means that the individual motifs do not share amino acid residues but, rather, are fused to other motifs or amino acid residues in a linear fashion. In other embodiments, at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 97%, or about 99% to about 100% of the XTEN sequence consists of non-overlapping sequence motifs wherein each of the motifs has 9 to 14 amino acid residues. In still other embodiments, at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 97%, or about 99% to about 100% of the XTEN sequence consists of non-overlapping sequence motifs wherein each of the motifs has 12 amino acid residues. In these embodiments, it is preferred that the sequence motifs are composed of substantially (e.g., 90% or more) or exclusively small hydrophilic amino acids, such that the overall sequence has an unstructured, flexible characteristic. Examples of amino acids that are included in XTEN are, e.g., arginine, lysine, threonine, alanine, asparagine, glutamine, aspartate, glutamate, serine, and glycine. In one embodiment, XTEN sequences have predominately four to six types of amino acids selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) or proline (P) that are arranged in a substantially non-repetitive sequence that is about 36 to about 3000, or about 100 to about 2000, or about 144 to about 1000 amino acid residues in length. In some embodiment, an XTEN sequence is made of 4, 5, or 6 types of amino acids selected from the group consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) or proline (P). In some embodiments, XTEN have sequences of about 36 to about 1000, or about 100 to about 2000, or about 400 to about 3000 amino acid residues wherein at least about 80% of the sequence consists of non-overlapping sequence motifs wherein each of the motifs has 9 to 36 amino acid residues and wherein at least 90%, or at least 91%, or at least 92%,

or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or 100% of each of the motifs consists of 4 to 6 types of amino acids selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the content of any one amino acid type in the full-length XTEN does not exceed 30%. In other embodiments, at least about 90% of the XTEN sequence consists of non-overlapping sequence motifs wherein each of the motifs has 9 to 36 amino acid residues wherein the motifs consist of 4 to 6 types of amino acids selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the content of any one amino acid type in the full-length XTEN does not exceed 40%, or about 30%, or 25%, or about 17%, or about 12%, or about 8%. In other embodiments, at least about 90% of the XTEN sequence consists of non-overlapping sequence motifs wherein each of the motifs has 12 amino acid residues consisting of 4 to 6 types of amino acids selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), and wherein the content of any one amino acid type in the full-length XTEN does not exceed 40%, or 30%, or about 25%, or about 17%, or about 12%, or about 8%. In yet other embodiments, at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99%, to about 100% of the XTEN sequence consists of non-overlapping sequence motifs wherein each of the motifs has 12 amino acid residues consisting of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P).

[00232] In some embodiments, the invention provides XTEN-payload, XTEN-cross-linker, and XTEN-click-chemistry reactant conjugates comprising one, or two, or three, or four or more substantially non-repetitive XTEN sequence(s) of about 36 to about 1000 amino acid residues, or cumulatively about 100 to about 3000 amino acid residues wherein at least about 80%, or at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% to about 100% of the sequence consists of multiple units of four or more non-overlapping sequence motifs selected from the amino acid sequences of Table 1, wherein the overall sequence remains substantially non-repetitive. In some embodiments, the XTEN comprises non-overlapping sequence motifs in which about 80%, or at least about 85%, or at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% or about 100% of the sequence consists of multiple units of non-overlapping sequences selected from a single motif family selected from Table 1, resulting in a family sequence. Family, as applied to motifs, means that the XTEN has motifs selected from a single motif category from Table 1; i.e., AD, AE, AF, AG, AM, AQ, BC, or BD. In other embodiments, the XTEN comprises multiple units of motif sequences from two or more of the motif families of Table 1 selected to achieve desired physicochemical characteristics, including such properties as net charge, hydrophilicity, lack of secondary structure, or lack of repetitiveness that may be conferred by the amino acid

composition of the motifs, described more fully below. In the embodiments hereinabove described in this paragraph, the motifs or portions of the motifs incorporated into the XTEN can be selected and assembled using the methods described herein to achieve an XTEN of about 36, about 42, about 72, about 144, about 288, about 576, about 864, about 1000, about 2000 to about 3000 amino acid residues, or any intermediate length. Non-limiting examples of XTEN family sequences useful for incorporation into the subject conjugates are presented in Table 2. It is intended that a specified sequence mentioned relative to Table 2 has that sequence set forth in Table 2, while a generalized reference to an AE144 sequence, for example, is intended to encompass any AE sequence having 144 amino acid residues; e.g., AE144_1A, AE144_2A, etc., or a generalized reference to an AG144 sequence, for example, is intended to encompass any AG sequence having 144 amino acid residues, e.g., AG144_1, AG144_2, AG144_A, AG144_B, AG144_C, etc.

Table 1: XTEN Sequence Motifs of 12 Amino Acids and Motif Families

Motif Family*	MOTIF SEQUENCE
AD	GESPGGSSGSES
AD	GSEGSSGPGESS
AD	GSSESGSSEGGP
AD	GSGGEPSESGSS
AE, AM	GSPAGSPTSTEE
AE, AM, AQ	GSEPATSGSETP
AE, AM, AQ	GTSESATPESGP
AE, AM, AQ	GTSTEPSEGSAP
AF, AM	GSTSESPSGTAP
AF, AM	GTSTPESGSASP
AF, AM	GTSPSGESSTAP
AF, AM	GSTSSTAESPGP
AG, AM	GTPGSGTASSSP
AG, AM	GSSTPSGATGSP
AG, AM	GSSPSASTGTGP
AG, AM	GASPGTSSTGSP
AQ	GEPAGSPTSTSE
AQ	GTGEPSSTPASE
AQ	GSGPSTESAPTE
AQ	GSETPSGPSETA
AQ	GPSETSTSEPGA
AQ	GSPSEPTEGTSA
BC	GSGASEPTSTEP
BC	GSEPATSGTEPS
BC	GTSEPSTSEPGA
BC	GTSTEPSEPGSA
BD	GSTAGSETSTEA
BD	GSETATSGSETA
BD	GTSESATSESGA
BD	GTSTEASEGSAS

* Denotes individual motif sequences that, when used together in various permutations, results in a "family sequence"

Table 2: XTEN Polypeptides

XTEN Name	Amino Acid Sequence
AE42	GAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPASS
AE42_1	TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGS
AE42_2	PAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSG
AE42_3	SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSP
AG42_1	GAPSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGPSGP
AG42_2	GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASP
AG42_3	SPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA
AG42_4	SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG
AE48	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGS
AM48	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGS
AE144	GSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSA PGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAP
AE144_1A	SPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPG
AE144_2A	TSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGTSESATPESGPG
AE144_2B	TSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGTSESATPESGPG
AE144_3A	SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPG
AE144_3B	SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPG
AE144_4A	TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPG
AE144_4B	TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPG
AE144_5A	TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESG PGSPAGSPTSTEEGSPAGSPTSTEEG
AE144_6B	TSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPG
AF144	GTSTPESGSASPGTSPSGESSTAPGTSPSGESSTAPGSTSSTAESPGPGSTSESPSGTA PGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSASPGSTSSTAESPGPGTSPSGESST APGTSPSGESSTAPGTSPSGESSTAP
AG144_1	SGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSS PSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG SSPSASTGTGPGSSPSASTGTGPGASP
AG144_2	PGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSS TGSPGASPGTSSTGSPGTPGSGTASSS
AG144_A	GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSP

XTEN Name	Amino Acid Sequence
AG144_B	GTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSST GSPGASPGTSSTGSPGASPGTSSTGSP
AG144_C	GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGT GPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSP
AG144_F	GSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATG SPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGAT GSPGSSTPSGATGSPGASPGTSSTGSP
AG144_3	GTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGT GPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTG TGPGASPGTSSTGSPGASPGTSSTGSP
AG144_4	GTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSP
AE288_1	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESG PGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPES GPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPE SGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP
AE288_2	GSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSA PGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPT STEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP
AG288_1	PGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTAS SSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSAST GTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSAS TGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPS ASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGS
AG288_2	GSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSS TGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP
AF504	GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSXPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSXPSASTGTGPGSSPSASTGTGPGSSTPS GATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGS STPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSP GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSP
AF540	GSTSSTAESPGPGSTSSTAESPGPGSTSESPSGTAPGSTSSTAESPGPGSTSSTAESPG PGTSTPESGSASPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGT APGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSG TAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPSGTAPGTSTPESG SASPGSTSSTAESPGPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPS GTAPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGSTSESP SGTAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSES PSGTAPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSPS GESSTAPGSTSSTAESPGPGTSPSGESSTAPGSTSSTAESPGPGTSTPESGSASPGSTS ESPSGTAP
AD576	GSSESGSSEGGPGSGGEPSESGSSGSSESGSSEGGPGSSESGSSEGGPGSSESGSSEG GPGSSESGSSEGGPGSSESGSSEGGPGESPGGSSGSESGSEGSSGPGESSGSSESGSSE GGPGSSESGSSEGGPGSSESGSSEGGPGSGGEPSESGSSGESPGGSSGSESGESPGGS

XTEN Name	Amino Acid Sequence
	SGSESGSGGEPSESGSSGSSESGSSEGGPGSGGEPSESGSSGSGGEPSESGSSGSEGSS GPGESSGESPGGSSGSESGSGGEPSESGSSGSGGEPSESGSSGSGGEPSESGSSGSSES GSSEGGPGESPGGSSGSESGESPGGSSGSESGESPGGSSGSESGESPGGSSGSESGES PGGSSGSESGSSESGSSEGGPGSGGEPSESGSSGSEGSSGPGESSGSSESGSSEGGPGS GGEPSESGSSGSSESGSSEGGPGSGGEPSESGSSGESPGGSSGSESGESPGGSSGSES GSSESGSSEGGPGSGGEPSESGSSGSSESGSSEGGPGSGGEPSESGSSGSGGEPSESG SSGESPGGSSGSESGSEGSSGPGESSGSSESGSSEGGPGSEGSSGPGESS
AE576	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSG SETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP
AF576	GSTSSTAESPGPGSTSSTAESPGPGSTSESPSGTAPGSTSSTAESPGPGSTSSTAESPG PGTSTPESGSASPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGT APGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSG TAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPSGTAPGTSTPESG SASPGSTSSTAESPGPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPS GTAPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGSTSESP SGTAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSES PSGTAPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSPS GESSTAPGSTSSTAESPGPGTSPSGESSTAPGSTSSTAESPGPGTSTPESGSASPGSTS ESPSGTAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASP
AG576	PGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGAT GSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGT ASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSS TPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTA SSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGS
AE624	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESAT PESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEP SEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTE PSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEE GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP
AD836	GSSESGSSEGGPGSSESGSSEGGPGESPGGSSGSESGSGGEPSESGSSGESPGGSSGS ESGESPGGSSGSESGSSESGSSEGGPGSSESGSSEGGPGSSESGSSEGGPGESPGGSS GSESGESPGGSSGSESGESPGGSSGSESGSSESGSSEGGPGSSESGSSEGGPGSSESGS SEGGPGSSESGSSEGGPGSSESGSSEGGPGSSESGSSEGGPGSGGEPSESGSSGESPG GSSGSESGESPGGSSGSESGSGGEPSESGSSGSEGSSGPGESSGSSESGSSEGGPGSG GEPSESGSSGSEGSSGPGESSGSSESGSSEGGPGSGGEPSESGSSGESPGGSSGSESGS GGEPSESGSSGSGGEPSESGSSGSSESGSSEGGPGSGGEPSESGSSGSGGEPSESGSS GSEGSSGPGESSGESPGGSSGSESGSEGSSGPGESSGSEGSSGPGESSGSGGEPSESG SSGSSESGSSEGGPGSSESGSSEGGPGESPGGSSGSESGSGGEPSESGSSGSEGSSGPG ESSGESPGGSSGSESGSEGSSGPGSSESGSSEGGPGSGGEPSESGSSGSEGSSGPGESS

XTEN Name	Amino Acid Sequence
	GSEGSSGPGESSGSEGSSGPGESSGSGGEPSESGSSGSGGEPSESGSSGESPGGSSGS ESGESPGGSSGSESGSGGEPSESGSSGSEGSSGPGESSGESPGGSSGSESGSSESGSSE GGPGSSESGSSEGGPGSSESGSSEGGPGSGGEPSESGSSGSSESGSSEGGPGESPGGS SGSESGSGGEPSESGSSGSSESGSSEGGPGESPGGSSGSESGSGGEPSESGSSGESPG GSSGSESGSGGEPSESGSS
AE864	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSG SETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESG PGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGS APGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP
AF864	GSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSAS PGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGT APGTSPSGESSTAPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSPSGESS TAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSESPS GTAPGTSTPESGSASPGSTSSTAESPGPGTSTPESGSASPGSTSESPSGTAPGTSPSGE SSTAPGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSASPGSTSSTAESPGPGSTSST AESPGPGSTSSTAESPGPGSTSSTAESPGPGTSPSGESSTAPGSTSESPSGTAPGSTSE SPSGTAPGTSTPESGPXXXGASASGAPSTXXXXSESPSGTAPGSTSESPSGTAPGSTS ESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTS PSGESSTAPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSASPGS TSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGTSTPESGSASPG TSTPESGSASPGSTSESPSGTAPGTSTPESGSASPGSTSSTAESPGPGSTSESPSGTAP GSTSESPSGTAPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSAS PGTSPSGESSTAPGTSPSGESSTAPGTSPSGESSTAPGSTSSTAESPGPGSTSSTAESP GPGTSPSGESSTAPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSP
AG864_2	GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPS GATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGS STPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSP GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTA SSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASP GTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTP GSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSP
AM875	GTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSE TPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEG SAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATP ESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPS EGSAPGSEPATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPA GSPTSTEEGTSTEPSEGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSP

XTEN Name	Amino Acid Sequence
	AGSPTSTEEGSTSSTAESPGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGS STPSGATGSPGSSPSASTGTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPG STSSTAESPGPGSTSSTAESPGPGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETP GTSTEPSEGSAPGSTSSTAESPGPGTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSA PGTSTEPSEGSAPGTSTEPSEGSAPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTG SPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSSTPSGATGSPGSSPSASTG TGPGASPGTSSTGSPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP
AM1318	GTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSE TPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEG SAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATP ESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPS EGSAPGSEPATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPA GSPTSTEEGTSTEPSEGSAPGPEPTGPAPSGGSEPATSGSETPGTSESATPESGPGSPA GSPTSTEEGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGSTSSTAESPGPGSTSESPSGTAPGTSPSGESSTAPGS TSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGTSTEPSEGSAPGTSPSGESSTAPGTSPSGESSTAPGTSPSGESSTA PGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGSSPSASTGTGPGSSTPSGATG SPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASASGAP STGGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSESATPESGPGTSTEPSE GSAPGTSTEPSEGSAPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGTSTPES GSASPGTSPSGESSTAPGTSPSGESSTAPGTSESATPESGPGSEPATSGSETPGTSTEP SEGSAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSPAGSPTSTEEGTSES ATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGSST PSGATGSPGASPGTSSTGSPGSSTPSGATGSPGSTSESPSGTAPGTSPSGESSTAPGST SSTAESPGPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSPAGSPTSTEEGS PAGSPTSTEEGTSTEPSEGSAP
BC 864	GTSTEPSEPGSAGTSTEPSEPGSAGSEPATSGTEPSGSGASEPTSTEPGSEPATSGTE PSGSEPATSGTEPSGSEPATSGTEPSGSGASEPTSTEPGTSTEPSEPGSAGSEPATSG TEPSGTSTEPSEPGSAGSEPATSGTEPSGSEPATSGTEPSGTSTEPSEPGSAGTSTEPS EPGSAGSEPATSGTEPSGSEPATSGTEPSGTSEPSTSEPGAGSGASEPTSTEPGTSEP STSEPGAGSEPATSGTEPSGSEPATSGTEPSGTSTEPSEPGSAGTSTEPSEPGSAGSG ASEPTSTEPGSEPATSGTEPSGSEPATSGTEPSGSEPATSGTEPSGSEPATSGTEPSGT STEPSEPGSAGSEPATSGTEPSGSGASEPTSTEPGTSTEPSEPGSAGSEPATSGTEPS GSGASEPTSTEPGTSTEPSEPGSAGSGASEPTSTEPGSEPATSGTEPSGSGASEPTST EPGSEPATSGTEPSGSGASEPTSTEPGTSTEPSEPGSAGSEPATSGTEPSGSGASEPT STEPGTSTEPSEPGSAGSEPATSGTEPSGTSTEPSEPGSAGSEPATSGTEPSGTSTEPS EPGSAGTSTEPSEPGSAGTSTEPSEPGSAGTSTEPSEPGSAGTSTEPSEPGSAGTSTE PSEPGSAGTSEPSTSEPGAGSGASEPTSTEPGTSTEPSEPGSAGTSTEPSEPGSAGTS TEPSEPGSAGSEPATSGTEPSGSGASEPTSTEPGSEPATSGTEPSGSEPATSGTEPSG SEPATSGTEPSGSEPATSGTEPSGTSEPSTSEPGAGSEPATSGTEPSGSGASEPTSTEP GTSTEPSEPGSAGSEPATSGTEPSGSGASEPTSTEPGTSTEPSEPGSA
BD864	GSETATSGSETAGTSESATSESGAGSTAGSETSTEAGTSESATSESGAGSETATSGS ETAGSETATSGSETAGTSTEASEGSASGTSTEASEGSASGTSESATSESGAGSETAT SGSETAGTSTEASEGSASGSTAGSETSTEAGTSESATSESGAGTSESATSESGAGSE TATSGSETAGTSESATSESGAGTSTEASEGSASGSETATSGSETAGSETATSGSETA GTSTEASEGSASGSTAGSETSTEAGTSESATSESGAGTSTEASEGSASGSETATSGS ETAGSTAGSETSTEAGSTAGSETSTEAGSETATSGSETAGTSESATSESGAGTSESA TSESGAGSETATSGSETAGTSESATSESGAGTSESATSESGAGSETATSGSETAGSE TATSGSETAGTSTEASEGSASGSTAGSETSTEAGSETATSGSETAGTSESATSESGA GSTAGSETSTEAGSTAGSETSTEAGSTAGSETSTEAGTSTEASEGSASGSTAGSETS TEAGSTAGSETSTEAGTSTEASEGSASGSTAGSETSTEAGSETATSGSETAGTSTEA SEGSASGTSESATSESGAGSETATSGSETAGTSESATSESGAGTSESATSESGAGSE TATSGSETAGTSESATSESGAGSETATSGSETAGTSTEASEGSASGTSTEASEGSAS GSTAGSETSTEAGSTAGSETSTEAGSETATSGSETAGTSESATSESGAGTSESATSE

XTEN Name	Amino Acid Sequence
	SGAGSETATSGSETAGSETATSGSETAGSETATSGSETAGTSTEASEGSASGTSESA TSESGAGSETATSGSETAGSETATSGSETAGTSESATSESGAGTSESATSESGAGSE TATSGSETA
AE948	GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGTSTEPSE GSAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSEPATSGSETPGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGSEPAT SGSETPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTS ESATPESGPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGT STEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPG SEPATSGSETPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTE EGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTST EEGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATP ESGP
AE1044	GSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTE EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSE TPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGS ETPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGSPAGSP TSTEEGTSTEPSEGSAPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSES ATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTS TEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGS PAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPG SEPATSGSETPGTSESATPESGPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGSEPATSGSE TPGSPAGSPTSTEEGTSESATPESGPGTSESATPESGPGSEPATSGSETPGTSTEPSEG SAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSG SETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESAT PESGPGTSESATPESGPGTST
AE1140	GSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESG PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEP SEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTE PSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSE PATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGS PAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPG SEPATSGSETPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPES GPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGS ETPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSG SETPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGSPAGSPTSTEEGSPA
AE1236	GSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGS

XTEN Name	Amino Acid Sequence
	APGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPT STEEGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESAT PESGPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESA TPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGTSTE PSEGSAPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT SESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPG TSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTSTEPSEGSAPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSET PGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSE TPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGSEPATSGS ETPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSG SETPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEPS EGSAPGTSTEPSEGSAPGSEP
AE1332	GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPES GPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEPATSGS ETPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPS EGSAPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSEPAT SGSETPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGTS TEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGS EPATSGSETPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSE TPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSESAT PESGPGTSTEPSEGSAPGTST
AE1428	GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGTSESATPESG PGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSTEPSE GSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESAT PESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEP SEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGSPAG SPTSTEEGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSPA GSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTS ESATPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGT SESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGTSTEPSEGSAPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSEPATSGSETPGTSESATPESGPGTSESATPESGPGTSESATPESGPGTSTEPSEG SAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSP TSTEEGTSESATPESGPGSPA
AE1524	GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTE EGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSESATPES GPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEG SAPGSEPATSGSETPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPT STEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESAT PESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGTSTEP

XTEN Name	Amino Acid Sequence
	SEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAG SPTSTEEGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSE SATPESGPGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGS EPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG SPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETP GSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGTSTEPSEGSA PGTSTEPSEGSAPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSG SETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSTEPS EGSAPGTSESATPESGPGSPA
AE1620	GSEPATSGSETPGTSTEPSEGSAPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESG PGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPES GPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPE SGPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSESA TPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSTE PSEGSAPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGT SESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG SPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSA PGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSE TPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSG SETPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPS EGSAPGSPAGSPTSTEEGTST
AE1716	GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPES GPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGTSESATPE SGPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSPAGSP TSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSES ATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPG SEPATSGSETPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESG PGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTST EEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGSPAGSP TSTEEGTSESATPESGPGTSE
AE1812	GTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTS TEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATP ESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSESAT PESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEP SEGSAPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSESATPESGPGTSTE PSEGSAPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT

XTEN Name	Amino Acid Sequence
	SESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP GSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSESATPESGPGTSESATPESG PGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSTEPSEGS APGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGSPAGSPT STEEGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGSPAGSP TSTEEGTSTEPSEGSAPGSEP
AE1908	GSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSA PGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSE TPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPE SGPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSP TSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGSEPAT SGSETPGTSESATPESGPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTS ESATPESGPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGT SESATPESGPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSESATPESG PGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPE SGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSESATP ESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSPAGSP TSTEEGTSESATPESGPGSEP
AE2004A	GTSTEPSEGSAPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSET PGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSTEPSEGS APGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGTSESATPESGPGSPAGSPTS TEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPAT SGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSEPATSGSETPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGS EPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGTSTEPS EGSAPGTSESATPESGPGTSE
AG948	GSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTASSSPGSSPSASTG TGPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSPGASPGTS STGSPGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGSSPSA STGTGPGASPGTSSTGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGTPG SGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGSS PSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTG SPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGAT GSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSS TGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSTP SGATGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGAS

XTEN Name	Amino Acid Sequence
	PGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSP
AG1044	GTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTG SPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSST GSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGT ASSSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGTPGSG TASSSPGASPGTSSTGSPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPGASPG TSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSP SASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGS SPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGSSPSASTGTGP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASS SPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGAT GSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSS TGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPG TSSTGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGASP GTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGS SPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTGSP GSSTPSGATGSPGTPGSGTASSSPGSST
AG1140	GASPGTSSTGSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTG SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTA SSSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGSSP SASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGA SPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPG TPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGP GASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGA SPGTSSTGSPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSP GASPGTSSTGSPGSSPSASTGTGPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGASPGTSSTGSPGSST
AG1236	GSSPSASTGTGPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASS SPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTA SSSPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGASPGTS STGSPGSSPSASTGTGPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGASPG TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGTPGSGTASSSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGSS PSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPG SSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATG SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTG TGPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGTPGSGT ASSSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGTPGS GTASSSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGTP GSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPG TPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSPSASTGT GPGSSPSASTGTGPGASPGTSSTGSPGASP
AG1332	GSSTPSGATGSPGSSPSASTGTGPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTG

XTEN Name	Amino Acid Sequence
	SPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTG TGPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGSSTPSGATGSPG SSPSASTGTGPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSP GASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGASPGTSSTGSPGSSTPSGATG SPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTA SSSPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSPGTPGSGTASSSPGTPGSGT ASSSPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSA STGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGSSPS ASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTP GSGTASSSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPG TPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSP GSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGASPGTSSTGSPGASPGTSSTGSPGTPG
AG1428	GTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASS SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTG TGPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTS STGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGASPGTSSTGSPGASPG TSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPGASP GTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTGSPGSSTPSGATGSPG ASPGTSSTGSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTA SSSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTS STGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSTPSGATGSPGTPGS GTASSSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSST PSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSP GTPGSGTASSSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGTPGSGTASSSPGASP
AG1524	GSSTPSGATGSPGTPGSGTASSSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATG SPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSPGTPGSGTA SSSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGTPGSGT ASSSPGASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGAS PGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSP GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGTPGSGTASS SPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTA SSSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSAS TGTGPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGTPGSGTASSSPGSSPS ASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSP GSSPSASTGTGPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGASPGTSST GSPGASPGTSSTGSPGSSTPSGATGSPGTPG
AG1620	GSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTASS SPGASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSST GSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSPSAST GTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPS GATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPS

XTEN Name	Amino Acid Sequence
	ASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGAS PGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPG ASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSP GASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGASPGTSSTG SPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSST GSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGA TGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSAS TGTGPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSPGSSP SASTGTGPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGT PGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPG SSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSP GTPGSGTASSSPGSSTPSGATGSPGSST
AG1716	GASPGTSSTGSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGTPGSGTASS SPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSPGTPGSGTA SSSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPGSSPSAS TGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPG TSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPGSSP SASTGTGPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGS SPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSPSASTGTGP GASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTG SPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGAT GSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSAST GTGPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPS GATGSPGASPGTSSTGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGASP GTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGTP GSGTASSSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGS SPSASTGTGPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSP GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTG TGPGASPGTSSTGSPGASPGTSSTGSPGTPG
AG1812	GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGSSPSASTGTGPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSST GSPGSSPSASTGTGPGTPGSGTASSSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGA TGSPGSSTPSGATGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSG ATGSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPGTPGSGTASSSPGSSPSA STGTGPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGTPG SGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGAS PGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSPSASTGTGPGTPGSGTASSSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSST GSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSPSAST GTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSST PSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSS PSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPG ASPGTSSTGSPGSSTPSGATGSPGASP
AG1908	GSSPSASTGTGPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSPSASTGT GPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGTPGSGTA SSSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGSSTPSG ATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGASPGTSSTGSPGASPG TSSTGSPGTPGSGTASSSPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGTPG SGTASSSPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGATGSPGSS PSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTGTGPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASS

XTEN Name	Amino Acid Sequence
	SPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGASPGTSSTGSPGASPGTSST GSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSAST GTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGASPGT SSTGSPGTPGSGTASSSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSGATGSPGSSTP SGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGTPGSGTASSSPGSSP SASTGTGPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSPGA SPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSPSASTGTGPGSSTPSGATGSPG ASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSP GASPGTSSTGSPGSSPSASTGTGPGSSP
AG2004A	GSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTA SSSPGASPGTSSTGSPGSSTPSGATGSPGTPGSGTASSSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGASPG TSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSPGSSPSASTGTGPGSST PSGATGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGA SPGTSSTGSPGTPGSGTASSSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGTPGSGTASSSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSPSAST GTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGSSPSASTGTGPGSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGASPGTSSTGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGT PGSGTASSSPGSSPSASTGTGPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSP GSSPSASTGTGPGSSPSASTGTGPGASP
AE72B	SPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPG
AE72C	TSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEE GTSTEPSEGSAPG
AE108A	TEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS
AE108B	GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESG PGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP
AE144A	STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG TSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSPAGSPTSTEEGSPAGSPTSTEEGS
AE144B	SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSTEPSEGSAPG
AE180A	TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGS PTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPA TSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEP ATS
AE216A	PESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSES ATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESAT
AE252A	ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEP SEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPA TSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSE SATPESGPGTSTEPSE
AE288A	TPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTS

XTEN Name	Amino Acid Sequence
	ESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGS PAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESA
AE324A	PESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEP SEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGT STEPSEGSAPGTSTEPSEGSAPGSEPATS
AE360A	PESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGS PTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTS TEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGS EPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESAT
AE396A	PESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGT SESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPS
AE432A	EGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPG TSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGSEPATS
AE468A	EGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSE SATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPG TSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESAT
AE504A	EGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGS PTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPA GSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGS PAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEG SPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPS
AE540A	TPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS PAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESG PGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPES GPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEP

XTEN Name	Amino Acid Sequence
AE576A	TPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPG TSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSET PGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPES GPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESA
AE612A	GSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGS PTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGS PAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESAT
AE648A	PESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEP SEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESAT
AE684A	EGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEP SEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPE SGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATS
AE720A	TSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS TEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGT SESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPE SGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATS GSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESA TPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG SPTSTEEGTSTE
AE756A	TSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTST

XTEN Name	Amino Acid Sequence
	EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS TEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGT SESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPE SGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATS GSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESA TPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG SPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSES
AE792A	EGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESA TPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTE PSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTS TEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATS GSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPAT SGSETPGTSESATPESGPGTSTEPS
AE828A	PESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESA TPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTE PSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSE SATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTS TEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESG PGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPAT SGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSES AT
AG72A	GPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSS TGSPGTPGSGTASS
AG72B	GSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTG SPGTPGSGTASSSP
AG72C	SPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSPGA
AG108A	SASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGA SPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASP
AG108B	PGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGAT GSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS
AG144A	PGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSS TGSPGASPGTSSTGSPGTPGSGTASSS
AG144B	PSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSS PSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGASPGTSSTGSPGASP

XTEN Name	Amino Acid Sequence
AG180A	TSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPG TPGS
AG216A	TGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSG
AG252A	TSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPG TPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSP GSSTPSGATGSPGASPG
AG288A	TSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPG TPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSP GSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGS
AG324A	TSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTP GSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTG SPGSSPSASTGTGPGTPGSGTASSSPGSSTP
AG360A	TSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGA TGSPGASPG
AG396A	GATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGS STPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSP GTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGT
AG432A	GATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG TPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSP GSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTG SPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSST GSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSAST GTGPGTPGSGTASSSPGSSTPS
AG468A	TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTG TGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSAST GTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPG
AG504A	TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPG

XTEN Name	Amino Acid Sequence
	ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTG TGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSAST GTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGT SSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTP
AG540A	TSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASP GTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTP GSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTG TGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSAST GTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGASPG
AG576A	TSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSP SASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGT SSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPG TSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSP SASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPG
AG612A	STGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGA SPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPG ASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSP GTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSS TGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPS ASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSS PSASTGTGPGSSPSASTGTGPGASPGTS
AG648A	GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSST PSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSP GASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSST GSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSST PSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSS TP
AG684A	TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSST PSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATG SPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPG

XTEN Name	Amino Acid Sequence
	SGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGAS PGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGT PGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPG
AG720A	TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSST PSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGA SPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPG ASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSP GASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTG SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTG TGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTS STGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGS GTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSP SASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGS SPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGASPG
AG756A	TSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPG TPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSP GSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSG ATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPG
AG792A	TSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPG TPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSP GSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSG ATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGSSTPSGATGSPGSSPSASTGTGPGASPG
AG828A	TSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPG TPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSP GSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSG ATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGSSTP

XTEN Name	Amino Acid Sequence
AE869	GSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPA GSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGS PAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPG SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPS EGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGR
AE144_R1	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG SPTSTEEGTSESATPESGPGTESASR
AE288_R1	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPG TSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPSASR
AE432_R1	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG SPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSE PATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGS PAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTESASR
AE576_R1	SAGSPTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGS PAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPG SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPS EGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPSASR
AE864_R1	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG SPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSE PATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGS PAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESA TPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTE PSEGSAPGSEPATSGSETPGTSESATPESGPGTESASR
AF864_R1	SAGSPGSTSSTAESPGPGSTSSTAESPGPGSTSESPSGTAPGSTSSTAESPGPGSTSST AESPGPGTSTPESGSASPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSE

XTEN Name	Amino Acid Sequence
	SPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGSTS ESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPSGTAPGTS TPESGSASPGSTSSTAESPGPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGS TSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPG STSESPSGTAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAP GSTSESPSGTAPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSAS PGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGSTSSTAESPGPGTSTPESGSA SPGSTSESPSGTAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSSTAESP GPGTSPSGESSTAPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGS ASPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGSTSSTAESPGPGSTSSTAE SPGPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPS GTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGSTSESP SGTAPGSTSSTAESPGPGTSPSGESSTAPGTSSASR
AG864_R1	SAGSPGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGAS PGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGT GPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGS STPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSP GTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASSASR

[00233] In some embodiments wherein the XTEN has less than 100% of its amino acids consisting of 4, 5, or 6 types of amino acid selected from glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P), or less than 100% of the sequence consisting of the sequence motifs from Table 1 or the XTEN sequences of Tables 2, 3 and 22-25 the other amino acid residues of the XTEN are selected from any of the other 14 natural L-amino acids, but are preferentially selected from hydrophilic amino acids such that the XTEN sequence contains at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least about 99% hydrophilic amino acids. An individual amino acid or a short sequence of amino acids other than glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P) may be incorporated into the XTEN to achieve a needed property, such as to permit incorporation of a restriction site by the encoding nucleotides, or to facilitate linking to a payload component, or incorporation of a cleavage sequence. As one exemplary embodiment, described more fully below, the invention provdes XTEN that incorporates from 1 to about 20, or 1 to about 15, or 1 to about 10, or 1 to 5 lysine residues wherein the reactive lysines are utilized for linking to cross-linkers or payloads, as described herein. In another embodiment, described more fully below, the XTEN incorporates from 1 to about 20, or 1 to about 15, or 1 to about 10, or 1 to 5 cysteine residues wherein the reactive cysteines are utilized for linking to cross-linkers or payloads, as described herein. In

another embodiment, the XTEN incorporates from 1 to about 20 cysteine and lysine residues wherein the lysines and cysteines are utilized for linking to different cross-linkers or payloads, as described herein. In another embodiment, the XTEN incorporations 1, 2, 3, 4, 5 or more arginine residues that are not followed by proline residues to provide cleavage sequences that can be cleaved by trypsin to create XTEN segments, described more fully herein, below. The XTEN amino acids that are not glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P) are either interspersed throughout the XTEN sequence, are located within or between the sequence motifs, or are concentrated in one or more short stretches of the XTEN sequence such as at or near the N- or C-terminus. As hydrophobic amino acids impart structure to a polypeptide, the invention provides that the content of hydrophobic amino acids in the XTEN utilized in the conjugation constructs will typically be less than 5%, or less than 2%, or less than 1% hydrophobic amino acid content. Hydrophobic residues that are less favored in construction of XTEN include tryptophan, phenylalanine, tyrosine, leucine, isoleucine, valine, and methionine. Additionally, one can design the XTEN sequences to contain less than 5% or less than 4% or less than 3% or less than 2% or less than 1% or none of the following amino acids: methionine (to avoid oxidation), asparagine and glutamine (to avoid desamidation). In other embodiments, the amino acid content of methionine and tryptophan in the XTEN component used in the conjugation constructs is typically less than 5%, or less than 2%, and most preferably less than 1%. In other embodiments, the XTEN of the subject XTEN conjugates will have a sequence that has less than 10% amino acid residues with a positive charge, or less than about 7%, or less that about 5%, or less than about 2% amino acid residues with a positive charge, the sum of methionine and tryptophan residues will be less than 2%, and the sum of asparagine and glutamine residues will be less than 5% of the total XTEN sequence.

3. Cysteine- and Lysine-Engineered XTEN Sequences

[00234] In another aspect, the invention provides XTEN with defined numbers of incorporated cysteine or lysine residues; "cysteine-engineered XTEN" and "lysine-engineered XTEN", respectively. It is an object of the invention to provide XTEN with defned numbers of cysteine and/or lysine residues to permit conjugation between the thiol group of the cysteine or the epsilon amino group of the lysine and a reactive group on a payload or a cross-linker to be conjugated to the XTEN backbone. In one embodiment of the foregoing, the XTEN of the invention has between about 1 to about 100 lysine residues, or about 1 to about 70 lysine residues, or about 1 to about 50 lysine residues, or about 1 to about 30 lysine residues, or about 1 to about 20 lysine residues, or about 1 to about 10 lysine residues, or about 1 to about 5 lysine residues, or 1 to about 3 lysine residues, or alternatively only a single lysine residue. In another embodiment of the foregoing, the XTEN of the invention has between about 1 to about 100 cysteine residues, or about 1 to about 70 cysteine residues, or about 1 to about 50 cysteine

residues, or about 1 to about 30 cysteine residues, or about 1 to about 20 cysteine residues, or about 1 to about 10 cysteine residues, or about 1 to about 5 cysteine residues, or 1 to about 3 cysteine residues, or alternatively only a single cysteine residue. In another embodiment of the foregoing, the XTEN of the invention has about 1 to about 10 lysine residues and about 1 to about 10 cysteine residues. Using the foregoing lysine- and/or cysteine-containing XTEN, conjugates can be constructed that comprise XTEN, an optional cross-linker, plus a payload useful in the treatment of a condition in a subject wherein the maximum number of molecules of the payload agent linked to the XTEN component is determined by the numbers of lysines, cysteines or other amino acids with a reactive side group (e.g., a terminal amino or thiol) incorporated into the XTEN.

[00235] In one embodiment, the invention provides cysteine-engineered XTEN where nucleotides encoding one or more amino acids of an XTEN are replaced with a cysteine amino acid to create the cysteine-engineered XTEN gene. In another embodiment, the invention provides cysteine-engineered XTEN where nucleotides encoding one or more cysteine amino acids are inserted into an-XTEN encoding gene to create the cysteine-engineered XTEN gene. In other cases, oligonucleotides encoding one or more motifs of about 9 to about 14 amino acids comprising codons encoding one or more cysteines are linked in frame with other oligos encoding XTEN motifs or full-length XTEN to create the cysteine-engineered XTEN gene. In one embodiment of the foregoing, where the one or more cysteines are inserted into an XTEN sequence during the creation of the XTEN gene, nucleotides encoding cysteine can be linked to codons encoding amino acids used in XTEN to create a cysteine-XTEN motif with the cysteine(s) at a defined position using the methods described herein (see Example 61 and FIGS. 40-41), or by standard molecular biology techniques, and the motifs subsequently assembled into the gene encoding the full-length cysteine-engineered XTEN. In such cases, where, for example, nucleotides encoding a single cysteine are added to the DNA encoding a motif selected from Table 1, the resulting motif would have 13 amino acids, while incorporating two cysteines would result in a motif having 14 amino acids, etc. In other cases, a cysteine-motif can be created *de novo* and be of a pre-defined length and number of cysteine amino acids by linking nucleotides encoding cysteine to nucleotides encoding one or more amino acid residues used in XTEN (e.g., G, S, T, E, P, A) at a defined position, and the encoding motifs subsequently assembled by annealing with other XTEN-encoding motif sequences into the gene encoding the full-length XTEN, as described herein and illustrated in FIGS. 7-8. In cases where a lysine-engineered XTEN is utilized to make the conjugates of the invention, the approaches described above would be performed with codons encoding lysine instead of cysteine. Thus, by the foregoing, a new XTEN motif can be created that could comprise about 9-14 amino acid residues and have one or

more reactive amino acids; i.e., cysteine or lysine. Non-limiting examples of motifs suitable for use in an engineered XTEN that contain a single cysteine or lysine are:

GGSPAGSCTSP
GASASCAPSTG
TAEAAGCGTAEAA
GPEPTCPAPSG
GGSPAGSKTSP
GASASKAPSTG

However, the invention contemplates motifs of different lengths, such as those of Table 5 and Table 11, for incorporation into XTEN.

[00236] In such cases where a gene encoding an XTEN with one or more cysteine and/or lysine motifs is to be constructed from existing XTEN motifs or segments, the gene can be designed and built by linking existing "building block" polynucleotides encoding both short- and long-length XTENs; e.g., AE48, AE144, AE288, AE432, AE576, AE864, AM48, AM875, AE912, AG864, or the nucleotides encoding the 36'mers of Examples 1-4, and Tables 22-25, which can be fused in frame with the nucleotides encoding the cysteine- and/or lysine-containing motifs or, alternatively, the cysteine- and/or lysine-encoding nucelotides can be PCR'ed into an existing XTEN sequence (as described more fully below and in the Examples) using, for example, nucleotides encoding the islands of Tables 4 and 5 to build an engineered XTEN in which the reactive cysteine and/or lysines are placed in one or more designed locations in the sequence in the desired quantity. Non-limiting examples of such engineered XTEN are provided in Table 3. Thus, in one embodiment, the invention provides an XTEN sequence having at least about 80% sequence identity, or at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity, or is identical to a sequence or a fragment of a sequence selected from of Table 3, when optimally aligned. However, application of the cysteine- or lysine-engineered methodology to create XTEN encompassing cysteine or lysine residues is not meant to be constrained to the precise compositions or range of composition identities of the foregoing embodiments. As will be appreciated by those skilled in the art, the precise location and numbers of incorporated cysteine or lysine residues in an XTEN can be varied without departing from the invention as described.

Table 3: Cysteine- and lysine-engineered XTEN

Name	Amino Acid Sequence
Seg 1	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPAT

Name	Amino Acid Sequence
	SGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPR
Seg 2	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 3	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 4	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPTA EAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPTAEAA GCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESA TPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCG TAEAAR
Seg 5	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEA AGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP

Name	Amino Acid Sequence
	GTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPG SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTS TEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSE PATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSE SATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG SPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPS EGSAPTAEAAGCGTAEAAR
Seg 6	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTETAEAAGCGTAEAAPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSTAEAAGCGTAEAAAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGSTAEAAGCGTAEAAPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSE PATSGSETPGTSESATTAEAAGCGTAEAAPESGPGSPAGSPTSTEEGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEP ATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 7	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEA AGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG TSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEETA EAAGCGTAEAAGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPG SEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 8	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSTAEAAGCGTAEAAESATPESGPGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSTEPSTAEAAGCGTAEAAEGSAPGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSTAEAAGCGTAEAA APGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTTAEAAGCGTAEAASTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSEPATAEAAGCGTAEAATSGSETPGTSESATPESGPGTSTEPSEGSA PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPETAEAAGCGTAEAASGPGTSESATPESG PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP

Name	Amino Acid Sequence
	GTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 9	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 10	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 11	ATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 12	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTTAEAAGCGTAEAAEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATTAEAAGCGTAEAASGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGTSESATPESGPGTSTEP

Name	Amino Acid Sequence
	SEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 13	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPAT SGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 14	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGGKPGGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPA GSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPR
Seg 15	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPA GSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPGGKPGR
Seg 16	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGGKPGGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE

Name	Amino Acid Sequence
	EGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG TSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEP ATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGGKPGR
Seg 17	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGGKPGGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGGTSESATPESGPGSEPATS GSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPT STEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTS TEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 18	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGGKPGGTSESATPESGPGSEPAT SGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSP TSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEGSAPGGKPGGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGS PTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGKPGGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPA GSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPA TSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPAT SGSETPGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 19	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEGGKP GPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGS PTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSGGKPGAPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSP AGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSGGKPGPAGSPTSTEE GSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATGGKPGPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPG SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 20	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGGKPGGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGGKPGG SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSP

Name	Amino Acid Sequence
	AGSPTSTEEGTSTEPSEGSAPGGKPGGTSESATPESGPGSEPATSGSETPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGGKPGGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESA TPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 21	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSGGKPGESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSGGKPGEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPG SPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGTSTEPSEGSGGKPGAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGTGGKPGSTEPSEGSAPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPAGGKPGTSGSETPGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPEGGKPGSGPGTSESATPESGPG TSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 22	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPA GSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPR
Seg 23	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAP GTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPG SPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGGKPGR
Seg 24	AGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEE

Name	Amino Acid Sequence
	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGGKPGGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG TSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEP ATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPR
Seg 25	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTGGKPGEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSESATPESGPGSEPATGGKPGSGSETPGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTST EEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEG TSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGS EPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPR
Seg 26	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGT STEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGGKPGGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPA GSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPGGKPGR
Seg 27	AEATTAAGGAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSP AGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGS PTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSA PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPG SEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 28	AEATTAAGGATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG SEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSP

Name	Amino Acid Sequence
	AGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSES ATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPS EGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSA PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPG SEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 29	AEATTAAGGATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG SEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSP AGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSES ATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPS EGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPAT SGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSE GSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPES GPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESG PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEA AR
Seg 30	AEATTAAGGATAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG SEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSP AGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSES ATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPAT SGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSE GSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSG SETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPES GPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP TAEAAGCGTAEAAR
Seg 31	ATGTATSEGSPEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSP AGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGS PTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSA PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPG SEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGS

Name	Amino Acid Sequence
	EPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 32	ATGTATSEGSPETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESG PGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 33	ATGTATSEGSPETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSE PATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESAT PESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATP ESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGT AEAAR
Seg 34	ATGTATSEGSPETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEP SEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPAT SGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESAT PESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APTAEAAGCGTAEAAR
Seg 35	EPTAATTGESAGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSP AGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGS PTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPES

Name	Amino Acid Sequence
	GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSA PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPG SEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 36	EPTAATTGESAGTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESG PGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 37	EPTAATTGESAGTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSE PATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESAT PESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATP ESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGT AEAAR
Seg 38	EPTAATTGESAGTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEP SEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPAT SGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESAT PESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APTAEAAGCGTAEAAR
Seg 39	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST

Name	Amino Acid Sequence
	EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 40	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 41	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESAT PESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCG TAEAAR
Seg 42	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPTAEAAGCGTAEAAR
Seg 43	ATGTATSEGSPEEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSET

Name	Amino Acid Sequence
	PGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 44	ATGTATSEGSPEEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 45	ATGTATSEGSPEEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPG SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTS TEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESA TPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCG TAEAAR
Seg 46	ATGTATSEGSPEEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGS APGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTS TEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSE PATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSE SATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAG

Name	Amino Acid Sequence
	SPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPS EGSAPTAEAAGCGTAEAAR
Seg 47	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPRPRPRPRP
Seg 48	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAARPRPRPRP
Seg 49	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESAT PESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCG TAEAARPRPRPRP
Seg 50	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST

Name	Amino Acid Sequence
	EPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPTAEAAGCGTAEAARPRPRPRP
Seg 51	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPR
Seg 52	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAG SPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 53	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESAT PESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCG TAEAAR
Seg 54	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP

Name	Amino Acid Sequence
	GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPTAEAAGCGTAEAAR
Seg 55	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGGKPGGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPT AEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTS TEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGKP GR
Seg 56	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSES ATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGGKPGR
Seg 57	AEATTAAGGAEEEGGKPGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATS GSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESG PGGKPGGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPS EGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSE GSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSE GSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 58	AEATTAAGGAEEETAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEG

Name	Amino Acid Sequence
	SAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGGKPGGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPT AEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGT SESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTS TEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGKP GR
Seg 59	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 60	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 61	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPTAE AAGCGTAEAAR
Seg 62	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 63	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 64	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST

Name	Amino Acid Sequence
	EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 65	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPTAE AAGCGTAEAAR
Seg 66	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAR
Seg 67	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 68	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGGKPGR
Seg 69	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGGK PGR
Seg 70	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 71	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPT STEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 72	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPGGKPGR
Seg 73	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP

Name	Amino Acid Sequence
	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGGK PGR
Seg 74	AEATTAAGGAEEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTE EGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGGKPGR
Seg 75	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTP SGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGAT GSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPR
Seg 76	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSST PSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGAT GSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 77	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 78	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPT AEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP

Name	Amino Acid Sequence
	GSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG SSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGS STPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPTAEA AGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTP GSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASP GTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPG TSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSA STGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAG CGTAEAAR
Seg 79	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPTAEAAGCGTAE AAGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGS PGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASS SPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGS PGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPG TPGSGTASSSPGSSTPSGATGSPTAEAAGCGTAEAAGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGA SPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGAS PGTSSTGSPTAEAAGCGTAEAAR
Seg 80	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTAEAAGCGTAEAATSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GSSPSASTGTTAEAAGCGTAEAAGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSP GASPGTSSTGSPGTTAEAAGCGTAEAAPGSGTASSSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGASPGTSTAEAAGCGTAEAASTGSPGTPGSGTASSSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGS PGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 81	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTA SSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTG TGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSST GSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTA EAAGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGAT GSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGS PTAEAAGCGTAEAAGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSST GSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR

Name	Amino Acid Sequence
Seg 82	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASTAEAAGCGTAEAAPGTSSTGSPGASPGTSSTGSPGTPGSGTA SSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTG TGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGTAEAAGCGTAEAAATGSPGASPGTS STGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSS TGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGTAEAAGCGTA EAASPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSS TGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTG TGPGATAEAAGCGTAEAASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTS STGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGTPGSGTASSSPGSSTPTAEAAGCGTAEAASGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTAEAAGCGTAEAATGPGASPGT SSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSAS TGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGC GTAEAAR
Seg 83	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSST PSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGAT GSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPR
Seg 84	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSS TGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTAS SSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTG PGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPG ASPGTSSTGSPTAEAAGCGTAEAAR
Seg 85	ATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSST PSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGAT GSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST

Name	Amino Acid Sequence
	PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 86	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTTAEAAGCGTAEAAPSGATGSPGSST PSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSTAEAAGCGTAEAAGATGSPGSS TPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTS STGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 87	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTP SGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGAT GSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 88	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGS SPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGAS PGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPG SGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPS ASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSA STGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGA TGSPGASPGTSSTGSPR
Seg 89	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPG

Name	Amino Acid Sequence
	ASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGT PGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSS PSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPS ASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGASPGTSSTGSPGGKPGR
Seg 90	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGS PGASPGTSSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSS TGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGAT GSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGASPGTSSTGSPGGKPGR
Seg 91	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGGKPGGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGGKPGGTPGSGTASSSPGS STPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSS TPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSST PSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTP SGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGASPGTSSTGSPGGKPGR
Seg 92	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGGKPGGSSPSASTGTGPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPS GATGSPGASPGTSSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGA SPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGGK PGGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSP GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPG SSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGGKPGR
Seg 93	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGGG KPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGGKPGGP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPG

Name	Amino Acid Sequence
	SSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGS STPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTGGKPGPGSGTAS SSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGS PGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSGGKPGSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTS STGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGGKPGR
Seg 94	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGG KPGGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGT GPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGS PGSSTPSGATGSPGASPGTSSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGT ASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGGKPGGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGGKPGGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSP GASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPG TPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGGKPGR
Seg 95	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASGGKPGPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGGGKPGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGT GPGTPGSGTASSSPGASPGTSSTGGGKPGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPS GATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGAGGKPGSPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPGGKPGSGATGSPGTPGSGTASS SPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGS PGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGGGKPGTGPGASPGT SSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSAS TGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGGKPGR
Seg 96	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPG ASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGT PGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSS PSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSP SASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPS ASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGASPGTSSTGSPR
Seg 97	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP

Name	Amino Acid Sequence
	GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSS TGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTAS SSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTG PGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPG ASPGTSSTGSPGGKPGR
Seg 98	AGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGA TGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASS SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGS PGASPGTSSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSS TGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGAT GSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGASPGTSSTGSPR
Seg 99	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTGGKPGPSGATGSPGSSTPSGATGSP GASPGTSSTGSPGTPGSGTASSSPGSSTPSGGKPGGATGSPGSSTPSGATGSPGSSTPSG ATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSS TGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGAT GSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGASPGTSSTGSPR
Seg 100	AGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGT PGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASP GTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPG TSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPGGKPGGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGS SPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGAS PGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPG SGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPS ASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSA STGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGA TGSPGASPGTSSTGSPGGKPGR
Seg 101	AEATTAAGGAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGS STPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASP

Name	Amino Acid Sequence
	GTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTP SGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSG ATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGA TGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 102	AEATTAAGGATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTG PGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPG SSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGS SPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSP SASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTP SGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGA TGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTG SPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 103	AEATTAAGGATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTG PGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPG SSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGS SPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSP SASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTP SGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSS TGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGT AEAAR
Seg 104	AEATTAAGGATAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTG PGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPG SSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGS SPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGAS PGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPG TSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST PSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSA STGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTS STGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSS

Name	Amino Acid Sequence
	TGSPTAEAAGCGTAEAAR
Seg 105	ATGTATSEGSPEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSP GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGA SPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPS GATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 106	ATGTATSEGSPETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS PSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTP SGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 107	ATGTATSEGSPETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS PSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSS TGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGT AEAAR
Seg 108	ATGTATSEGSPETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPG TSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST

Name	Amino Acid Sequence
	PSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSA STGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTS STGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSS TGSPTAEAAGCGTAEAAR
Seg 109	EPTAATTGESAGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSP GSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGA SPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPS GATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 110	EPTAATTGESAGTAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS PSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTP SGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 111	EPTAATTGESAGTAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS PSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTP SGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 112	EPTAATTGESAGTAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGT GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGA SPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGA

Name	Amino Acid Sequence
	SPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSS TPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASP GTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPG TSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST PSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSA STGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTS STGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSS TGSPTAEAAGCGTAEAAR
Seg 113	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTP SGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSS TPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTS STGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 114	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 115	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 116	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS

Name	Amino Acid Sequence
	PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGS STPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPG TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPTAEAAGCGTAEAAR
Seg 117	ATGTATSEGSPEEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG TPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPG SSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 118	ATGTATSEGSPEEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSAST GTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTA SSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG SSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGS STPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTP SGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 119	ATGTATSEGSPEEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSAST GTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTA SSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP GSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG SSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGS STPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTP SGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR

Name	Amino Acid Sequence
	CGTAEAAR
Seg 120	ATGTATSEGSPEEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSAST GTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTA SSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTAS SSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSST GSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSP GASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSP GSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPG SSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGS SPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGAS PGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASP GTSSTGSPTAEAAGCGTAEAAR
Seg 121	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSS TPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTS STGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPRPRPRPRP
Seg 122	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAARPRPRPRP
Seg 123	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAARPRPRPRP
Seg 124	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAARPRPRPRP

Name	Amino Acid Sequence
	SGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGT SSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSAS TGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGC GTAEAARPRPRPRP
Seg 124	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGS STPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPG TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPTAEAAGCGTAEAARPRPRPRP
Seg 125	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGSS TPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPS GATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTS STGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTA SSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPR
Seg 126	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGTSS TGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTAS SSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 127	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGS SPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSS

Name	Amino Acid Sequence
	TPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPG SSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGA SPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPG SGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGT SSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSAS TGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGC GTAEAAR
Seg 128	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGS STPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPG TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPTAEAAGCGTAEAAR
Seg 129	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGGKPGGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSS TGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGS PGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP TAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTG PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPG SSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGG KPGR
Seg 130	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGS STPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGAS PGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPTAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSS TPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPS ASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPG TSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGT SSTGSPGGKPGR
Seg 131	AEATTAAGGAEEEGGKPGGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGS

Name	Amino Acid Sequence
	GTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSG ATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSAST GTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSPGGKPGGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPS ASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPS GATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSG ATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGT ASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGGKPGGTP GSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSST PSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 132	AEATTAAGGAEEETAEAAGCGTAEAAGASPGTSSTGSPGSSPSASTGTGPGSSPSASTG TGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGGKPGGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSS TGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSST GSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATG SPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGS PGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSP TAEAAGCGTAEAAGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATG SPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTG PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGP GASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPG SSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGG KPGR
Seg 133	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 134	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 135	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGAS PGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGAS PGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPTAE AAGCGTAEAAR
Seg 136	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 137	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS

Name	Amino Acid Sequence
	PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 138	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 139	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPTAE AAGCGTAEAAR
Seg 140	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPTAEAAGCGTAEAAR
Seg 141	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGGKPGR
Seg 142	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGGKPGR
Seg 143	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGG KPGR
Seg 144	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGGKPGR
Seg 145	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP

Name	Amino Acid Sequence
	GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPS GATGSPGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGT SSTGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGGKPGR
Seg 146	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTP GSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPG SGTASSSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGGKPGR
Seg 147	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGS STPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGG KPGR
Seg 148	AEATTAAGGAEEEGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGGKPGR
Seg 149	GSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPG SEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGGGSPAGSCTSPGGSPAGSPTSTEEGTSESATPESGPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTE PSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPS EGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATP ESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPG
Seg 150	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTST EPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPS EGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEG SAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPES GPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGT STEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGA SASCAPSTGGGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTS TEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPG
Seg 151	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGT SESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTS TEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEP

Name	Amino Acid Sequence
	SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGGGSPAGSCTSPGGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPG
Seg 152	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGGPEPTCPAPS GGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGT STEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPG
Seg 153	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTE PSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGGSPAGSCTSPGGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGGSPAGSCTSPGGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPG SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG
Seg 154	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGGASASCAPST GGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGT STEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGGASASCAPSTGGGSEPATSGSETPGTSESA TPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATS GSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSE GSAPG
Seg 155	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGGSPAGSCTS PGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT

Name	Amino Acid Sequence
	STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAES PGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTSSTAESPG PGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSTSSTAESPGP GTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPG
Seg 156	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGASASCAPST GGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGPEPTGPAPSGGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESATPE SGPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGSPAGSPTST EEGSTSSTAESPGPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAP GTSPSGESSTAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT SPSGESSTAPGTSPSGESSTAPGTSPSGESSTAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGASASGAPSTGGTSPSGESSTAPGSTSSTAESPGPGTSPSGE SSTAPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSSPSASTGTGPGSSTPSGA TGSPGASPGTSSTGSPGTSTPESGSASPGTSPSGESSTAPGTSPSGESSTAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPG SEPATSGSETPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGATGSPGSTSESPSGTAPGT SPSGESSTAPGSTSSTAESPGPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPG
Seg 157	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGPEPTCPAPS GGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAES PGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTSSTAESPG PGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSTSSTAESPGP GTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPG
Seg 158	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGPEPTCPAPS GGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE

Name	Amino Acid Sequence
	PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAES PGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTSSTAESPG PGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSTSSTAESPGP GTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGGPEPTCPAPSGGMAEPAGSPTSTEEGASPGTSSTGSPG SSTPSGATGSPGSSTPSGATGSPG
Seg 159	GSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPG SEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGS EPATSGSETPGTSTEPSEGSAPGGGSPAGSKTSPGGSPAGSPTSTEEGTSESATPESGPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTE PSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPS EGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATP ESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGS APGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGP GSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPG
Seg 160	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPG TSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGT STEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTST EPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPS EGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEG SAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPES GPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSET PGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPG TSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGT STEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGA SASKAPSTGGGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTS TEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPG
Seg 161	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGT SESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTS TEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTST EPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGGGSPAGSKTSPGGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPG
Seg 162	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGGASASKAPST GGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEE

Name	Amino Acid Sequence
	GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGT STEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPG
Seg 163	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTE PSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGGSPAGSKTSPGGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGGSPAGSKTSPGGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPG SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG
Seg 164	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGGGSPAGSKTS PGGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGT STEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGGGSPAGSKTSPGGSEPATSGSETPGTSESAT PESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSG SETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGS APG
Seg 165	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGGSPAGSKTS PGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAES PGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTSSTAESPG PGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSTSSTAESPGP GTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPG

Name	Amino Acid Sequence
Seg 166	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGASASKAPST GGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGPEPTGPAPSGGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESATPE SGPGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGSPAGSPTST EEGSTSSTAESPGPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAP GTSPSGESSTAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT SPSGESSTAPGTSPSGESSTAPGTSPSGESSTAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSTP SGATGSPGASPGTSSTGSPGASASGAPSTGGTSPSGESSTAPGSTSSTAESPGPGTSPSGE SSTAPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSSPSASTGTGPGSSTPSGA TGSPGASPGTSSTGSPGTSTPESGSASPGTSPSGESSTAPGTSPSGESSTAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASP GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPG SEPATSGSETPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGATGSPGSTSESPSGTAPGT SPSGESSTAPGSTSSTAESPGPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPG
Seg 167	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGASASKAPST GGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAES PGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTSSTAESPG PGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSTSSTAESPGP GTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPG
Seg 168	MAEPAGSPTSTEEGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGGASASKAPST GGGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTS ESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGSEP ATSGSETPGSPAGSPTSTEEGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTE PSEGSAPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPS EGSAPGASASGAPSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAES PGPGSTSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGT GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTSSTAESPG PGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGSTSSTAESPGP GTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTSESATPESGPGTS TEPSEGSAPGTSTEPSEGSAPGGASASKAPSTGGMAEPAGSPTSTEEGASPGTSSTGSPG SSTPSGATGSPGSSTPSGATGSPG
Seg 169	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSP

Name	Amino Acid Sequence
	AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTE PSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGGSPAGSCTSPGGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSP TSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGGGSPAGSKTSPGGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTE EGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPG SEPATSGSETPGTSESATPESGPGTSTEPSEGSAPG
Seg 170	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGGGSPAGSCTS PGGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSA PGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGTSTEPSEGSAPGGGSPAGSCTSPGSEPATSGSETPGTSESATPESGPG SEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGS EPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGGG SPAGSCTSPGGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTS TEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGGGSPAGSCTSPGGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPA TSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPS EGSAPG
Seg 171	MAEPAGSPTSTEEGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGGGSPAGSKTS PGGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSA PGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGTSTEPSEGSAPGGGSPAGSKTSPGSEPATSGSETPGTSESATPESGPG SEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGS EPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGGG SPAGSKTSPGGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTS TEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGGGSPAGSKTSPGGSEPATSGSETPGTSE SATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPA TSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPS EGSAPG
Seg 172	SAGSPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESAT PESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGT AEAASASR
Seg 173	SAGSPGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEG TSESATPESGPGTSTEPSEGSAGPTKPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPTKPGTSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPG TSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGT SESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTST EPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPA

Name	Amino Acid Sequence
	TSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAG CGTAEAASASR
Seg 174	SAGSPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATS GSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESG PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SPAGSPTSTEEGTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPG SPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGT SESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSES ATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEP SEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAASASR
Seg 175	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPTAEAAGCGTAEAAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTAEAAGCGTAEAASTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPATAEAAGC GTAEAASPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATTAEAAGCGTAEAASET PGTSESATPESGPGSEPATSGSETPGTSESATPESGTAEAAGCGTAEAAGSPAGSPTSTE EGTSESATPESGPGSEPATSGSETPGTTAEAAGCGTAEAAAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSET PGSEPATSGTAEAAGCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSET PTAEAAGCGTAEAASASR
Seg 176	SAGSPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEP SEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESAT PESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSG SETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGT AEAASASR
Seg 177	SAGSPTAEAAGCGTAEAAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTAE AAGCGTAEAASTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPATAEAAGCGTAE AASPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATTAEAAGCGTAEAASETPGTS ESATPESGPGSEPATSGSETPGTSESATPESGTAEAAGCGTAEAAGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTTAEAAGCGTAEAAAGSPTSTEEGSPAGSPTSTEEGTS TEPSEGSAPGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSE PATSGTAEAAGCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAE AAGCGTAEAASASR
Seg 178	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPSASR
Seg 179	GSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGT

Name	Amino Acid Sequence
	SESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGS PTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGR
Seg 180	GSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGT SESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPTAEAAGKPGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAG SPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSG SETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPGK
Seg 181	SAGSPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATS GSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESG PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAG SPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSG SETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPSASR
Seg 182	CGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSA PGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETP GTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEG TSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGT STEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTS TEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSE SATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAG SPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEG SAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSE TPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESG PGTSTEPSEGSAPGR
Seg 183	MKNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGPGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTST EEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTE

Name	Amino Acid Sequence
	EGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPSASRSAHHHHHHHHH
Seg 184	MKNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPRPSASRSAGSPTAEAAGCGTA EAAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTAEAAGCGTAEAASTEPSE GSAPGTSESATPESGPGSPAGSPTSTEEGSPATAEAAGCGTAEAASPTSTEEGTSESATP ESGPGTSTEPSEGSAPGTSESATTAEAAGCGTAEAASETPGTSESATPESGPGSEPATSG SETPGTSESATPESGTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSG SETPGTTAEAAGCGTAEAAAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESTAE AAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGTAEAAGCGTAE AATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAEAASASRS AHHHHHHHH
Seg 185	MKNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPG TSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGT SESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTS TEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPTAEAAG CGTAEAAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTAEAAGCGTAEAAS TEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPATAEAAGCGTAEAASPTSTEEGTS ESATPESGPGTSTEPSEGSAPGTSESATTAEAAGCGTAEAASETPGTSESATPESGPGSE PATSGSETPGTSESATPESGTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSE PATSGSETPGTTAEAAGCGTAEAAAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTS ESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGTAEAAG CGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAEAA SASRSAHHHHHHHHH
Seg 186	GSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPG TSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGT SESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTS TEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTST EPSEGSAPTAEAAGKPGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAG SPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSG SETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPGK
Seg 187	SAGSPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGS PTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATS GSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESG PGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG SPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGS EPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAG SPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSG SETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPSASR

Name	Amino Acid Sequence
Seg 188	SAGSPTEGTSTEPSEGSAPGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPA TSGSETPGSEPATSGTAEAAGCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPA TSGSETPTAEAAGCGTAEAASASR
Seg 189	SAGSPTPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSET PGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAE AASASR
Seg 190	SAGSPTGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPS EGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATP ESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEG SAPGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGT AEAASASR
Seg 191	SAGSPTPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSP TSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGTA EAAGCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGT AEAASASR
Seg 192	SAGSPGSTSSTAESPGPGSTSSTAESPGPGCTSESPSGTAPGSTSSTAESPGPGSTSSTAES PGPGTSTPESGSASPGSTSCSPSGEAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTA PETSPSGESCTAPGSTSASR
Seg 193	SAGSPGTPGSGTASSSPGSSTPSGATGSPGCAGSGTASSSPGSSTPSGATGSPGTPGSGT ASSSPGSSTPSGATGSPGSSTCSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSS TGSPGTPGSGTACSSPGSSSASR
Seg 194	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSET PGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPA GSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESA TPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPES GPGTESASK
Seg 195	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTACSEGSAPSASR
Seg 196	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATP ESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEG SAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSCASASR

Name	Amino Acid Sequence
Seg 197	SAGSPGSCAGSPTSTEEGTSESACPESGPGTSTEPSEGSCPGSPAGSPTSTEEGTCTEPSE GSAPGTSTEPCSGSAPGTSESATPESCPGSEPATSGSETPGSCPATSGSETPGSPAGSCTS TEEGTSESATPESCPGTESASR
Seg 198	SAGSPTGCGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGS PTSTEEGSPAGSPTSTEEGTSCTPSEGSAPGTSESATPESGPGTSESATPESGPGTSESAT PESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGSEPATSGSETPGTSESATPESGPGTSTEPSCGSAPSASR
Seg 199	SAGSPTGCGSEPATSGSETPGTSESATPESGPGSEPATSGSCTPGTSESATPESGPGTSTE PSEGSAPGSPAGSPCSTEEGTSESATPESGPGSEPATSGSETPGTSESCTPESGPGSPAGS PTSTEEGSPAGSPTSTEEGTSCTPSEGSAPGTSESATPESGPGTSESATPESGPGCSESAT PESGPGSEPATSGSETPGSEPATSGSETCGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSE GCAPGSEPATSGSETPGTSESATPESGPGTSTEPSCGSAPSASR

[00237] In another embodiment, the invention provides inserts of lysine as part of a longer sequence defined as a lysine island. Examples of lysine island are shown in Table 4. The benefit of flanking all lysine residues in an XTEN with similar or identical sequence is that it results in a more uniform chemical reactivity for each lysine. Another benefit results from the ability to perform peptide mapping to measure the degree of payload linking. Examples include the islands I_L6, I_L7, and I_L8 of Table 4. These islands comprise glutamate residues that facilitate peptide mapping using GluC protease. In another embodiment, the invention provides inserts of cysteine as part of a longer sequence defined as a cysteine island. Examples of cysteine island are shown in Table 5. The benefit of flanking all cysteine residues in an XTEN with similar or identical sequence is that it results in a more uniform chemical reactivity for each cysteine. Another benefit results from the ability to perform peptide mapping to measure the degree of payload conjugation. Examples include islands I_C4, I_C7, I_C8, and I_C9 of Table 5. These islands comprise glutamate residues that facilitate peptide mapping using GluC protease. The islands can be inserted into constructs encoding the existing XTEN by conventional PCR methods, as described above and in the Examples. Oligonucleotides encoding the islands can be inserted into constructs encoding the existing XTEN by conventional PCR methods. For example, in one embodiment, where an existing full-length XTEN gene is to be modified with nucleotides encoding one or more reactive cysteine or lysine residues, an oligonucleotide can be created that encodes a cysteine or lysine and that exhibits partial homology to and can hybridize with one or more short sequences of the XTEN, resulting in a recombination event and substitution of a cysteine or the lysine codon for an existing codon of the XTEN gene (see, e.g., Examples 6 and 7 for a description of the general methods). In one exemplary embodiment, the recombination results in a replacement with the amino acid sequence GGSPAGSCTSP of the I_C1 island. However, the oligonucleotides can be designed to place the cysteine (or lysine) in a different location in the motif or to include a second cysteine (or lysine) in the motif. The cysteine- or lysine-encoding oligonucleotides can be designed to hybridize with a given sequence segment at different points along the known XTEN sequence to permit their insertion into an

XTEN-encoding gene. Thus, the invention contemplates that multiple XTEN gene constructs can be created with cysteines or lysines inserted at different locations within the XTEN sequence by the selection of restriction sites within the XTEN sequence and the design of oligonucleotides appropriate for the given location and that encode a cysteine or lysine, including use of designed oligonucleotides that result in multiple insertions in the same XTEN sequence. By the design and selection of one or more such oligonucleotides in consideration of the known sequence of the XTEN, and the appropriate use of the methods of the invention, the potential number of substituted reactive cysteine or lysine residues inserted into the full-length XTEN can be estimated and then confirmed by sequencing the resulting XTEN gene.

Table 4: Examples of lysine islands

Designator	Amino Acid Sequence
I_L1	GGSPAGSKPTSP
I_L2	GASASKPAPSTG
I_L3	PKP
I_L4	PPKPP
I_L5	GGKPG
I_L6	EGGKPGES
I_L7	EGGSPAGSKPTSPE
I_L8	EGASASKPAPSTGE

Table 5: Examples of cysteine islands

Designator	Sequence
I_C1	GGSPAGSCTSP
I_C2	GASASCAPSTG
I_C3	GPEPTCPAPSG
I_C4	TAEAAGCGTAEAA
I_C5	GECEP
I_C6	GRPCRP
I_C7	GETSPAGSCTSPTET
I_C8	TESGRPCRPSET
I_C9	GPEPTCPAPSEG

[00238] XTEN can be designed to comprise both lysine and cysteine residues for conjugation as illustrated in Figure 1D. This enables one to conjugate two different payloads to the same XTEN polymer using conjugations methods tailored to react with the functional group or linker attached to the cysteine or lysine. Such mixed payloads can have additive and/or synergistic pharmacologic effects when administered to a subject in a single composition. Alternatively, the mixed payloads can be a combination of a targeting moiety and an active payload in order to deliver the pharmacophore to a desired location in the subject. By controlling the number and position of lysine and cysteine residues one can control the number and position of conjugated payloads. This enables one to adjust the relative potency or selectivity of the payloads in the resulting XTEN-payload conjugate.

[00239] The design, selection, and preparation methods of the invention enable the creation of engineered XTEN that are reactive with electrophilic functionality. The methods to make the

subject conjugates provided herein enable the creation of XTEN-payload conjugates, XTEN-cross-linker conjugates, and XTEN-azide/alkyne reactant conjugates with the linker or payload molecules added in a quantified fashion at designated sites, as illustrated schematically in FIG. 1. Payloads, cross-linkers, and azide/alkyne reactants may be site-specifically and efficiently linked to the N- or C-terminus of XTEN, to cysteine-engineered XTEN with a thiol-reactive reagent, or to lysine-engineered XTEN of the invention with an amine-reactive reagent, and to an alpha amino group at the N-terminus of XTEN, as described more fully, below, and then are purified and characterized as shown schematically in FIG. 40 using, for example, the non-limiting methods described more specifically in the Examples.

4. Length of Sequence

[00240] In another aspect, the invention provides XTEN of varying lengths for incorporation into the compositions wherein the length of the XTEN sequence(s) are chosen based on the property or function to be achieved in the composition. Depending on the intended property or function, the XTEN-payload conjugates comprise short or intermediate length XTEN or longer XTEN sequences, or multimers of short, intermediate or longer XTEN that can serve as carriers. While not intended to be limiting, the XTEN or fragments of XTEN include short segments of about 6 to about 99 amino acid residues, intermediate lengths of about 100 to about 399 amino acid residues, and longer lengths of about 400 to about 1000 and up to about 3000 amino acid residues. Thus, the XTEN utilized as conjugation partners for incorporation into the subject conjugates encompass XTEN or fragments of XTEN with lengths of about 6, or about 12, or about 36, or about 40, or about 48, or about 72 or about 96, or about 144, or about 288, or about 400, or about 432, or about 500, or about 576, or about 600, or about 700, or about 800, or about 864, or about 900, or about 1000, or about 1500, or about 2000, or about 2500, or up to about 3000 amino acid residues in length. In other cases, the XTEN sequences can be about 6 to about 50, about 50 to about 100, about 100 to 150, about 150 to 250, about 250 to 400, about 400 to about 500, about 500 to about 900, about 900 to 1500, about 1500 to 2000, or about 2000 to about 3000 amino acid residues in length. The precise length of an XTEN incorporated into the subject XTEN-payload conjugates can vary without adversely affecting the biological activity of the conjugate. In one embodiment, one or more of the XTEN may be selected from one of the XTEN family sequences; e.g., AD, AE, AF, AG, AM, AQ, BC, or BD. In some embodiments, the XTEN utilized to create the subject conjugates comprise XTEN selected from any one of the sequences in Table 2, Table 3, and Tables 22-25, which may be linked to the payload component directly or via cross-linkers disclosed herein. In other embodiments, the one or more XTEN utilized to create the subject conjugates individually comprise an XTEN sequence having at least about 80% sequence identity, or alternatively 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity

compared to an XTEN selected from Tables 2, 3, 22-25 or a fragment thereof, when optimally aligned with a sequence of comparable length. In some embodiments, the subject conjugates comprise 2, 3, 4, or more XTEN sequence, wherein the cumulative length of the residues in the XTEN sequences is greater than about 100 to about 3000, or about 400 to about 2000, or about 800 to 1000 amino acid residues and the XTEN can be identical or they can be different in sequence or in length. As used herein, cumulative length is intended to encompass the total length, in amino acid residues, when more than one XTEN is incorporated into the conjugate.

[00241] As described more fully below, methods are disclosed in which the XTEN-payload conjugates are designed by selecting the length of the XTEN and a method of linking with a cross-linker reactant or the payload to confer a physicochemical property (e.g., stability or solubility) or to result in a target half-life or retention of activity when an XTEN-payload conjugate is administered to a subject.

[00242] XTEN are used as a carrier in the compositions, the invention taking advantage of the discovery that increasing the length of the non-repetitive, unstructured polypeptides enhances the unstructured nature of the XTENs and correspondingly enhances the physicochemical and pharmacokinetic properties of constructs comprising the XTEN carrier. In general, XTEN as monomers or as multimers with cumulative lengths longer that about 400 residues incorporated into the conjugates result in longer half-life compared to shorter cumulative lengths, e.g., shorter than about 280 residues. As described more fully in the Examples, proportional increases in the length of the XTEN, even if created by a repeated order of single family sequence motifs (e.g., the four AE motifs of Table 1), result in a sequence with a higher percentage of random coil formation, as determined by GOR algorithm, or reduced content of alpha-helices or beta-sheets, as determined by Chou-Fasman algorithm, compared to shorter XTEN lengths. In addition, increasing the length of the unstructured polypeptide fusion partner, as described in the Examples, results in a construct with a disproportionate increase in terminal half-life compared to polypeptides with unstructured polypeptide partners with shorter sequence lengths. In some embodiments, where the XTEN serve primarily as a carrier, the invention encompasses XTEN conjugate compositions comprising two, three, four or more XTEN wherein the cumulative XTEN sequence length of the XTEN proteins is greater than about 100, 200, 400, 500, 600, 800, 900, or 1000 to about 3000 amino acid residues, wherein the construct exhibits enhanced pharmacokinetic properties when administered to a subject compared to a payload not linked to the XTEN and administered at a comparable dose. In one embodiment of the foregoing, the two or more XTEN sequences each exhibit at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, or 98% or more identity to a sequence selected from any one of Table 2, Table 3, or Tables 22-25, and the remainder, if any, of the carrier sequence(s) contains at least 90% hydrophilic amino acids and less than about 2% of the overall sequence consists of hydrophobic

or aromatic amino acids or cysteine. The enhanced pharmacokinetic properties of the XTEN-payload conjugate, in comparison to payload not linked to XTEN, are described more fully, below.

5. XTEN Segments from XTEN Precursors

[00243] In another aspect, the invention provides methods to create XTEN of short or intermediate lengths from longer "donor" XTEN sequences, wherein the longer donor XTEN sequence is truncated at the N-terminus, or the C-terminus, or segments are created by protealysis of XTEN comprising cleavage sequences, thereby resulting in a short or intermediate length XTEN. In non-limiting examples, an AG864 sequence of 864 amino acid residues can be truncated to yield an AG144 with 144 residues, an AG288 with 288 residues, an AG576 with 576 residues, or other intermediate lengths, while the AE864 sequence can be truncated to yield multiple AE144 sequences, an AE288 sequence or an AE576 sequence with 288 or 576 residues or other shorter or intermediate lengths. Similarly, the DNA encoding the longer "donor" sequences can be manipulated to incorporate cysteine or lysine residues intended for use in conjugates with short or intermediate length XTEN. It is specifically contemplated that such an approach can be utilized with any of the XTEN embodiments described herein or with any of the sequences listed in Tables 2, 3, 21 and 22 to result in XTEN of a desired length.

[00244] In another aspect, the invention provides XTEN with cleavage sequences incorporated internal to the sequence at defined intervals such that the XTEN can be processed by cleavage into 2, 3, 4, 5, or 6 shorter XTEN of uniform lengths. As illustrated in FIG. 96A, a monomeric XTEN is designed with two internal cleavage sequences that, when treated with a protease under conditions effective to result in the cleavage of all cleavage sequences, results in three XTEN segments of uniform length. In addition, the XTEN are designed with a sequence such that the resulting XTEN segments also have the identical amino acid sequence, inclusive of the residual cleavage sequence. In one embodiment, the invention provides an XTEN with a defined, sequence comprising 1, 2, 3, 4, or 5 arginine (R) residues internal to the XTEN sequence and spaced at uniform intervals along the XTEN sequence bridging identical XTEN segments wherein treatment with trypsin results in cleavage of the XTEN into XTEN segments to having an identical length and sequence. In the foregoing embodiment, the arginine residue does not have a proline residue at the adjacent P1' position. Thus, by treatment of the foregoing with trypsin, an XTEN with 1 internal arginine would result in 2 identical XTEN segments, an XTEN with 2 internal argninines would result in 3 identical XTEN segments, etc. In another embodiment, each arginine of the foregoing embodiments is replaced with lysine residues. In another embodiment, the invention provides an XTEN with a defined sequence comprising 1, 2, 3, 4, or 5 cleavage sequences internal to the XTEN sequence and spaced at uniform intervals along the XTEN sequence, wherein each cleavage sequence is SASRSA, and wherein treatment

with trypsin results in cleavage of the XTEN into XTEN segments to having an identical length and sequence. In another embodiment, the invention provides an XTEN with at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity to a sequence selected from the group of sequences set forth in Table 6. In another embodiment, the invention provides an XTEN with at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity to a sequence selected from the group of sequences set forth in Table 6, wherein the XTEN further comprises a first and a second affinity tag wherein each affinity tags are linked to the XTEN by a cleavage sequence at the N- and C-termini of the XTEN, respectively, wherein each cleavage sequence is capable of being cleaved by trypsin, and wherein the first affinity tag is different from the second affinity tag and each is independently selected from the group consisting of the affinity tags set forth in Table 7. The foregoing embodiment is illustrated in FIG. 96B, wherein the treatment with protease of the XTEN with two internal cleavage sequences and an N-terminal and a C-terminal affinity tag each linked to the XTEN by cleavage sequence results in cleavage of the construct into three XTEN segments of uniform length and liberation of the two affinity tags, the resulting preparation of which can be subsequently processed into substantially homogeneous XTEN as described herein, below. Variations of XTEN comprising such uniform cleavage sequences and their distribution in the sequence are contemplated by the invention.

Table 6: Precursor XTEN with Internal Cleavage Sequences

XTEN Name	Amino Acid Sequence
AE864_R2 (2x AE432_R1)	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGS PTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPAT SGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGS PTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTESASRSAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEP ATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSE SATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGSPAGSPTSTEEGTESASR
AE864_R3 (3x AE288_R1)	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTST EPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPSASRSAGSPTGPGSEP ATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPA

XTEN Name	Amino Acid Sequence
	GSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPA GSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEP ATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEP ATSGSETPGTSESATPESGPGTSTEPSEGSAPSASRSAGSPTGPGSEPATSGSETPGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTS TEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSE PATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTS ESATPESGPGTSTEPSEGSAPSASR
AE864_R6 (6x AE144_ R1)	SAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGS PTSTEEGTSESATPESGPGTESASRSAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEP SEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPAT SGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTESASRSAGSPGSPAG SPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTE PSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSES ATPESGPGTESASRSAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEP ATSGSETPGSPAGSPTSTEEGTSESATPESGPGTESASRSAGSPGSPAGSPTSTEEGTS ESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTS ESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTE SASRSAGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSP AGSPTSTEEGTSESATPESGPGTESASR
Seg 200 (3x Seg 195)	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTST EPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTACSEGSAPSASRSAGSPTGPGSE PATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSE PATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGSE PATSGSETPGTSESATPESGPGTSTACSEGSAPSASRSAGSPTGPGSEPATSGSETPGT SESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGT SESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGS EPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGT SESATPESGPGTSTACSEGSAPSASR
Seg 201 (3x Seg 196)	SAGSPTGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSE SATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTST EPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSCASASRSAGSPTGPGSE PATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSP AGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSE PATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSPAGSPTSTEEGSE PATSGSETPGTSESATPESGPGTSTEPSEGSCASASRSAGSPTGPGSEPATSGSETPGT SESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGT SESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGS EPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGT SESATPESGPGTSTEPSEGSCASASR

6. Net charge

[00245] In other embodiments, the XTEN polypeptides have an unstructured characteristic imparted by incorporation of amino acid residues with a net charge and containing a low percentage or no hydrophobic amino acids in the XTEN sequence. The overall net charge and net charge density is controlled by modifying the content of charged amino acids in the XTEN sequences, either positive or negative, with the net charge typically represented as the percentage of amino acids in the polypeptide contributing to a charged state beyond those residues that are cancelled by a residue with an opposing charge. In some embodiments, the net charge density of the XTEN of the conjugates may be above +0.1 or below -0.1 charges/residue. By "net charge density" of a protein or peptide herein is meant the net charge divided by the total number of amino acids in the protein. In other embodiments, the net charge of an XTEN can be about 0%, about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10% about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, or about 20% or more. Based on the net charge, some XTENs have an isoelectric point (pI) of 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, or even 6.5. In one embodiment, the XTEN will have an isoelectric point between 1.5 and 4.5 and carry a net negative charge under physiologic conditions.

[00246] Since most tissues and surfaces in a human or animal have a net negative charge, in some embodiments the XTEN sequences are designed to have a net negative charge to minimize non-specific interactions between the XTEN containing compositions and various surfaces such as blood vessels, healthy tissues, or various receptors. Not to be bound by a particular theory, an XTEN can adopt open conformations due to electrostatic repulsion between individual amino acids of the XTEN polypeptide that individually carry a net negative charge and that are distributed across the sequence of the XTEN polypeptide. In some embodiments, the XTEN sequence is designed with at least 90% to 95% of the charged residues separated by other non-charged residues such as serine, alanine, threonine, proline or glycine, which leads to a more uniform distribution of charge, better expression or purification behavior. Such a uniform distribution of net negative charge in the extended sequence lengths of XTEN also contributes to the unstructured conformation of the polymer that, in turn, can result in an effective increase in hydrodynamic radius. In preferred embodiments, the negative charge of the subject XTEN is conferred by incorporation of glutamic acid residues. Generally, the glutamic residues are spaced uniformly across the XTEN sequence. In some cases, the XTEN can contain about 10-80, or about 15-60, or about 20-50 glutamic residues per 20kDa of XTEN that can result in an XTEN with charged residues that would have very similar pKa, which can increase the charge homogeneity of the product and sharpen its isoelectric point, enhance the physicochemical properties of the resulting XTEN-payload for, and hence, simplifying purification procedures.

For example, where an XTEN with a negative charge is desired, the XTEN can be selected solely from an AE family sequence, which has approximately a 17% net charge due to incorporated glutamic acid, or can include varying proportions of glutamic acid-containing motifs of Table 1 to provide the desired degree of net charge. Non-limiting examples of AE XTEN include, but are not limited to the AE36, AE42, AE144, AE288, AE432, AE576, AE624, AE864, and AE912 sequences of Tables 2 and 21 or fragments thereof. In one embodiment, an XTEN sequence of Tables 2 or 3 can be modified to include additional glutamic acid residues to achieve the desired net negative charge. Accordingly, in one embodiment the invention provides XTEN in which the XTEN sequences contain about 1%, 2%, 4%, 8%, 10%, 15%, 17%, 20%, 25%, or even about 30% glutamic acid. In some cases, the XTEN can contain about 10-80, or about 15-60, or about 20-50 glutamic residues per 20kDa of XTEN that can result in an XTEN with charged residues that would have very similar pKa, which can increase the charge homogeneity of the product and sharpen its isoelectric point, enhance the physicochemical properties of the resulting XTEN conjugate composition, and hence, simplifying purification procedures. In one embodiment, the invention contemplates incorporation of up to 5% aspartic acid residues into XTEN in addition to glutamic acid in order to achieve a net negative charge.

[00247] Not to be bound by a particular theory, the XTEN of the XTEN-payload conjugates with the higher net negative charge are expected to have less non-specific interactions with various negatively-charged surfaces such as blood vessels, tissues, or various receptors, which would further contribute to reduced active clearance. Conversely, it is believed that the XTEN of the XTEN-payload conjugates with a low (or no) net charge would have a higher degree of interaction with surfaces that can potentiate the activity of the associated conjugate in the vasculature or tissues.

[00248] In other embodiments, where no net charge is desired, the XTEN can be selected from, for example, AG XTEN components, such as the AG motifs of Table 1, or those AM motifs of Table 1 that have no net charge. Non-limiting examples of AG XTEN include, but are not limited to 36, 42, 144, 288, 576, and 864 AG family sequences of Tables 2 and 22, or fragments thereof. In another embodiment, the XTEN can comprise varying proportions of AE and AG motifs in order to have a net charge that is deemed optimal for a given use or to maintain a given physicochemical property.

[00249] The XTEN of the conjugates of the present invention generally have no or a low content of positively charged amino acids. In some embodiments, the XTEN may have less than about 10% amino acid residues with a positive charge, or less than about 7%, or less than about 5%, or less than about 2%, or less than about 1% amino acid residues with a positive charge. However, the invention contemplates constructs where a defined number of amino acids with a positive charge, such as lysine, are incorporated into XTEN to permit conjugation between the epsilon

amine of the lysine and a reactive group on a payload or a cross-linker to be conjugated to the XTEN backbone. In one embodiment of the foregoing, the XTEN of the subject conjugates has between about 1 to about 100 lysine residues, or about 1 to about 70 lysine residues, or about 1 to about 50 lysine residues, or about 1 to about 30 lysine residues, or about 1 to about 20 lysine residues, or about 1 to about 10 lysine residues, or about 1 to about 5 lysine residues, or about 1 to about 3 lysine residues, or alternatively only a single lysine residue. Using the foregoing lysine-containing XTEN, conjugates can be constructed that comprise XTEN, an optional linker, plus a payload useful in the treatment of a condition in a subject wherein the maximum number of molecules of the payload agent linked to the XTEN component is determined by the numbers of lysines with a reactive side group (e.g., a terminal amine) incorporated into the XTEN.

7. Low immunogenicity

[00250] In another aspect, the invention provides XTEN compositions having a low degree of immunogenicity or are substantially non-immunogenic. Several factors can contribute to the low immunogenicity of XTEN, e.g., the non-repetitive sequence, the unstructured conformation, the high degree of solubility, the low degree or lack of self-aggregation, the low degree or lack of proteolytic sites within the sequence, and the low degree or lack of epitopes in the XTEN sequence.

[00251] Conformational epitopes are formed by regions of the protein surface that are composed of multiple discontinuous amino acid sequences of the protein antigen. The precise folding of the protein brings these sequences into a well-defined, stable spatial configurations, or epitopes, that can be recognized as "foreign" by the host humoral immune system, resulting in the production of antibodies to the protein or the activation of a cell-mediated immune response. In the latter case, the immune response to a protein in an individual is heavily influenced by T-cell epitope recognition that is a function of the peptide binding specificity of that individual's HLA-DR allotype. Engagement of a MHC Class II peptide complex by a cognate T-cell receptor on the surface of the T-cell, together with the cross-binding of certain other co-receptors such as the CD4 molecule, can induce an activated state within the T-cell. Activation leads to the release of cytokines further activating other lymphocytes such as B cells to produce antibodies or activating T killer cells as a full cellular immune response.

[00252] The ability of a peptide to bind a given MHC Class II molecule for presentation on the surface of an APC (antigen presenting cell) is dependent on a number of factors; most notably its primary sequence. In one embodiment, a lower degree of immunogenicity is achieved by designing XTEN sequences that resist antigen processing in antigen presenting cells, and/or choosing sequences that do not bind MHC receptors well. The invention provides XTEN-payload, XTEN-cross-linker, and XTEN-click-chemistry reactant conjugates with substantially non-repetitive XTEN polypeptides designed to reduce binding with MHC II receptors, as well as

avoiding formation of epitopes for T-cell receptor or antibody binding, resulting in a low degree of immunogenicity. Avoidance of immunogenicity can attribute to, at least in part, a result of the conformational flexibility of XTEN sequences; i.e., the lack of secondary structure due to the selection and order of amino acid residues. For example, of particular interest are sequences having a low tendency to adapt compactly folded conformations in aqueous solution or under physiologic conditions that could result in conformational epitopes. The administration of polypeptides comprising XTEN, using conventional therapeutic practices and dosing, would generally not result in the formation of neutralizing antibodies to the XTEN sequence, and also reduce the immunogenicity of the payload in the conjugates.

[00253] In one embodiment, the XTEN sequences utilized in the subject polypeptides can be substantially free of epitopes recognized by human T cells. The elimination of such epitopes for the purpose of generating less immunogenic proteins has been disclosed previously; see for example WO 98/52976, WO 02/079232, and WO 00/3317 which are incorporated by reference herein. Assays for human T cell epitopes have been described (Stickler, M., *et al.* (2003) *J Immunol Methods*, 281: 95-108). Of particular interest are peptide sequences that can be oligomerized without generating T cell epitopes or non-human sequences. This is achieved by testing direct repeats of these sequences for the presence of T-cell epitopes and for the occurrence of 6 to 15-mer and, in particular, 9-mer sequences that are not human, and then altering the design of the XTEN sequence to eliminate or disrupt the epitope sequence. In some embodiments, the XTEN sequences are substantially non-immunogenic by the restriction of the numbers of epitopes of the XTEN predicted to bind MHC receptors. With a reduction in the numbers of epitopes capable of binding to MHC receptors, there is a concomitant reduction in the potential for T cell activation as well as T cell helper function, reduced B cell activation or upregulation and reduced antibody production. The low degree of predicted T-cell epitopes can be determined by epitope prediction algorithms such as, e.g., TEPITOPE (Sturniolo, T., *et al.* (1999) Nat Biotechnol, 17: 555-61), as shown in Example 46. The TEPITOPE score of a given peptide frame within a protein is the log of the K_d (dissociation constant, affinity, off-rate) of the binding of that peptide frame to multiple of the most common human MHC alleles, as disclosed in Sturniolo, T. *et al.* (1999) *Nature Biotechnology* 17:555). The score ranges over at least 20 logs, from about 10 to about -10 (corresponding to binding constraints of $10e^{10}$ K_d to $10e^{-10}$ K_d), and can be reduced by avoiding hydrophobic amino acids that serve as anchor residues during peptide display on MHC, such as M, I, L, V, F. In some embodiments, an XTEN component incorporated into either a XTEN-payload, XTEN-cross-linker, or XTEN-click-chemistry reactant conjugate does not have a predicted T-cell epitope at a TEPITOPE threshold score of about -5, or -6, or -7, or -8, or -9, or at a TEPITOPE score of -10. As used herein, a score of "-9" is a more stringent TEPITOPE threshold than a score of -5.

8. Increased Hydrodynamic radius

[00254] In another aspect, a subject XTEN useful as a fusion partner has a high hydrodynamic radius; a property that confers a corresponding increased apparent molecular weight to the XTEN-payload composition compared to the payload without the XTEN. As detailed in Example 26, the linking of XTEN to therapeutic protein sequences results in compositions that can have increased hydrodynamic radii, increased apparent molecular weight, and increased apparent molecular weight factor compared to a therapeutic protein not linked to an XTEN. For example, in therapeutic applications in which prolonged half-life is desired, compositions in which one or more XTEN with a high hydrodynamic radius are conjugated to a payload can effectively enlarge the hydrodynamic radius of the conjugate beyond the glomerular pore size of approximately 3-5 nm (corresponding to an apparent molecular weight of about 70 kDa) (Caliceti. 2003. Pharmacokinetic and biodistribution properties of poly(ethylene glycol)-protein conjugates. Adv Drug Deliv Rev 55:1261-1277), resulting in reduced renal clearance of circulating proteins with a corresponding increase in terminal half-life and other enhanced pharmacokinetic properties. The hydrodynamic radius of a protein is conferred by its molecular weight as well as by its structure, including shape or compactness. Not to be bound by a particular theory, the XTEN can adopt open conformations due to the electrostatic repulsion between individual charges of incorporated charged residues in the XTEN as wells as because of the inherent flexibility imparted by the particular amino acids in the sequence that lack potential to confer secondary structure. The open, extended and unstructured conformation of the XTEN polypeptide has a greater proportional hydrodynamic radius compared to polypeptides of a comparable sequence length and/or molecular weight that have secondary or tertiary structure, such as typical globular proteins. Methods for determining the hydrodynamic radius are well known in the art, such as by the use of size exclusion chromatography (SEC), as described in U.S. Patent Nos. 6,406,632 and 7,294,513. Example 26 demonstrates that increases in XTEN length result in proportional increase in the hydrodynamic radius, apparent molecular weight, and/or apparent molecular weight factor, and thus permit the tailoring of an XTEN-payload to desired cut-off values of apparent molecular weights or hydrodynamic radii. Accordingly, in certain embodiments, the XTEN-payload can be configured with an XTEN such that the resulting conjugate can have a hydrodynamic radius of at least about 5 nm, or at least about 8 nm, or at least about 10 nm, or about 12 nm, or about 15 nm, or about 20 nm, or about 30 nm or more. In the foregoing embodiments, the large hydrodynamic radius conferred by the XTEN in a XTEN-payload conjugate can lead to reduced clearance of the resulting conjugate, an increase in terminal half-life, and an increase in mean residence time. As described in the Examples, when the molecular weights of the XTEN-containing compositions are derived from size exclusion chromatography analyses, the open conformation of the XTEN due to the low degree of

secondary structure results in an increase in the apparent molecular weight of the conjugates into which they are incorporated. In one embodiment, the present invention makes use of the discovery that the increase in apparent molecular weight can be accomplished by the linking not ony of a single XTEN of a given length, but also by the linking of 2, 3, 4 or more XTEN of proportionally shorter lengths, either in linear fashion or as a trimeric or tetrameric, branched configuration, as described more fully, below. In some embodiments, the XTEN comprising a payload and one or more XTEN exhibits an apparent molecular weight of at least about 400 kD, or at least about 500 kD, or at least about 700 kD, or at least about 1000 kD, or at least about 1400 kD, or at least about 1600 kD, or at least about 1800kD, or at least about 2000 kD. Accordingly, the XTEN-payload conjugate exhibits an apparent molecular weight that is about 1.3-fold greater, or about 2-fold greater, or about 3-fold greater or about 4-fold greater, or about 8-fold greater, or about 10-fold greater, or about 12-fold greater, or about 15-fold, or about 20-fold greater than the actual molecular weight of the conjugate. In one embodiment, the isolated XTEN-payload conjugate of any of the embodiments disclosed herein exhibit an apparent molecular weight factor under physiologic conditions that is greater than about 1.3, or about 2, or about 3, or about 4, or about 5, or about 6, or about 7, or about 8, or about 10, or greater than about 15. In another embodiment, the XTEN-payload has, under physiologic conditions, an apparent molecular weight factor that is about 3 to about 20, or is about 5 to about 15, or is about 8 to about 12, or is about 9 to about 10 relative to the actual molecular weight of the conjugate. Generally, the increased apparent molecular weight of the subject XTEN-payload conjugates enhances the pharmacokinetic properties of the composition by a combination of factors, which include reduced active clearance, reduced renal clearance, and reduced loss through capillary and venous junctions.

9. Compositions and methods of purifying XTEN as substantially homogeneous preparations

[00255] It is an object of the invention to provide compositions of XTEN and methods of making preparations comprising XTEN with a high level of purity and uniformity in the length and composition of the XTEN described herein.

[00256] The expression of recombinant XTEN protein or a recombinant fusion protein comprising XTEN in a host cell normally, like any globular protein, results in a mixture of different compounds in which a portion are truncated versions of the desired protein length. The truncation can be the result of early termination of translation, mRNA instability, or proteolysis in the host cell. Because globular proteins generally have efficient or complete folding into their three-dimensional structure while truncated versions do not, typical purification and recovery processes can successfully separate and remove the truncated versions such that a high level of product homogeneity is achieved in a given preparation of globular proteins. However, protein

polymers such as XTEN are unique in that, given their unstructured nature, generally lack three-dimensional structures. It has been difficult to obtain a homogeneous preparation of full-length XTENs due to one or more of the above-mentioned reasons. This is because incomplete or truncated XTEN chains differ only slightly in their physicochemical properties from the desired full-length sequences such that traditional processes that would be sufficient for purification of globular proteins are not effective in the removal of truncated XTEN from the expression product in order to obtain a substantially homogeneous preparation of full-length sequences. While the subject XTEN of the invention, including XTEN linked to payload, can be purified to a moderate degree of homogeneity by conventional means used for proteins, such as salt fractionation, ion exchange chromatography, size exclusion chromatography, hydroxyapatite adsorption chromatography, hydrophobic interaction chromatography or gel electrophoresis, these methods alone do not result in preparations wherein the XTEN are substantially homogeneous in sequence length.

[00257] The subject methods provided herein permit production of substantially homogenous preparation of XTENs via one or a few simple purification steps. In one embodiment, the practice of any of such methods of the present invention can utilize an XTEN designed to further comprise, as a fusion protein, affinity tags located at either or both of the N- and C-termini of the XTEN such that the expressed product can be subject to purification methods to selectively capture the full-length expressed polypeptide, thereby removing truncated XTEN by-products (see FIGS. 41-42). Non-limiting examples of affinity tags that can be added to the termini of XTEN are presented in Table 7. Non-limiting examples of methods of the design, expression, and purification methods to achieve substantially homogeneous XTEN are described in the Examples.

[00258] In some embodiments, the invention provides substantially homogeneous polypeptide compositions with XTEN fused directly to one affinity tag (such as, but not limited to the tags of Table 7) linked to either the N- or C-terminus of the XTEN. In other embodiments, the invention provides substantially homogeneous polypeptide compositions with XTEN fused to one affinity tag (such as, but not limited to the tags of Table 7) by a cleavage sequence linked to either the N- or C-terminus of the XTEN. In other embodiments, the invention provides substantially homogeneous polypeptide compositions with XTEN fused directly to one or two different affinity tags (such as, but not limited to the tags of Table 7) linked to the N- and/or C-termini of the XTEN, as shown in FIG. 41. In other embodiments, the invention provides substantially homogeneous compositions with XTEN fused to one or two cleavage sequences (such as, but not limited to the cleavage sequences of Table 8 or Table 9) which, in turn, are each fused to different affinity tags (such as, but not limited to the tags of Table 7) linked to the N- or C-termini or both the N- and C-termini of the XTEN, as shown in FIG. 41. In yet other

embodiments, the invention provides substantially homogeneous polypeptide compositions with XTEN fused directly to one or two different affinity tags (such as, but not limited to the tags of Table 7) linked to the N- and/or C-termini of the XTEN that further comprise a helper sequence (such as, but not limited to the sequences of Table 12) fused to the N-terminus of the protein. As used in the context of the proteins described herein, "substantially homogeneous" means that at least about 85%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, 96%, 97%, 98%, 99% or even higher of the polypeptide sequences of the preparation have identical sequence length. The percent values are based on the area percentage of the chromatogram of the preparation analyzed by HPLC or the area percentage of the scan of the preparation analyzed by SDS-PAGE, or by other such standard procedures known in the art for assessing the purity of proteins.

[00259] In one embodiment, the invention provides a substantially homogenous polypeptide having the configuration of formula I:

(HS)-(AT1)-(CS1)-(XTEN) I

wherein HS is the helper sequence, AT1 is the first affinity tag, CS1 is the first cleavage sequence, and XTEN is the extended recombinant polypeptide.

[00260] In another embodiment, the invention provides a substantially homogenous polypeptide having the configuration of formula II

(HS)-(CS1)-(XTEN)-(CS2)-(AT1) II

wherein HS is the helper sequence, AT1 is the first affinity tag, CS1 is the first cleavage sequence, CS2 is the second cleavage sequence and XTEN is the extended recombinant polypeptide.

[00261] In another embodiment, wherein the composition has the configuration of formula III:

(HS)-(AT1)-(CS1)-(XTEN)-(CS2)-(AT2) III

wherein HS is the helper sequence, AT1 is the first affinity tag, AT2 is the second affinity tag, CS1 is the first cleavage sequence, CS2 is the second cleavage sequence and XTEN is the extended recombinant polypeptide.

[00262] The polypeptide constructs comprising affinity tags have the advantageous property, compared to XTEN not linked to affinity tags, of being able to be purified to substanially homogeneous length by use of chromatography substrates to which the affinity tags will bind. In some embodiments, the categories of chromatography substrates used in the method of purification are selected from the chromatography substrates set forth in Table 7, which are utilized for the purification of XTEN linked to the corresponding the indicated affinity tag in the tables. As will be appreciated by one of skill in the art, the categories of chromatography substrate can encompass different chemical groups linked to different matrices or resins; e.g.,

anion exchange substrates include quaternary trimethylammonium and diethylaminoethyl bound to resins, cation exchange substrates include sulfo or sulfopropyl or carboxymethyl or phosphate groups bound to resins, HIC substrates include ethyl, isopropyl, butyl, phenyl or octyl groups bound to resins, and IMAC substrates include iminodiacetic acid and nitriloacetic acid groups bound to resins. The foregoing substrates are listed for illustrative purposes and are not intended to limit the scope of substrates that can be employed to practice the invention.

[00263] In some embodiments, the invention provides substantially homogeneous XTEN prepared from the a polypeptide comprising an XTEN fused to a first or a first and a second affinity tag by cleavage sequences (such as, but not limited to the cleavage sequences of Table 8) capable of being cleaved by a protease, wherein the preparation is treated with the protease to cleave the cleavage sequences to release the XTEN from the polypeptide, followed by a chromatography step to bind and then elute, and then recover the substantially homogeneous XTEN. In one embodiment of the foregoing, the protease is trypsin and the cleavage sequences are capable of being cleaved by trypsin, non-limiting examples of which are listed in Tables 11 and 15. In another embodiment of the foregoing, the protease is TEV and the cleavage sequences are capable of being cleaved by TEV. In another embodiment of the foregoing, the cleaved XTEN is purified by binding to MacoCap SP chromatography substate followed by elution with a salt or buffer solution such as, but not limited to, sodium phosphate/NaCl, resulting in the substantially homogenous XTEN. As used in the context of XTEN and/or polypeptides comprising XTEN, a preparation that is "substantially purified" means that at least about 85%, and more preferably at least about 90%, and more preferably at least about 91%, and more preferably at least about 92%, and more preferably at least about 93%, and more preferably at least about 94%, and more preferably at least about 95% or more of the individual molecules of a given preparation have identical sequence length; in other words, the same number of amino acids. The methods that can be utilized to assay for homogeneity of length include mass spectroscopy, size exclusion chromatography/HPLC, or SDS-PAGE followed by silver staining; the methods can be used individually or collectively to quantitate the degree of homogeneity. A generalized scheme for purification of polypeptides comprising XTEN with affinity tag sequences optimized for purification is shown in FIGS. 41-42. After purification the tags can be proteolytically cleaved (FIG. 41B) or retained (FIG. 41C). The XTEN can be purified from contaminants due to the unique amino acid composition of XTEN, as illustrated in FIG. 42.

[00264] In one embodiment, the invention provides a method to produce a substanially purified preparation of a polypeptide comprising an XTEN, comprising the steps of designing a gene encoding an XTEN and a first affinity tag, creating an expression vector suitable for transforming a host cell comprising the encoding gene operably linked to control sequences, transforming the host cell with the expression vector, culturing the host cell under conditions

suitable for the expression of the XTEN with linked affinity tag, subjecting the crude expression product to a purification process that comprises an affinity purification step wherein the crude expression product is loaded onto a first chromatography substrate that selectively binds the first affinity tag, washing the chromatography substrate to elute material not bound to the chromatography substrate, eluting the retained protein under appropriate conditions and recovering the eluate wherein the recovered polypeptide is substantially homogeneous in length. In another embodiment, the invention provides a method to produce a substanialy homogeneous preparation of a polypeptide comprising an XTEN, comprising the steps of designing a gene encoding an XTEN comprising a first and a second affinity tag, creating an expression vector suitable for transforming a host cell comprising the encoding gene operably linked to control sequences, transforming the host cell with the expression vector, culturing the host cell under conditions suitable for the expression of the polypeptide, subjecting the crude expression product to a purification process that comprises an affinity purification step wherein the lysate is loaded onto a first chromatography substrate that selectively binds the first affinity tag, washing the chromatography substrate to elute material not bound to the chromatography substrate, eluting the retained protein under appropriate conditions and recovering the eluate, loading the recovered XTEN polypeptide onto a second chromatography substrate under conditions effective to capture the polypeptide with the second affinity tag onto the chromatography substrate, washing the chromatography substrate to elute material not bound to the chromatography substrate, eluting the XTEN polypeptide under conditions effective to elute the XTEN polypeptide with the second affinity tag, recovering the eluate containing the polypeptide comprising the XTEN polypeptide with the first and the second affinity tag wherein the recovered polypeptide is substantially homogeneous in length. In yet another embodiment, the invention provides a method to produce a substanially homogeneous preparation of a polypeptide comprising an XTEN, comprising the steps of designing a gene encoding an XTEN comprising a first affinity tag linked by a cleavage sequence to the N-terminus of the encoded XTEN and a second affinity tag linked by a cleavage sequence to the C-terminus of the encoded XTEN, creating an expression vector suitable for transforming a host cell comprising the encoding gene operably linked to control sequences, transforming the host cell with the expression vector, culturing the host cell under conditions suitable for the expression of the polypeptide, subjecting the crude expression product to a purification process that comprises an affinity purification step wherein the lysate is loaded onto a first chromatography substrate that selectively binds the first affinity tag, washing the chromatography substrate to elute material not bound to the chromatography substrate, eluting the retained protein under appropriate conditions and recovering the eluate, loading the recovered polypeptide onto a second chromatography substrate under conditions effective to capture the polypeptide with the second affinity tag onto the chromatography substrate, washing the

chromatography substrate to elute material not bound to the chromatography substrate, eluting the polypeptide under conditions effective to elute the polypeptide with the second affinity tag, then treating the recovered polypeptide with a protease under conditions effective to release the XTEN from the polypeptide and loading the material onto a chromatography substrate capable of capturing the XTEN but not the affinity tags, washing the chromatography substrate to elute material not bound to the chromatography substrate, eluting the XTEN, recovering the eluate containing the XTEN polypeptide wherein the recovered XTEN is substantially homogeneous in length. In one embodiment of the foregoing methods described in this paragraph, the first and second affinity tags are selected from the group of affinity tags set forth in Table 7. In one embodiment of the method, the first affinity tag linked to the XTEN as a fusion protein comprises the sequence RPRPRPRPRPRPR and the chromatography substrate used to bind the polypeptide is MacroCap SP. In another embodiment of the foregoing methods, the first affinity tag linked to a first terminus of the XTEN as a fusion protein comprises the sequence RPRPRPRPRPRPRPRPRPRPRPR, the second affinity tag linked to a second terminus of the XTEN comprises the sequence HHHHHHHH, the first chromatography substrate used to bind the polypeptide is MacroCap SP, and the second chromatography substrate used to bind the polypeptide is a immobilized metal on affinity (IMAC) substrate. In another embodiment of the foregoing methods, the first affinity tag fused to a cleavage sequence fused to a first terminus of the XTEN as a fusion protein comprises the sequence RPRPRPRPRPRPR or RPRPRPRPRPRPRPRPRPRPRPR, the second affinity tag fused to a cleavage sequence to a second terminus of the XTEN comprises the sequence HHHHHH or HHHHHHHH, the first chromatography substrate used to bind the polypeptide is MacroCap SP, the second chromatography substrate used to bind the polypeptide is a immobilized metal on affinity (IMAC) substrate, the cleavage sequences comprise an arginine or lysine (including, but not limited to the sequences of Tables 8 and 9) and are cleaved by trypsin, and Macrocap Q is the chromatography substrate used to bind the XTEN freed from the affinity tags or, in the alternative, the freed XTEN is captures as flow-through by passing the protease-treated preparation through one or more of cation exchange, HIC and/or IMAC to capture the cleavage products and protease, leaving the XTEN in the flow-through, which is then recovered as a substantially homogeneous preparation.

[00265] It will be appreciated by one of skill in the art that the order and specific conditions of the steps of the method will vary depending on the composition of the XTEN-affinity tag polypeptide as well as the starting expression level and degree of contamination of truncated contaminants. For example, with certain XTEN compositions, the use of a single affinity tag linked to the XTEN will be sufficient to achieve a preparation in which the polypeptide molecules are substantially homogeneous in length. In such cases, in one embodiment the single

affinity tag is selected from the affinity tags set forth in Table 7. With other XTEN compositions, the use of a first and a second affinity tag will be sufficient to achieve a preparation in which the polypeptide molecules are substantially homogeneous in length and in such cases, in one embodiment, the first and second affinity tags are different and each is selected from the affinity tags set forth in Table 7. It will be further appreciated by one of skill in the art that once the polypeptides comprising cleavage sequences are purified, the recovered polypeptide can be subsequently treated by proteolysis to release the one or two affinity tags, followed by passing the treated XTEN through a chromatography substrate to recover the XTEN without linked affinity tags. A schematic of the method is illustrated in FIG. 42 and exemplary methodologies are described in the Examples. Many different proteases can be utilized for the release of terminal purification tags, depending on the sequence linking the affinity tag to the XTEN, including but not limited to a protease selected from Table 9. In one embodiment, the protease is selected from the group consisting of trypsin, chymotrypsin, tobacco etch mosaic virus protease (TEV), FXa, and enterokinase. In another embodiment, the cleavage sequence incorporated into the polypeptide comprises an arginine residue that can be cleaved and the affinity tag removed by treatment with trypsin, thereby releasing the XTEN that is subsequently recovered in substantilly purified form by chromatography such as, by capture using anion exchange (including but not limited to, MacroCap Q) or recovered as flow-through wherein the non-XTEN cleavage products and protease are captured by one or more of HIC, cation exchange, or IMAC chromatography, leaving substantially homogeneous XTEN in the flow-through.

Table 7: Affinity Tags and Chromatography Substrate Categories that Bind Affinity Tags

Affinity Tag Amino Acid Sequence	Chromatography Substrate
LYPYPYP, LYYYPP, WPWP, FPFPFP	HIC
$(Y)_n$, $(W)_n$, $(YP)_n$, $(WP)_n$, $(FP)_n$, $(LP)_n$ with n=3-20	HIC
$(RP)_n$, $(KP)_n$, $(HP)_n$, $(H)_n$, $(R)_n$ with n=3-20	Cation exchange, IMAC
$(E)_n$, $(D)_n$, $(ED)_n$, $(EP)_n$, $(DP)_n$ with n=3-20	Anion exchange
RPRPRPRPRP	Cation exchange
RPRPRPRPRPGR	Cation exchange
RPRPRPRPRPRPRP	Cation exchange
RPRPRPRPRPRPRPGR	Cation exchange
KPKPKPKPKP	Cation exchange
KPKPKPKPKPGR	Cation exchange
RPRPRPRPRPRPRPRPRP	Cation exchange
RPRPRPRPRPRPRPRPRPGR	Cation exchange
RPRPRPRPRPRPRPRPRPRPRP	Cation exchange
RPRPRPRPRPRPRPRPRPRPRPGR	Cation exchange
RPRPRPRPRPRPRPRPRPRPRPRPRP	Cation exchange
RPRPKPRPKPRPKPRPKP	Cation exchange
PRPKPRPKPRPKPRPKPGR	Cation exchange
RPRPKPRPKPRPKPRPKPRPKP	Cation exchange

RPRPKPRPKPRPKPRPKPRPKPGR	Cation exchange
GSPYGYPYSYS, GSPWGSPTSTE, GSPAGSPTSTE,	HIC
GSPXGXPXSXS, GSPSGXPXSXS, GSPSGTPXSXS where X = Ile, Leu, Val, Phe, Trp, or Tyr	HIC
GSPXGXPXSXS, GSPSGXPXSXS, GSPSGTPXSXS where X = Arg, Lys, or His	Cation exchange, IMAC
HHHHHH, HHHHHHHH	IMAC
STRPSRRSRRG, STRRGTRRGTRRG,	Cation exchange
STRPSRGRARG, STRPSRRARG, STRPSRRRRG,	Cation exchange
STEPSEESEEG, STEEGTEEGTEEG,	Anion exchange
STEPSEGEAEG, STEPSEEAEG, STEPSEEEEG,	Anion exchange

Table 8: Trypsin Cleavage Sequences

P4	P3	P2	P1	P1'	P2'
S	A	S	R	S	A
S	A	S	K	S	A
G	S	G	R	A	T
E	A	A	R	H	H
A	P	G	R	H	H
G	S	G	R	G	S
			R	X*	
			K	X*	

* X = any L-amino acid other than proline

Table 9: Proteases and Protease Cleavage Sequences

Protease Acting Upon Sequence	Exemplary Cleavage Sequence	Cleavage Sequences*
FXIa	KLTR↓AET	KD/FL/T/R/VA/VE/GT/GV
FXIa	DFTR↓VVG	KD/FL/T/R/VA/VE/GT/GV
FXIIa	TMTR↓IVGG	
Kallikrein	SPFR↓STGG	-/-/FL/RY/SR/RT/-/-
FVIIa	LQVR↓IVGG	
FIXa	PLGR↓IVGG	-/-/G/R/-/-/-/-
FXa	IEGR↓TVGG	IA/E/GFP/R/STI/VFS/-/G
FIIa (thrombin)	LTPR↓SLLV	-/-/PLA/R/SAG/-/-/-
Elastase-2	LGPV↓SGVP	-/-/-/VIAT/-/-/-/-
Granzyme-B	VAGD↓SLEE	V/-/-/D/-/-/-/-
MMP-12	GPAG↓LGGA	G/PA/-/G/L/-/G/-
MMP-13	GPAG↓LRGA	G/P/-/G/L/-/GA/-
MMP-17	APLG↓LRLR	-/PS/-/-/LQ/-/LT/-
MMP-20	PALP↓LVAQ	
TEV	ENLYFQ↓G	ENLYFQ/G/S
Enterokinase	DDDK↓IVGG	DDDK/IVGG
Protease 3C (PreScission™)	LEVLFQ↓GP	LEVLFQ/GP
Sortase A	LPKT↓GSES	L/P/KEAD/T/G/-/EKS/S

Trypsin	K↓X** or R↓X	K/X or R/X
Trypsin	R↓X**	SASRSA

↓indicates cleavage site
* the listing of multiple amino acids before, between, or after a slash indicate alternative amino acids that can be substituted at the position; "-" indicates that any amino acid may be substituted for the corresponding amino acid indicated in the middle column
** x is any L-amino acid other than proline

[00266] In another embodiment, XTEN can be designed such that one or both affinity tags linked to the termini and used to facilitate purification can remain part of the final product, eliminating the requirement for a protease release step. If purification tags are designed to remain a part of a drug product, then tag sequences are selected that do not elicit a pronounced immune response. Immunogenicity can be predicted using computational prediction algorithms or experimental assays. Sequence, that avoid T-cell and B-cell epitopes are preferred. Non-limiting examples of sequences incorporated into the terminus of XTEN sequences that facilitate capture and that may optionally remain associated with the conjugate constructs are provided in Table 7.

10. Compositions for Increased Expression of XTEN

[00267] In another aspect, the invention provides constructs comprising polynucleic acid sequences encoding XTEN and methods of making the XTEN for use in the subject conjugates in which additional encoding polynucleotide helper sequences are added to the 5' end of polynucleotides encoding the XTEN or are added to the 5' end of sequences encoding an affinity tag linked to the 5' end of sequences encoding an XTEN to enhance and facilitate the expression of the XTEN or XTEN with cleavage sequences linked to affinity tag polypeptides in transformed host cells, such as bacteria. Examples of such encoded helper sequences are given in Table 10 and in the Examples. In one embodiment, the invention provides a polynucleotide sequence construct encoding a polypeptide comprising a helper sequence having at least about 80%, or at least about 90%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity to a sequence selected from Table 10 linked to the N-terminus of a first affinity tag selected from the group of sequences set forth in Table 7 that, in turn, is either linked to a cleavage sequence described herein or directly to the N-terminus of an XTEN having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94% sequence identity, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99% to a sequence selected from the group of sequences set forth in Tables 2 and 3. The invention provides expression vectors encoding the constructs useful in methods to produce substantially homogeneous preparations of polypeptides and XTEN at high expression levels. In some embodiments, the invention provides methods for producing a substantially homogenous population of polypeptides comprising an XTEN and a first and a second affinity tag and a helper

sequence, the method comprising culturing in a fermentation reaction a host cell that comprises a vector encoding a polypeptide comprising an XTEN and the first and second affinity tag under conditions effective to express the polypeptide such that more than about 2 g/L, or more than about 3 g/L, or more than about 4 g/L, or more than about 5 g/L, or more than about 6 g/L, or more than about 7 grams per liter (7 g/L) of the polypeptide is produced as a component of a crude expression product of the host cell when the fermentation reaction reaches an optical density of at least 130 at a wavelength of 600 nm. In one embodiment, the method further comprises the steps of adsorbing the polypeptide onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate; eluting and recovering the polypeptide; adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag of the polypeptide onto the chromatography substrate; eluting the polypeptide; and recovering the substantially homogeneous polypeptide preparation. In one embodiment of the foregoing method, the vector further comprises nucleotides encoding a helper sequence at the N-terminus of the encoded polypeptide wherein the helper sequence has at least 80%, or at least 90%, or at least 95% sequence identity to a sequence set forth in Table 10. In other embodiments, the invention provides methods for producing a substantially homogenous population of polypeptides comprising an XTEN and a first and a second affinity tag and a helper sequence, the method comprising culturing in a fermentation reaction a host cell that comprises a vector encoding a polypeptide comprising an XTEN and the first and second affinity tag under conditions effective to express the polypeptide product at a concentration of more than about 10 milligrams/gram of dry weight host cell (mg/g), or at least about 250 micromoles/L, or about 300 micromoles/L, or about 350 micromoles/L, or about 400 micromoles/L, or about 450 micromoles/L, or about 500 micromoles/L of said polypeptide when the fermentation reaction reaches an optical density of at least 130 at a wavelength of 600 nm. In one embodiment of the foregoing, the method further comprises the steps of adsorbing the polypeptide onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate; eluting and recovering the polypeptide; adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag of the polypeptide onto the chromatography substrate; eluting the polypeptide; and recovering the substantially homogeneous polypeptide preparation. In one embodiment of the foregoing method, the vector further comprises nucleotides encoding a helper sequence at the N-terminus of the encoded polypeptide wherein the helper sequence has at least 80%, or at least 90%, or at least 95% sequence identity to a sequence set forth in Table 10. In other embodiments, the invention provides methods for producing a substantially homogenous population of polypeptides comprising an XTEN and a first and a second affinity tag and a helper

sequence, the method comprising culturing in a fermentation reaction a host cell that comprises a vector encoding a polypeptide comprising an XTEN and the first and second affinity tag under conditions effective to express the polypeptide product at a concentration of more than about 10 milligrams/gram of dry weight host cell (mg/g), or at least about 15 mg/g, or at least about 20 mg/g, or at least about 25 mg/g, or at least about 30 mg/g, or at least about 40 mg/g, or at least about 50 mg/g of said polypeptide when the fermentation reaction reaches an optical density of at least 130 at a wavelength of 600 nm. In one embodiment of the foregoing, the method further comprises the steps of adsorbing the polypeptide onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate; eluting and recovering the polypeptide; adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag of the polypeptide onto the chromatography substrate; eluting the polypeptide; and recovering the substantially homogeneous polypeptide preparation. In one embodiment of the foregoing method, the vector further comprises nucleotides encoding a helper sequence at the N-terminus of the encoded polypeptide wherein the helper sequence has at least 80%, or at least 90%, or at least 95% sequence identity to a sequence set forth in Table 10. In another embodiment, the constructs of the foregoing methods of the paragraph further comprise nucleotides encoding protease cleavage sequences between the affinity tags and the XTEN and the method provides that the recovered polypeptides of the preparation are treated with a protease capable of cleaving the cleavage sequences, such as but not limited to trypsin, thereby releasing the XTEN from the polypeptide; the XTEN is adsorbed onto a chromatography substrate under conditions effective to capture the XTEN; the XTEN is then eluted and recovered as a substantially homogeneous XTEN.

Table 10: Examples of helper sequences to facilitate protein expression, secretion and processing in bacteria

Amino Acid Sequence*	Amino Acid at Position**					
	X1	X2	X3	X4	X5	Z
ADAQKAADNKKP						
KTLVYCSEGSPE						
ENNAQTTNESAG						
KDTIALVVSTLN						
APKDNTWYTGA						
ADVPAGVTLAEK						
KIEEGKLVIWIN						
AEATTAAGGA						
ATGTATSEGSPE						
EPTAATTGESAG						
AETTAPAGST						
APTEATAGTGA						
AETPAGATGAE						

Amino Acid Sequence*	Amino Acid at Position**					
	X1	X2	X3	X4	X5	Z
APEEGTAGGA						
SLSTEATAKIVSEFGRDAN						
ANPEQLEEQREETRLIIEE						
SASTEATAKAASEAGRDAN						
ANPEQAEEQREETR						
ANPEQAEEQREET						
ANPEQAEEQSEET						
KNPEQAEEQREET						
KNPEQAEEQSEET						
KNPEQAEEQAEEQREET						
KNPEQAEEQAEEQSEET						
KNHEQAEEQAEEQSEET						
KKHEQAEEQAEEQSEET						
KKPEQAEEQAEEQREET						
KNHEQEKEKAEEQSEET						
KKQEQEEKKAEEQREET						
KNHEKDEKKAEEQSEET						
KKQEQEKEQAEEQREET						
KNPEQEKEKAEEQREET						
KKPEQEEKQAEEQREET						
KKQEQEKEQAEEQAESEREET						
KKQEQEKEQAEEQSQSQREET						
KKQEQEKEQAEEQSESEREET						
KKQEQEKEQAEEQAKAESEAEREET						
KKQEQEKEQAEEQSKSQAEAEREET						
KKQEQEKEQAEEQAQAQAEDEREET						
KKQEQEKEQAEEQSKSKAEDEREET						
KKQEQEKEQAEEQPEVQREET						
KKQEQEKEQAEEQVENPREET						
KKQEQEKEQAEEQELCEREET						
KKQEQEKEQAEEQGIDTREET						
KNPEQAEEQX1EET	S/R					
ANPEQAEEQX1EET	S/R					
KNPEQAEEQAEEQX1EET	S/R					
KX2X3EQAEEQAEEQX1EET	S/R	K/N	K/N/T/Q/H/P/E/D/A/R/S			
$KX2(X3)_{10}QX1EET$	S/R	K/N	K/N/T/Q/H/P/E/D/A/R/S			
$KX2(X3)_{7}AEEQX1EET$	S/R	K/N	K/N/T/Q/H/P/E/D/A/R/S			
$KX2X3EQE(X3)_{3}AEEQREET$		K/N	K/N/T/Q/H/P/E/D/A/R/S			
$KX2X3EQE(X3)_{3}AEE(X3)_{5}$		K/N	K/N/T/Q/H/P/E/D/A/R/S			
$KKQEQEKEQAEEQ(X4X5)_{2}REET$				A/S	K/Q/E	
$KKQEQEKEQAEEQ(X4X5)_{4}REET$				A/S	K/Q/E	
$KKQEQEKEQAEEQ(Z)_{4}REET$						any
$KX2(X3)_{n}$, where n=10-40		K/N	K/N/T/Q/H/P/E/D/A/R/S			
$(X3)_{n}$, where n=10-50			K/N/T/Q/H/P/E/D/A/R/S			
$KX2QEQEKEQAEEQ(X4X5)_{n}X1EET$, where n=0-10	S/R	K/N		A/S	K/Q/E	
$KX2(X3)_{n}(X4X5)_{m}X1EET$, where n=5-20 and m=0-10	S/R	K/N	K/N/T/Q/H/P/E/D/A/R/S	A/S	K/Q/E	
$KX2(X3)_{n}(Z)_{m}X1EET$,where n=5-20 and m=0-20	S/R	K/N	K/N/T/Q/H/P/E/D/A/R/S			any

* where n or m=0, the adjoining amino acids are contiguous
** indicates the amino acid(s) that can be utilized at the given position in the amino acid sequence entries, with the alternatives separated by "/"

III). PAYLOADS

[00268] The present invention relates in part to XTEN conjugates linked to one or more payload molecules. It is contemplated that XTEN can be linked to a broad diversity of payload molecules, including biologically active peptides, proteins, polymers, pharmacologically active small-molecules, polynucleic acids, targeting peptides and proteins, targeting small molecules, antibodies and antibody fragments, and imaging small-molecule payloads, as well as combinations of these types of payloads resulting in compositions with 2, 3, 4 or more types of payloads. The invention addresses a long-felt need in increasing the terminal half-life of exogenously administered therapeutic and diagnostic payloads to a subject in need thereof, as well as combinations of payloads that may include a therapeutic component and a targeting component.

[00269] Non-limiting examples of functional classes of pharmacologically active payload agents for use in linking to an XTEN of the invention may be any one or more of the following: hypnotics and sedatives, psychic energizers, tranquilizers, respiratory drugs, anticonvulsants, muscle relaxants, antiparkinson agents (dopamine antagnonists), analgesics, anti-inflammatories, antianxiety drugs (anxiolytics), appetite suppressants, antimigraine agents, muscle contractants, anti-infectives (antibiotics, antivirals, antifungals, vaccines), antiarthritics, antimalarials, antiemetics, anepileptics, bronchodilators, coagulation factors, cytokines, chemokines, interleukins, growth factors, growth hormones, endocrine hormones, exocrine hormones, insulin, glucose-regulating peptides, anti-cancer agents, antithrombotic agents, antihypertensives, cardiovascular drugs, antiarrhythmics, antioxicants, anti-asthma agents, hormonal agents (including contraceptives), sympathomimetics, diuretics, lipid regulating agents, antiandrogenic agents, antiparasitics, anticoagulants, neoplastics, antineoplastics, hypoglycemics, nutritional agents and supplements, growth supplements, antienteritis agents, vaccines, antibodies, diagnostic agents, contrasting agents, and radioactive imaging agents.

[00270] More particularly, the active payload may fall into one of a number of structural classes, including but not limited to small molecule drugs, biologically active proteins (peptides, polypeptides, proteins, recombinant proteins, antibodies, and glycoproteins), steroids, nucleotides, oligonucleotides, polynucleotides, fats, electrolytes, and the like. For the XTEN-payload conjugation compositions, it is specifically contemplated that a payload can be a pharmacologically active agent that possesses a suitably reactive functional group, including, but not limited to a native amino group, a sulfydryl group, a carboxyl group, an aldehyde group, a ketone group, an alkene group, an alkyne group, an azide group, an alcohol group, a heterocycle,

or, alternatively, is modified to contain at least one of the foregoing reactive groups suitable for coupling to either an XTEN, XTEN-cross-linker, or XTEN-click-chemistry reactant of the invention using any of the conjugation methods described herein or are otherwise known to be useful in the art for conjugating such reactive groups. Specific functional moieties and their reactivities are described in Organic Chemistry, 2nd Ed. Thomas Sorrell, University Science Books, Herndon, VA (2005). Further, it will be understood that any payload containing a reactive group or that is modified to contain a reactive group will also contain a residue after conjugation to which either the XTEN, the XTEN-cross-linker, or the XTEN-click-chemistry reactant is linked.

[00271] Exemplary payloads suitable for covalent attachment to either an XTEN polymer, XTEN-cross-linker, or XTEN-click-chemistry reactant include biologically active proteins and pharmacologically active small molecule drugs with activity. Exemplary drugs suitable for the inventive compositions can be found as set forth in the official United States Pharmacopeia, official Homeopathic Pharmacopeia of the United States, or official National Formulary, in the Physician's Desk Reference (PDR) and in the Orange Book maintained by the U.S. Food and Drug Administration (FDA). Preferred drugs are those having the needed reactive functional group or those that can be readily derivatized to provide the reactive functional group for conjugation and will retain at least a portion of the pharmacologic activity of the unconjugated payload when conjugated to XTEN.

1. Drugs as payloads

[00272] In some embodiments, the drug payload for conjugation to either the subject XTEN, the XTEN-cross-linkers, or the XTEN-click-chemistry reactants described herein is one or more agents described herein or selected from the payloads of Table 11, or a pharmaceutically acceptable salt, acid or derivative or agonist thereof. In one embodiment, the drug is derivatized to introduce a reactive group for conjugation to the subject XTEN, the XTEN-cross-linkers, or the XTEN-click-chemistry reactants described herein. In another embodiment, the drug for conjugation is derivatized to introduce a cleavable linker such as, but not limited to, valine-citrulline-PAB, wherein the linker is capable of being cleaved by a circulating or an intracellular protease after administration to a subject, thereby freeing the drug from the conjugate.

Table 11: Drugs for Conjugation to XTEN

Drugs
Erlotinib; Bortezomib; Alitretinoin, Allopurinol, arsenic trioxide, clofarabine, dexrazoxane, Fulvestrant; Sutent (SU11248), Letrozole; Imatinib mesylate; PTK787/ZK 222584; Bendamustine; Romidepsin; Pralatrexate; Cabazitaxel (XRP-6258); Everolimus (RAD-001); Abirateron; Oxaliplatin; 5-FU (5-fluorouracil), leucovorin, rapamycin; lapatinib; lonafarnib; sorafenib; gefitinib; cyclosphosphamide; busulfan; improsulfan; piposulfan; benzodopa; carboquone; meturedopa; uredopa; altretamine; triethylenemelamine; triethylenephosphoramide; triethylenethiophosphoramide; trimethylomelamine; bullatacin; bullatacinone; camptothecin; topotecan; bryostatin; callystatin; CC-1065; adozelesin; calicheamycin; auristatin; monomethyl auristatin E (MMAE); monomethyl auristatin F (MMAF); (valine-

Drugs
citrulline-PAB)-monomethyl auristatin E; (valine-citrulline-PAB)-monomethyl auristatin F; carzelesin; bizelesin; cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin; eleutherobin; pancratistatin, sarcodictyin; spongistatin; chlorambucil; chlornaphazine; cholophosphamide; estramustine; ifosfamide; mechlorethamine; mechlorethamine oxide hydrochloride; melphalan; novembichin; phenesterine; prednimustine; trofosfamide; uracil mustard; carmustine; chlorozotocin; fotemustine; lomustine; nimustine; ranimnustine; calicheamicin; dynemicin; dynemicin A; clodronate; esperamicin; neocarzinostatin chromophore; aclacinomysins, actinomycin; anthramycin; azaserine; bleomycin; cactinomycin; carabicin; carminomycin; carzinophilin; chromomycinis; dactinomycin; daunorubicin; detorubicin; 6-diazo-5-oxo-L-norleucine; doxorubicin; morpholino-doxorubicin; lenalidomide, cyanomorpholino-doxorubicin; (valine-citrulline-PAB)-doxorubicin; 2-pyrrolino-doxorubicin and deoxydoxorubicin; epirubicin; esorubicin; idarubicin; marcellomycin; mitomycin C; mycophenolic acid; nogalamycin; olivomycin; pepiomycin; potfiromycin; puromycin; quelamycin; rodorubicin; streptonigrin; streptozocin; tubercidin; ubenimex; zinostatin; zorubicin; 5-fluorouracil (5-FU); fdenopterin; methotrexate; pteropterin; trimetrexate; fludarabine; 6-mercaptopurine; thiamiprine; ancitabine; azacitidine; 6-azauridine; carmofur; cytarabine; dideoxyuridine; doxifluridine; enocitabine; meclorethamine, floxuridine; calusterone; dromostanolone propionate; epitiostanol; mepitiostane; testolactone; aminoglutethimide; trilostane; frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elformithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansine; ansamitocins; mitoguazone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; methoxsalen, podophyllinic acid; 2-ethylhydrazide; procarbazine; razoxane; rhizoxin; ribavirin; zidovudine; acyclovir; gangcyclovir; vidarabine; idoxuridine; trifluridine; foscarnet; amantadine; rimantadine; saquinavir; indinavir; ritonavir; alpha-interferons and other interferons; AZT; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2''-trichlorotriethylamine; T-2 toxin; verracurin A; roridin A; anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids; epaclitaxel; paclitaxel; docetaxel; doxetaxel; irinotecan; pemetrexed; chloranbucil; gemcitabine; 6-thioguanine; cisplati; carboplatin; vinblastine; platinum; etoposide, VP-16; ifosfamide; mitoxantrone; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoic acid; capecitabine; mesna, lidocaine; bupivacaine; memantine; quinacrine, donepezil; rivastigmine; galantamine; morphine; oxycodone; hydromorphone; oxymorphone; metopon; apomorphine; normorphine, etorphine; buprenorphine; meperidine; loperamide; anileridine; ethoheptazine; piminidine; betaprodine; diphenoxylate; fentanil; sufentanil; alfentanil; remifentanil; levorphanol; dextromethorphan; phenazocine; pentazocine; cyclazocine; methadone; isomethadone; propoxyphene; naloxone; naltrexone; treprostinil; N-methylnaloxone; 6-amino-14-hydroxy-17-allylnordesomorphine; naltrendol;, N-methylnaltrexone; nalbuphine; butorphanol; cyclazocine; pentazocine,; nalmephene; naltrindole; nor-binaltorphimine; oxilorphan; 6-amino-6-desoxo-naloxone; pentazocine; levallorphanmethylnaltrexone; buprenorphine; cyclorphan; levalorphan; cyclosporine; cyclosporine A; mycophenylate mofetil; sirolimus; tacrolimus; prednisone; azathioprine; cyclophosphamide; prednisone; aminocaproic acid; chloroquine; hydroxychloroquine; dexamethasone; chlorambucil; danazol; bromocriptine; Nilotinib (AMN107) ; Nelarabine, amifostine, amiodarone, aminocaproic acid, aminohippurate sodium, aminoglutethimide, aminolevulinic acid, aminosalicylic acid, amsacrine, anagrelide, anastrozole, asparaginase, anthracyclines, bexarotene, bicalutamide, bleomycin, buserelin, busulfan, cabergoline, capecitabine, carboplatin, carmustine, chlorambucin, cilastatin sodium, cisplatin, cladribine, clodronate, cyclophosphamide, cyproterone, cytarabine, camptothecins, 13-cis retinoic acid, all trans retinoic acid; dacarbazine, dactinomycin, daunorubicin, deferoxamine, dexamethasone, diclofenac, diethylstilbestrol, docetaxel, doxorubicin, epirubicin, estramustine, etoposide, exemestane, fexofenadine, fludarabine, fludrocortisone, fluorouracil, fluoxymesterone, flutamide, gemcitabine, epinephrine, L-Dopa, hydroxyurea, idarubicin, ifosfamide, imatinib, irinotecan, itraconazole, goserelin acetate, letrozole, leucovorin, levamisole, lisinopril, lovothyroxine sodium, mechlorethamine, medroxyprogesterone, megestrol, melphalan, metaraminol bitartrate, metoclopramide, mexiletine, mitomycin, mitotane, naloxone, nicotine, nilutamide, octreotide, pamidronate, pilcamycin, porfimer, prednisone, prochlorperazine, ondansetron, raltitrexed, sirolimus, tacrolimus, tamoxifen, temozolomide, testosterone, tetrahydrocannabinol, thalidomide, thioguanine, topotecan, tretinoin, valrubicin, vincristine, vindesine, vinorelbine, dolasetron, granisetron; formoterol, fluticasone, leuprolide, midazolam, alprazolam, amphotericin B, podophylotoxins, nucleoside antivirals, aroyl hydrazones, sumatriptan; macrolides such as erythromycin, oleandomycin, troleandomycin, roxithromycin, clarithromycin, davercin, azithromycin, flurithromycin, dirithromycin,

Drugs
josamycin, spiromycin, midecamycin, leucomycin, miocamycin, rokitamycin, andazithromycin, and swinolide A; fluoroquinolones such as ciprofloxacin, ofloxacin, levofloxacin, trovafloxacin, alatrofloxacin, moxifloxicin, norfloxacin, enoxacin, grepafloxacin, sunitinib, gatifloxacin, lomefloxacin, sparfloxacin, temafloxacin, pefloxacin, amifloxacin, fleroxacin, tosufloxacin, prulifloxacin, irloxacin, pazufloxacin, clinafloxacin, and sitafloxacin; aminoglycosides such as gentamicin, netilmicin, paramecin, tobramycin, amikacin, kanamycin, neomycin, and streptomycin, vancomycin, teicoplanin, rampolanin, mideplanin, colistin, daptomycin, gramicidin, colistimethate; polymixins such as polymixin B, capreomycin, bacitracin, penems; penicillins including penicllinase-sensitive agents like penicillin G, penicillin V; penicllinase-resistant agents like methicillin, oxacillin, cloxacillin, dicloxacillin, floxacillin, nafcillin; gram negative microorganism active agents like ampicillin, amoxicillin, and hetacillin, cillin, and galampicillin; antipseudomonal penicillins like carbenicillin, ticarcillin, azlocillin, mezlocillin, and piperacillin; cephalosporins like cefpodoxime, cefprozil, ceftbuten, ceftizoxime, ceftriaxone, cephalothin, cephapirin, cephalexin, cephradrine, cefoxitin, cefamandole, cefazolin, cephaloridine, cefaclor, cefadroxil, cephaloglycin, cefuroxime, ceforanide, cefotaxime, cefatrizine, cephacetrile, cefepime, cefixime, cefonicid, cefoperazone, cefotetan, cefinetazole, ceftazidime, loracarbef, and moxalactam, monobactams like aztreonam; and carbapenems such as imipenem, meropenem, pentamidine isethiouate, albuterol sulfate, lidocaine, metaproterenol sulfate, beclomethasone diprepionate, triamcinolone acetamide, budesonide acetonide, fluticasone, ipratropium bromide, flunisolide, cromolyn sodium, and ergotamine tartrate; taxanes such as paclitaxel; SN-38, tyrphostines, 20-epi-1,25 dihydroxy vitaminD3, 5-ethynyluracil, abiraterone, Acivicin, Aclarubicin, Acodazole Hydrochloride, AcrQnine, acylfulvene, adecypenol, adramycin, Aldesleukin, ALL-TK antagonists, ambamustine, amidox, Ambomycin, Ametantrone Acetate, amrubicin, andrographolide, angiogenesis inhibitors, antagonist D, antagonist G, antarelix, anti-androgen, anti-dorselizing morphogenetic protein-1, anti-estrogen, antimetabolites, anti-neoplaston, anti-oestrogens, anti-sense oligonucleotides, anti-venom, aphidicolinglycinate, apoptosis gene modulators, apoptosis regulators, apurinic acid, ara-CDP-DL-PTBA, arginine deaminase, Asperlin, asulacrine, atamestane, atrimustine, atrsacrine, axinastatin 1, axinastatin 2, axinastatin 3, azasetron, azatoxin, azatyrosine, Azptepa:Azotomycin, baccatin III derivatives, balanol, Batimastat, BCR/ABLantagonists, benzochlorins, Benzodepa, benzoylstaurosporine, staurosporine, beta-alethine, betaclamycin B, betalactamderivatives, betamethasone, betulinic acid, bFGFinhibitor, Bicalutamide, Bisantrene Hydrochloride, bisaziridinylspermine, bisnafide, Bisnafide Dimesylate, bistrateneA, Bleomycin Sulfate, breflate, Brequinar Sodium, bromine epiandrosterone, Bropirimine, budotitane, buthionine sulfoximine, calcipotriol, calphostin C, camptothecin derivatives, canarypox IL-2, capedtabine, Caracemide, Carbetimer, carboxamide-amino-triazole:carboxyamidotriazole, CaRestM3, CARN700, cartilage derived inhibitor, Carubicin Hydrochloride, casein kinase inhibitors(ICOS), castanospermine, cecropin B, Cedefingol, cetrorelix, chlorins, chloroquinoxaline sulfonamide, , chlorotrianisene, cicaprost, Cirolemycin, cis-porphyrin, clomifene analogues, clotrimazole, collismycin A, collismycin B, combretastatin A4, combretastatin analogue, conagenin, crambescidin 816, crisnatol, Crisnatol Mesylate, cryptophycin 8, cryptophycin A derivatives, curacin A, cyclopentanthraquinones, cycloplatam, cypemycin, cytarabineocfosfate, cytolyticfactor, cytostatin, cytotoxic agents, Daunorubicin Hydrochloride, Decitabine, dehydrodidemnin B, deslorelin, dexifosfamide, Dexormaplatin, dexrmzoxane, dexverapamil, Dezaguanine, Dezaguanine Mesylate, DHEA, diaziquorie, dicarbazine, didemnin 13, didox, diethylnorspermine, dihydro-5-azacytidine:dihydrotaxol,9-, dioxamycin, diphenylspiromustine, docosanol, Doxorubicin Hydrochloride, Droloxifene, Droloxifene Citrate, Dromostanolone Propionate, dronabinol, Duazomycin, duocannycin SA, ebselen, ecorustine, edelfosine, edrocolomab, Eflomithine Hydrochloride, eflornithine, elemene, Elsamitrucin, emitefur, Enloplatin, Enpromate, epiandrosterone, Epipropidine, Epirubicin Hydrochloride, epristeride, Erbulozole, erythrocyte gene therapy, Esorubicin Hydrochloride, estramustine analogue, estrogen agonists, estrogen antagonists, Etanidazole, ethinyloestradiol, Ethiodized Oil I131, Etoposide Phosphate, Etoprine, fadrozole, Fadrozole Hydrochloride, Fazarabine, fazarabine, fenretinide, Fenretinide:Floxuridine, finasteride, flavopiridol, flezelastine, Fludarabine Phosphate, fluorodaunorunicin hydrochloride, Flurocitabine, forfenimex, formestane, Fosquidone, fostriecin, Fostriecin Sodium, gadoliniumtexaphyrin, galocitabine, ganirelix, gelatinase inhibitors:gemcitabine, Gemcitabine Hydrochloride, glutathione inhibitors, Gold Au198, goserelin, hepsulfam, heregulin, hexamethylenebisacetamide, hexamethylmelamine, human chorionic gonadotrophin:monophosphoryl lipid A + myobacterium cell walls k, hypericin, ibandronic acid, Idarubicin Hydrochloride, idoxifene, idramantone, Ilmofosine, ilomastat, imidazoacridones, imiquimod, immuno stimulant peptides:insulin-like growth factor-1 receptor inhibitor, interferon agonists, Interferon Alfa-2a, Interferon Alfa-2b, Interferon Alfa-n1, Interferon Alfa-n3, Interferon Beta-Ia, Interferon Gamma-Ib, iobenguane, iododoxorubicin, ipomeanol, Iproplatin, Irinotecan Hydrochloride, iroplact, irsogladine, isobengazole, isohomohalicondrin

Drugs
B, itasetron, jasplakinolide, kahalalide F, lamellarin-Ntriacetate, lanreotide, Lanreotide Acetate, leinamycin, lenograstim, lentinan sulfate, leptolstatin, leukemia inhibiting factor, leukocyte alpha interferon, Leuprolide Acetate, leuprolide+estrogen+progesterone, leuprorelin, liarozole, Liarozole Hydrochloride, linear polyamine analogue, lipophilic disaccharide peptide, lipophilic platinum compounds, lissoclinamide7, lobaplatin, lombricine, lometrexol, Lometrexol Sodium, lonidamine, Losoxantrone Hydrochloride, lovastatin, loxoribine, luprolide, lurtotecan, lutetlumtexaphyrin, lysofylline, lyticpeptides, maitansine, mannostatin A, marimastat, Masoprocol, maspin, matrilysin inhibitors, matrix metallo proteinase inhibitors, mecaptopurine, Mechlorethamine Hydrochloride, Megestrol Acetate, Melengestrol Acetate, Menogaril, merbarone, meterelin, methioninase, methlorethamine, Metoprine, Meturedepa, microalgal, mifepristone, MIFinhibitor, miltefosine, mirimostim, mismatched double stranded RNA, Mitindomide, Mitocarcin, Mitocromin, Mitogillin, mitoguazone, Mitomalcin, mitomycin analogues, mitonafide, Mitosper, mitotoxin fibroblast growth factor-saporin, mofarotene, molgramostim, monoclonal antibody, multiple drug resistance gene inhibitor, multiple tumor suppressor1-based therapy, mustard anticancer agent, mutamycin, mycaperoxide B, mycobacterial cell wall extract, Mycobacterium bovis, myriaporone, N-acetyldinaline:N-substitutedbenzamides, nafarelin, nagrestip, naloxone+pentazocine, napavin, naphterpin, nartograstim, nedaplatin, nemorubicin, neridronic acid, neutral endo peptidase, nisamycin, nitric oxide modulators, nitrogen mustard derivatives, nitroxide antioxidant, nitrullyn, Nocodazole:Nogalamycin, O6-benzylguanine, oestradiol, okicenone, oligonucleotides, onapristone:ondansetron, ondansetron, oracin, oral cytokine inducer, Ormaplatin, osaterone, oxaunomycin, Oxisuran, palauamine, palmitoylrizoxin, pamidronic acid, panaxytriol, panomifene, parabactin, pazelliptine:pegaspargase, Pegaspargase, peldesine:pentosanpolysulfatesodium, Peliomycin, Pentamustine, pentrozole, Peplomycin Sulfate, perflubron, Perfosfamide, perillyl alcohol, phenazinomycin, phenylacetate, phosphatase inhibitors, picibanil, pilocarpine hydrochloride, piritrexim, Piroxantrone Hydrochloride, placetin A, placetin B, plasminogen activator inhibitor, platinum complex, platinum compounds, platinum-triamine complex, Plicamycin, Plomestane, Porfimer Sodium, Procarbazine Hydrochloride, propylbis-acridone, prostaglandin J2, prostatic carcinoma, proteasome inhibitors, protein A-based immune modulator, protein kinase C inhibitor, protein tyrosine phosphatase inhibitors, purine nucleoside phosphorylase inhibitors, Puromycin Hydrochloride, purpurins, Pyrazofurin, pyrazoloacridine, pyridoxylated hemoglobin polyoxyethylene conjugate, raf antagonists, ramosetron, rasfarnesyl protein transferase inhibitors, ras inhibitors:ras-GAP inhibitor, retelliptine demethylated, rhenium Re186 etidronate, Riboprine, ribozymes, RII retinamide, RM-131 (ghrelin agonist), RM-493 (agonis for melanocortin type 4 receptor), Rogletimide, rohitumine, romurtide, roquinimex, rubiginone B1, ruboxyl, Safingol Hydrochloride, Safingol, saintopin:Sar CNU, sarcophytol A, sargramostim, Sdi1 mimetics, Semustine, senescence derived inhibitor 1, sense oligonucleotides, signal transduction inhibitors, signal transduction modulators, Simtrazene, single chain antigen binding protein, sobuzoxane, sodium borocaptate, sodium phenylacetate, solverol, somatomedin binding protein, sonermin, Sparfosate Sodium, sparfosic acid, Sparsomycin, Spirogermanium Hydrochloride, Spiromustine, spiromustine:splenopentin, Spiroplatin, splcamycin D, squalamine, stem cell inhibitor, stem-cell division inhibitors, stipiamide, stromelysin inhibitors, Strontium Chloride Sr89, sulfmosine, Sulofenur, superactive vasoactive intestinal peptide antagonist, suradista, suramin, swainsonine, synthetic glycosamino glycans, Talisomycin, tallimustine, tamoxifen methiodide, tauromustine, tazarotene, Tecogalan Sodium, Tegafur, tellurapyrylium, telnoporfin, telomerase inhibitors, Teloxantrone Hydrochloride, Temoporfin, ternozolomide, Teroxirone, tetrachlorodecaoxide, tetrazomine, texotere, thallblastine, thiocoraline, thrombopoietin mimetic, thymalfasin, thymopoietin receptor agonist, thymotrinan, thyroid stimulating hormone, Tiazofurin, tinethylotiopurpurin, Tirapazamine, titanocene dichloride, Topotecan Hydrochloride, topsentin, toremifene, Toremifene Citrate, totipotent stem cell factor, translation inhibitors, Trestolone Acetate, triacetyluridine, triciribine, Triciribine Phosphate:Trimetrexate, Trimetrexate Glucuronate, Triptorelin, triptorelin:tropisetron, tubulozole hydrochloride, turosteride, tyrosine kinase inhibitors, UBC inhibitors, urodepa, urogenital sinus-derived growth inhibitory factor, urokinase receptor antagonists, vapreotide, variolin B, vector system, velaresol, venom, veramine, verdins, Verleporfin, verteporfin, Vinblastine Sulfate, vincristine sulfate, vindesine, Vindesine Sulfate, Vinepidine Sulfate, Vinglycinate Sulfate, Vinleurosine Sulfate, vinorelbine tartrate, vinrosidine sulfate, vinxaltine, Vinzolidine Sulfate, vitaxin, Vorozole, zanoterone, Zeniplatin, zilascorb, zinostatin stimalamer, Zorubicin Hydrochloride, Bovine pancreatic RNase, Human pancreatic RNAse, Mammalian pancreatic RNase, onconase, ranpirnase, pokeweed antiviral protein, rachelmycin, ricin-A chain, gelonin, everolimus, carfilzomib, tubulysin, tubulysin B, tubulysin M, maytansinoid DM1, maytansinoid DM4, triptolide, SJG-136, apaziquone, irofulven, illudin S, tomaymycin, zoledronate

2. Biologically Active Proteins as Payloads

[00273] In another aspect, the invention provides XTEN-payload compositions in which the payload is a biologically active protein, either as a peptide or polypeptide. In some embodiments of XTEN-payload conjugates, the payload is any pharmacologically active peptide or polypeptide that can be expressed recombinantly as a fusion protein linked to one or more XTEN. In other embodiments of XTEN-payload conjugates, the payload is any pharmacologically active peptide or polypeptide that can be conjugated to one or more XTEN. The conjugates may be in a configuration as described herein, below. The exemplary peptide or polypeptide payloads are meant to encompass analogs, agonists, antagonists, inhibitors, and isomers. It will be understood that the subject peptides and proteins encompass synthetic, semi-synthetic, recombinant, native, glycosylated, and non-glycosylated forms, as well as biologically active fragments, sequence variants, species variants, homologs and mutations thereof as long as the resulting variant protein retains a portion of activity of the parent or native protein.

[00274] Biologically active protein sequences can be obtained from publicly available databases, patents, or literature references and other such sources that are well known in the art. For example, sequences can be obtained from Universal Protein Resource (UniProt)/Swiss-Prot, European Bioinformatics Institute (EBI), the SIB Swiss Institute of Bioinformatics, the Protein Information Resource (PIR). Chemical Abstracts Services (CAS) Registry Numbers (published by the American Chemical Society) and/or GenBank Accession Numbers (e.g., AAA-AZZ, HAA-HZZ, JAA-JZZ), Model Protein identifiers available through the National Center for Biotechnology Information (NCBI) webpage, available on the world wide web at ncbi.nlm.nih.gov that correspond to entries in the CAS Registry or GenBank database that contain an amino acid sequence of the protein of interest or of a fragment or variant of the protein. For such sequence identifiers provided herein, the summary pages associated with each of these CAS and GenBank and GenSeq Accession Numbers as well as the cited journal publications (e.g., PubMed ID number (PMID)) are each incorporated by reference in their entireties, particularly with respect to the amino acid sequences described therein.

[00275] In one embodiment, the XTEN-payload composition, whether in recombinant or conjuate form, comprises one or more molecules of a biologically active peptide or protein that includes, but is not limited to a peptide or polypeptide selected from the payloads set forth in Table 12, or a sequence variant thereof that retains at least a portion of the activity of the biologically active protein. By "sequence variant," it is meant that the biologically active protein exhibits at least about 80%, or 90%, or 91%, or 92%, or 93%, or 94%, or 95%, or 96%, or 97%, or 98%, or 99% sequence identity, when optimally aligned, to that of the known peptide or polypeptide, such as are listed in Table 12.

Table 12: Biologically Active Proteins for linking to XTEN

Protein/Peptide Name
EPO, IFN-α, IFN-β, IFN-γ, consensus IFN, factor VII, factor VIII, factor IX, IL-1, IL-2, remicade (infliximab), Rituxan (rituximab), Enbrel (etanercept), Synagis (palivizumab), Reopro (abciximab), Herceptin (trastuzimab), tPA, Cerizyme (imiglucerase), Hepatitus-B vaccine, rDNAse, alpha-1 proteinase inhibitor, C-peptide, fuzeon, G-CSF, GM-CSF, growth hormone, somatropin, growth hormone releasing hormone, insulin, insulin analogues, glucagon, GLP-1, GLP-2, FSH, TNF-receptor, uricase, VEGF, PTH, aspariginase, amdoxovir (DAPD), antide, becaplermin, calcitonins, cyanovirin, denileukin diftitox, erythropoietin (EPO), ceredase, cerezyme, alpha-glucosidase, collagen, cyclosporin, alpha defensins, beta defensins, exendin-4, granulocyte colony stimulating factor (GCSF), thrombopoietin (TPO), alpha-1 proteinase inhibitor, elcatonin, granulocyte macrophage colony stimulating factor (GMCSF), fibrinogen, filgrastim, growth hormones human growth hormone (hGH), growth hormone releasing hormone (GHRH), GRO-beta, GRO-beta antibody, bone morphogenic proteins such as bone morphogenic protein-2, bone morphogenic protein-6, OP-1; acidic fibroblast growth factor, basic fibroblast growth factor, CD-40 ligand, heparin, human serum albumin, low molecular weight heparin (LMWH), interferons such as interferon alpha, interferon beta, interferon gamma, interferon omega, interferon tau, consensus interferon; interleukins and interleukin receptors such as interleukin-1 receptor, interleukin-2, interluekin-2 fusion proteins, interleukin-1 receptor antagonist, interleukin-3, interleukin-4, interleukin-4 receptor, interleukin-6, interleukin-8, interleukin-12, interleukin-13 receptor, interleukin-17 receptor; lactoferrin and lactoferrin fragments, luteinizing hormone releasing hormone (LHRH), insulin, pro-insulin, insulin analogues (e.g., mono-acylated insulin as described in U.S. Pat. No. 5,922,675), amylin, somatostatin, somatostatin analogs including octreotide, vasopressin, follicle stimulating hormone (FSH), influenza vaccine, insulin-like growth factor (IGF), insulintropin, macrophage colony stimulating factor (M-CSF), plasminogen activators such as alteplase, urokinase, reteplase, streptokinase, pamiteplase, lanoteplase, and teneteplase; nerve growth factor (NGF), osteoprotegerin, platelet-derived growth factor, tissue growth factors, transforming growth factor-1, vascular endothelial growth factor, leukemia inhibiting factor, keratinocyte growth factor (KGF), glial growth factor (GGF), T Cell receptors, CD molecules/antigens, tumor necrosis factor (TNF), monocyte chemoattractant protein-1, endothelial growth factors, parathyroid hormone (PTH), thymosin alpha 1, thymosin alpha 1 IIb/IIIa inhibitor, thymosin beta 10, thymosin beta 9, thymosin beta 4, alpha-1 antitrypsin, phosphodiesterase (PDE) compounds, VLA-4 (very late antigen-4), VLA-4 inhibitors, bisphosponates, respiratory syncytial virus antibody, cystic fibrosis transmembrane regulator (CFTR) gene, deoxyreibonuclease (Dnase), bactericidal/permeability increasing protein (BPI), anti-CMV antibody, etanercept, abciximab, afeliomomab, basiliximab, daclizumab, infliximab, ibritumomab tiuexetan, mitumomab, muromonab-CD3, iodine 131 tositumomab conjugate, olizumab, rituximab, trastuzumab (herceptin), boxtox, Dysport, alglucosidase alfa, daptomycin, YH-16 , choriogonadotropin alfa, filgrastim, cetrorelix, interleukin-2, aldesleukin, teceleukin, denileukin diftitox, interferon alfa-n3 (injection), interferon alfa-n1, DL-8234, interferon, Suntory (gamma-1a), interferon gamma, thymosin alpha 1, tasonermin, DigiFab, ViperaTAb, EchiTAb, CroFab, nesiritide, abatacept , alefacept, Rebif , eptotermin alfa, teriparatide (osteoporosis), calcitonin injectable, bone disease), calcitonin (nasal, osteoporosis), etanercept , hemoglobin glutamer 250 (bovine), drotrecogin alfa, collagenase , carperitide, recombinant human epidermal growth factor (topical gel, wound healing), DWP-401, darbepoetin alfa , epoetin omega, epoetin beta, epoetin alfa, desirudin , lepirudin, bivalirudin, nonacog alpha, Mononine, eptacog alfa (activated), recombinant Factor VIII + VWF, Recombinate, recombinant Factor VIII, Factor VIII (recombinant), Alphanate, octocog alfa, Factor VIII, palifermin, Indikinase, tenecteplase, alteplase, pamiteplase, reteplase, nateplase,monteplase, follitropin alfa, rFSH, hpFSH, micafungin, pegfilgrastim, lenograstim, nartograstim, sermorelin, glucagon, exenatide, pramlintide, imiglucerase, galsulfase, Leucotropin, molgramostim, triptorelin acetate, histrelin, histrelin acetate, deslorelin, nafarelin, leuprolide sustained release depot (ATRIGEL), leuprolide implant (DUROS), somatropin, Eutropin, KP-102 program, somatropin, somatropin, mecasermin (growth failure), enfuvirtide, Org-33408, insulin glargine, insulin glulisine, insulin (inhaled), insulin lispro, insulin detemir, insulin (buccal, RapidMist), mecasermin rinfabate, anakinra, celmoleukin, 99mTc-apcitide injection, myelopid, Betaseron, glatiramer acetate, Gepon, oprelvekin, human leukocyte-derived alpha interferons, Bilive, insulin (recombinant), recombinant human insulin, insulin aspart, mecasermin, Roferon-A, interferon-alpha 2, Alfaferone, interferon alfacon-1, interferon alpha, Avonex' recombinant human luteinizing hormone, dornase alfa , trafermin, ziconotide, taltirelin, dibotermin alfa, atosiban, becaplermin, eptifibatide, Zemaira, CTC-111, Shanvac-B , HPV vaccine (quadrivalent), NOV-002, octreotide, lanreotide, ancestim, agalsidase beta,

Protein/Peptide Name
agalsidase alfa, laronidase, prezatide copper acetate (topical gel), rasburicase, ranibizumab, Actimmune, PEG-Intron, Tricomin, recombinant house dust mite allergy desensitization injection, recombinant human parathyroid hormone (PTH) 1-84 (sc, osteoporosis), epoetin delta, transgenic antithrombin III, Granditropin, Vitrase, recombinant insulin, interferon-alpha (oral lozenge), GEM-21S, vapreotide, idursulfase, omapatrilat, recombinant serum albumin, certolizumab pegol, glucarpidase, human recombinant C1 esterase inhibitor (angioedema), lanoteplase, recombinant human growth hormone, enfuvirtide (needle-free injection, Biojector 2000), VGV-1, interferon (alpha), lucinactant, aviptadil (inhaled, pulmonary disease), icatibant, ecallantide, omiganan, Aurograb, pexiganan acetate, ADI-PEG-20, LDI-200, degarelix, cintredekin besudotox, FavId , MDX-1379, ISAtx-247, liraglutide, teriparatide (osteoporosis), tifacogin, AA-4500, T4N5 liposome lotion, catumaxomab, DWP-413, ART-123, Chrysalin, desmoteplase, amediplase, corifollitropin alpha , TH-9507, teduglutide, Diamyd, DWP-412, growth hormone (sustained release injection), recombinant G-CSF, insulin (inhaled, AIR), insulin (inhaled, Technosphere), insulin (inhaled, AERx), RGN-303, DiaPep277, interferon beta (hepatitis C viral infection (HCV)), interferon alfa-n3 (oral), belatacept, transdermal insulin patches, AMG-531, MBP-8298, Xerecept , opebacan, AIDSVAX, GV-1001, LymphoScan, ranpirnase, Lipoxysan, lusupultide, MP52 (beta-tricalciumphosphate carrier, bone regeneration), melanoma vaccine, sipuleucel-T, CTP-37, Insegia, vitespen, human thrombin (frozen, surgical bleeding), thrombin, TransMID, alfimeprase, Puricase, terlipressin, EUR-1008M, recombinant FGF-1, BDM-E, rotigaptide, ETC-216, P-113, MBI-594AN, duramycin (inhaled, cystic fibrosis), SCV-07, OPI-45, Endostatin, Angiostatin, ABT-510, Bowman Birk Inhibitor Concentrate, XMP-629, 99mTc-Hynic-Annexin V, kahalalide F, CTCE-9908, teverelix (extended release), ozarelix, romidepsin, BAY-50-4798, interleukin-4, PRX-321, Pepscan, iboctadekin, rh lactoferrin, TRU-015, IL-21, ATN-161, cilengitide, Albuferon, Biphasix, IRX-2, omega interferon, PCK-3145, CAP-232, pasireotide, huN901-DM1, ovarian cancer immunotherapeutic vaccine, SB-249553, Oncovax-CL, OncoVax-P, BLP-25, CerVax-16, nemifitide, rAAT (inhaled), rAAT (dermatological), CGRP (inhaled, asthma), pegsunercept, thymosin beta-4, plitidepsin, GTP-200, ramoplanin, GRASPA, OBI-1, AC-100, salmon calcitonin (oral, eligen), calcitonin (oral, osteoporosis), examorelin, capromorelin, Cardeva, velafermin, 131I-TM-601, KK-220, TP-10, ularitide, depelestat , hematide, Chrysalin (topical), rNAPc2, recombinant Factor VIII (PEGylated liposomal), bFGF, PEGylated recombinant staphylokinase variant , V-10153, SonoLysis Prolyse, NeuroVax, CZEN-002, islet cell neogenesis therapy, rGLP-1, BIM-51077, LY-548806, exenatide, AVE-0010, GA-GCB, avorelin, AOD-9604, linaclotide acetate, CETi-1, Hemospan, VAL (injectable), insulin, recombinant methionyl human leptin, pitrakinra subcutaneous injection, eczema), pitrakinra (inhaled dry powder, asthma), Multikine, RG-1068, MM-093, NBI-6024, AT-001, PI-0824, Org-39141, Cpn10 (autoimmune iseases/inflammation), talactoferrin (topical), rEV-131 (ophthalmic), rEV-131 (respiratory disease), oral recombinant human insulin (diabetes), RPI-78M, CYT-99007 CTLA4-Ig, DTY-001, valategrast , interferon alfa-n3 (topical), IRX-3, RDP-58, Tauferon, bile salt stimulated lipase, Merispase, alkaline phosphatase, EP-2104R, Melanotan-II, bremelanotide, ATL-104, recombinant human microplasmin, AX-200, SEMAX, ACV-1, Xen-2174, CJC-1008, dynorphin A, SI-6603, LAB GHRH, AER-002, BGC-728, malaria vaccine (virosomes, PeviPRO), ALTU-135, parvovirus B19 vaccine, influenza vaccine (recombinant neuraminidase), malaria/HBV vaccine, anthrax vaccine, Vacc-5q, Vacc-4x, HIV vaccine (oral), HPV vaccine, Tat Toxoid, YSPSL, CHS-13340 , PTH(1-34) liposomal cream (Novasome), Ostabolin-C, PTH analog (topical, psoriasis), MBRI-93.02, MTB72F vaccine (tuberculosis), MVA-Ag85A vaccine (tuberculosis), FAR-404 , BA-210, recombinant plague F1V vaccine, AG-702, OxSODrol, rBetV1, Der-p1/Der-p2/Der-p7 allergen-targeting vaccine (dust mite allergy), PR1 peptide antigen (leukemia), mutant ras vaccine, HPV-16 E7 lipopeptide vaccine, labyrinthin vaccine (adenocarcinoma), CML vaccine, WT1-peptide vaccine (cancer), IDD-5, CDX-110, Pentrys, Norelin, CytoFab, P-9808, VT-111, icrocaptide, telbermin, rupintrivir, reticulose, rGRF, P1A, alpha-galactosidase A, ACE-011, ALTU-140, CGX-1160, angiotensin therapeutic vaccine, D-4F, ETC-642, APP-018, rhMBL, SCV-07 (oral, tuberculosis), DRF-7295, ABT-828, ErbB2-specific immunotoxin (anticancer), DT388IL-3, TST-10088, PRO-1762, Combotox, cholecystokinin-B/gastrin-receptor binding peptides, 111In-hEGF, AE-37, trastuzumab-DM1, Antagonist G, IL-12 (recombinant), PM-02734, IMP-321, rhIGF-BP3, BLX-883, CUV-1647 (topical), L-19 based radioimmunotherapeutics (cancer), Re-188-P-2045, AMG-386, DC/I540/KLH vaccine (cancer), VX-001, AVE-9633, AC-9301, NY-ESO-1 vaccine (peptides), NA17.A2 peptides, melanoma vaccine (pulsed antigen therapeutic), prostate cancer vaccine, CBP-501, recombinant human lactoferrin (dry eye), FX-06, AP-214, WAP-8294A2 (injectable), ACP-HIP, SUN-11031, peptide YY [3-36] (obesity, intranasal), FGLL, atacicept , BR3-Fc, BN-003, BA-058, human parathyroid hormone 1-34 (nasal, osteoporosis), F-

Protein/Peptide Name
18-CCR1, AT-1001 (celiac disease/diabetes), JPD-003, PTH(7-34) liposomal cream (Novasome), duramycin, CAB-2 , CTCE-0214, erythropoietin, EPO-Fc, CNTO-528, AMG-114 , JR-013, Factor XIII, aminocandin, PN-951, 716155, SUN-E7001, TH-0318 , BAY-73-7977 , teverelix (immediate release), EP-51216, hGH, OGP-I, sifuvirtide, TV-4710, ALG-889, Org-41259, rhCC10, F-991, thymopentin (pulmonary diseases), r(m)CRP, hepatoselective insulin, subalin, L19-IL-2 fusion protein, elafin, NMK-150, ALTU-139, EN-122004, rhTPO, thrombopoietin receptor agonist, AL-108, AL-208, nerve growth factor antagonists (pain), SLV-317, CGX-1007, INNO-105 , oral teriparatide (eligen), GEM-OS1, AC-162352, PRX-302, LFn-p24 fusion vaccine (Therapore), EP-1043, hPTH(1-34), 768974, SYN-101, PGN-0052, aviscumine, BIM-23190, enkastim , APC-8024, GI-5005, ACC-001, TTS-CD3 , TNF, desmopressin, onercept, TP-9201, AC165198, Activin receptor type IIA, Adenosine deaminase, Adipotide, Afostase alfa (alkaline phosphatase), Alpha melanocyte stimulating hormone, Alpha-1 antitrypsin, Alpha-galactosidase, Angiotensin, Anti-angiopoietin-1 inhibitor, Anti-angiopoietin-2 inhibitor, Apolipoprotein A1, Arcalyst, Arginine deiminase, Asparaginase, Atilmotin, AZD2820, Bradykinin receptor antagonist, Calcitonin, Calcitonin gene-related peptide, Cenderitide, Cholecystokinin, Ciliary neurotropic factor (CNTF), Ciligenitide, Coagulation factor IX, Coagulation factor VII, Coagulation factor VIII, Coagulation factor X, Coagulation factor XIII, Collagenase, Complement C1 esterase inhibitor (conestat alfa), Complement factor C3 inhibitor, Complement factor C5 inhibitor, Corticotropin-releasing factor, C-peptide, C-type natriuretic peptide, Defensins, DiaPep277, Diphenhydramine, Ecallantide, Endostatin, Eptifibatide, Fibrinogen, Fibroblast growth factor receptor agonist, Follicle-stimulating hormone (FSH), Follistatin, FP-1039 (FGF trap), Fuzeon, Gastrin, Ghrelin, Ghrelin antagonist, GIP-1, GIP-1/GLP-1 dual agonist, Glucagon, Glucagon-like peptide (GLP) 1 , Glucagon-like peptide (GLP) 2, Glucocerebrosidase (Cerezyme), Glutamate carboxypeptidase (carboxypeptidase G2), Glutaminase, Granulocyte colony stimulating factor (GCSF), Growth hormone, Growth hormone releasing hormone (GHRH), Hematide, Heparinase, Hirudin, Human chorionic gonadotropin (hCG), Human deoxyribonuclease I, Humanin, Hyaluronidase, Icatibant, Iduronate-2-sulfatase (Elaprase), INGAP (Exsulin), Insulin, Irisin, KAI-4169, Lepirudin (Refludan), Leukemia inhibiting factor, L-iduronidase, LRP5 inhibitor, LRP6 inhibitor, Luteinizing hormone (LH), Macrophage inflammatory protein 2 (GroBeta-T CXC chemokine), Mannose binding lectin, Melanocortin stimulating hormone, Methioninase (METase), Mirostipen, MUCI inhibitor, Myostatin inhibitor, N-acetylgalactosamine 4-sulfatase (Naglazyme), Nerve growth factor (Cerebrolysin), Neuropeptide Y2, Neurophilin, NU206, Onconase (Ranpirnase), Ontak (IL-2-toxin), Opioid growth factor, Oxyntomodulin, Oxytocin, Paliperidone, Pancreatic polypeptide, PanCyte, Parathyroid hormone (PTH), Parathyroid hormone related protein (PTHrP), Peptide YY (3-36), Phenylalanine ammonia lyase (PAL), Phenylalanine hydroxylase(PAH), Pituitary adenylate cyclase-activating polypeptide (PACAP), Platelet-activating factor acetylhydrolase, POT-4 (APL-1), Pramlintide, P-Selectin, Relaxin, rhDNase (Pulmozyme), RNase, Sanvar, Secretin, SN38, Somatostatin (Octreotide, Pasireotide, Sandostatin etc.), Somavert (human growth hormone receptor antagonist), Stem cell growth factor, Superoxide dismutase, TACI, Thrombin inhibitor (direct), Thrombomodulin, Thrombopoietin (TPO), Thymosin alpha 1 (Thymalfasin), Thyroid stimulating hormone (TSH), Thyrotropin releasing hormone, Tigapotide, Tissue plasminogen activator (tPA), TLN-232, Tripeptidyl peptidase 1, Tumour necrosis factor receptor, Tyrosine kinase receptor (TrkA), UGP281, Urate oxidase, Uricase, Urocortin 2, Urokinase plasminogen activator, Vascular endothelial growth factor (VEGF) inhibitor, Vasoactive intestinal peptide, Vasopressin, von Willebrand Factor (vWF), Ziconotide (Prialt), Zinc protoporphyrin, Adrenal corticotrophin hormone (ACTH), CD25, Interleukin-1 receptor, Interleukin-21, ABCF1, ACVR1, ACVR1B, ACVR2, ACVR2B, ACVRL1, ADORA2A, Aggrecan, AGR2, AICDA, AIF1, AIG1, AKAP1, AKAP2, AMH, AMHR2, ANGPT1, ANGPT2, ANGPTL3, ANGPTL4, ANPEP, APC, APOC1, APRIL, AR, AZGP1 (zinc-a-glycoprotein), A4 integrin, B7, B7.1, B7.2, BAD, BAFF, BAG1, BAI1, BCL2, BCL6, BDNF, BLNK, BLR1 (MDR15), BlyS, BMP1, BMP2, BMP3B (GDF10), BMP4, BMP6, BMP8, BMPR1A, BMPR1B, BMPR2, BPAG1 (plectin), BRCA1, C19orf10 (IL27w), C3, C4A, C5, C5R1, CANT1, CASP1, CASP4, CAV1, CCBP2 (D6/JAB61), CCL1 (1-309), CCL11 (eotaxin), CCL13 (MCP-4), CCL15 (MIP-1d), CCL16 (HCC-4), CCL17 (TARC), CCL18 (PARC), CCL19 (MIP-3b), CCL2 (MCP-1), MCAF, CCL20 (MIP-3a), CCL21 (MIP-2), SLC, exodus-2, CCL22 (MDC/STC-1), CCL23 (MPIF-1), CCL24 (MPIF-2/eotaxin-2), CCL25 (TECK), CCL26 (eotaxin-3), CCL27 (CTACK/ILC), CCL28, CCL3 (MIP-1a), CCL4 (MIP-1b), CCL5 (RANTES), CCL7 (MCP-3), CCL8 (mcp-2), CCNA1, CCNA2, CCND1, CCNE1, CCNE2, CCR1 (CKR1/HM145), CCR2 (mcp-1RB/RA), CCR3 (CKR3/CMKBR3), CCR4, CCR5 (CMKBR5/ChemR13), CCR6 (CMKBR6/CKR-L3/STRL22/DRY6), CCR7 (CKR7/EBI1), CCR8 (CMKBR8/TER1/CKR-L1), CCR9 (GPR-9-6), CCRL1 (VSHK1), CCRL2 (L-CCR), CD164, CD19, CD1C, CD20, CD200, CD-22, CD24, CD28, CD3, CD37, CD38, CD3E, CD3G, CD3Z, CD4, CD11a (LFA-1 integrin alphaL), CD40, CD40L, CD44, CD45RB,

Protein/Peptide Name
CD52, CD69, CD72, CD74, CD79A, CD79B, CD8, CD80, CD81, CD83, CD86, CD340, CDH1 (E-cadherin), CDH10, CDH12, CDH13, CDH18, CDH19, CDH20, CDH5, CDH7, CDH8, CDH9, CDK2, CDK3, CDK4, CDK5, CDK6, CDK7, CDK9, CDKN1A (p21Wap1/Cip1), CDKN1B (p27Kip1), CDKN1C, CDKN2A (p16INK4a), CDKN2B, CDKN2C, CDKN3, CEBPB, CER1, CHGA, CHGB, Chitinase, CHST10, CKLFSF2, CKLFSF3, CKLFSF4, CKLFSF5, CKLFSF6, CKLFSF7, CKLFSF8; CLDN3; CLDN7 (claudin-7); CLN3; CLU (clusterin); cMET; CMKLR1; CMKOR1 (RDC1); CNR1; COL18A1; COL1A1; COL4A3; COL6A1; CR2; CRP; CSF1 (M-CSF); CSF2 (GM-CSF); CSF3 (GCSF); CTLA4; CTNNB1 (b-catenin); CTSB (cathepsin B); CX3CL1 (SCYD1); CX3CR1 (V28); CXCL1 (GRO1); CXCL10(IP-10); CXCL11 (I-TAC/IP-9); CXCL12 (SDF1); CXCL13; CXCL14; CXCL16; CXCL2 (GRO2); CXCL3 (GRO3); CXCL5 (ENA-78/LIX); CXCL6 (GCP-2); CXCL9 (MIG); CXCR3 (GPR9/CKR-L2); CXCR4; CXCR6 (TYMSTR/STRL33/Bonzo); CYB5; CYC1; CYSLTR1; DAB2IP; DES; DKFZp451J0118; DNCL1; DPP4; E2F1; ECGF1; EDG1; EFNA1; EFNA3; EFNB2; EGF; EGFR; ELAC2; elastase; ENG; ENO1; ENO2; ENO3; EPHB4; EPO; ERBB-2 (Her2); EREG; ERK8; ESR1; ESR2; F3 (TF); FADD; FasL; FASN; FCER1A; FCER2; FCGR3A; FGF; FGF1 (aFGF); FGF10; FGF11; FGF12; FGF12B; FGF13; FGF14; FGF16; FGF17; FGF18; FGF19; FGF2 (bFGF); FGF20; FGF21; FGF22; FGF23; FGF3 (int-2); FGF4 (HST); FGF5; FGF6 (HST-2); FGF7 (KGF); FGF8; FGF9; FGFR3; FIGF (VEGFD); FIL1 (EPSILON); FIL1 (ZETA); FLJ12584; FLJ25530; FLRT1 (fibronectin); FLT1; FOS; FOSL1 (FRA-1); FY (DARC); GABRP (GABAa); GAGEB1; GAGEC1; GALNAC4S-6ST; GATA3; GDF5; GFI1; GGT1; GM-CSF; GNAS1; GNRH1; GPR2 (CCR10); GPR31; GPR44; GPR81 (FKSG80); GRCC10 (C10); GRP; GSN (Gelsolin); GSTP1; HAVCR2; HDAC4; HDAC5; HDAC7A; HDAC9; HER2; HGF; HIF1A; HIP1; histamine and histamine receptors; HLA-A; HLA-DRA; HM74; HMOX1; HUMCYT2A; ICEBERG; ICOSL; ID2; IFN-a; IFNA1; IFNA2; IFNA4; IFNA5; IFNA6; IFNA7; IFNB1; IFNgamma; IFNW1; IGBP1; IGF1; IGF1R; IGF2; IGFBP2; IGFBP3; IGFBP6; IL-1; IL10; IL10RA; IL10RB; IL11; IL11RA; IL-12; IL12A; IL12B; IL12RB1; IL12RB2; IL13; IL13RA1; IL13RA2; IL14; IL15; IL15RA; IL16; IL17; IL17B; IL17C; IL17R; IL18; IL18BP; IL18R1; IL18RAP; IL19; IL1A; IL1B; IL1F10; IL1F5; IL1F6; IL1F7; IL1F8; IL1F9; IL1HY1; IL1R1; IL1R2; IL1RAP; IL1RAPL1; IL1RAPL2; IL1RL1; IL1RL2; IL1RN; IL2; IL20; IL20RA; IL21R; IL22; IL22R; IL22RA2; IL23; IL24; IL25; IL26; IL27; IL28A; IL28B; IL29; IL2RA; IL2RB; IL2RG; IL3; IL30; IL3RA; IL4; IL4R; IL5; IL5RA; IL6; IL6R; IL6ST (glycoprotein 130); IL7; IL7R; IL8; IL8RA; IL8RB; IL8RB; IL9; IL9R; ILK; INHA; INHBA; INSL3; INSL4; IRAK1; IRAK2; ITGA1; ITGA2; ITGA3; ITGA6 (a6 integrin); ITGAV; ITGB3; ITGB4 (b 4 integrin); JAG1; JAK1; JAK3; JUN; K6HF; KAI1; KDR; KITLG; KLF5 (GC Box BP); KLF6; KLK10; KLK12; KLK13; KLK14; KLK15; KLK3; KLK4; KLK5; KLK6; KLK9; KRT1; KRT19 (Keratin 19); KRT2A; KRTHB6 (hair-specific type II keratin); LAMA5; LEP (leptin); LFA3; LIGHT; Lingo-p75; Lingo-Troy; LPS; LTA (TNF-b); LTB; LTB4R (GPR16); LTB4R2; LTBR; MACMARCKS; MAG or Omgp; MAP2K7 (c-Jun); MDK; MIB1; midkine; MIF; MIP-2; MKI67 (Ki-67); MMP2; MMP9; MS4A1; MSMB; MT3 (metallothionectin-III); MTSS1; MUC1 (mucin); MYC; MYD88; NCK2; neurocan; NFKB1; NFKB2; NGFB (NGF); NGFR; NgR-Lingo; NgR-Nogo66 (Nogo); NgR-p75; NgR-Troy; NME1 (NM23A); NOX5; NPPB; NR0B1; NR0B2; NR1D1; NR1D2; NR1H2; NR1H3; NR1H4; NRII2; NRII3; NR2C1; NR2C2; NR2E1; NR2E3; NR2F1; NR2F2; NR2F6; NR3C1; NR3C2; NR4A1; NR4A2; NR4A3; NR5A1; NR5A2; NR6A1; NRP1; NRP2; NT5E; NTN4; ODZ1; OPRD1; P2RX7; PAP; PART1; PATE; PAWR; PCA3; PCNA; PDGFA; PDGFB; PECAM1; PF4 (CXCL4); PGF; PGR; phosphacan; PIAS2; PIK3CG; PLAU (uPA); PLG; PLXDC1; PPBP (CXCL7); PPID; PR1; PRKCQ; PRKD1; PRL; PROC; PROK2; PSAP; PSCA; PTAFR; PTEN; PTGS2 (COX-2); PTN; RAC2 (p21Rac2); RANKL; RARB; RGS1; RGS13; RGS3; RNF110 (ZNF144); ROBO2; RSV; SI00A2; SCGB1D2 (lipophilin B); SCGB2A1 (mammaglobin 2); SCGB2A2 (mammaglobin 1); SCYE1 (endothelial Monocyte-activating cytokine); SDF2; SERPINA1; SERPINA3; SERPINB5 (maspin); SERPINE1 (PAI-1); SERPINF1; SHBG; SLA2; SLC2A2; SLC33A1; SLC43A1; SLIT2; SPP1; SPRR1B (Spr1); ST6GAL1; STAB1; STAT6; STEAP; STEAP2; TB4R2; TBX21; TCP10; TDGF1; TEK; TGFA; TGFB1; TGFB111; TGFB2; TGFB3; TGFBI; TGFBR1; TGFBR2; TGFBR3; TH1L; THBS1 (thrombospondin-1); THBS2; THBS4; THPO; TIE (Tie-1); TIMP3; tissue factor; TLR10; TLR2; TLR3; TLR4; TLR5; TLR6; TLR7; TLR8; TLR9; TNF; TNF-a; TNFAIP2 (B94); TNFAIP3; TNFRSF11A; TNFRSF1A; TNFRSF1B; TNFRSF21; TNFRSF5; TNFRSF6 (Fas); TNFRSF7; TNFRSF8; TNFRSF9; TNFSF10 (TRAIL); TNFSF11 (TRANCE); TNFSF12 (APO3L); TNFSF13 (April); TNFSF13B; TNFSF14 (HVEM-L); TNFSF15 (VEGI); TNFSF18; TNFSF4 (OX40 ligand); TNFSF5 (CD40 ligand); TNFSF6 (FasL); TNFSF7 (CD27 ligand); TNFSF8 (CD30 ligand); TNFSF9 (4-1BB ligand); TOLLIP; Toll-like receptors (TLR1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 to TLR-13); TOP2A (topoisomerase Iia); TP53; TPM1; TPM2; TRADD; TRAF1; TRAF2; TRAF3; TRAF4; TRAF5; TRAF6; TREM1; TREM2; TRPC6; TSLP; TWEAK; VAP1; VEGF; VEGFB; VEGFC; versican; VHL C5; VLA-1; VLA-4; XCL1

Protein/Peptide Name
(lymphotactin); XCL2 (SCM-1b); XCR1 (GPR5/CCXCR1); YY1; ZFPM2.

3. Exemplary Biologically active proteins as payloads

[00276] Proteinacious compounds that are specifically contemplated as payloads in the subject compositions are the following peptides and proteins:

[00277] "C-type Natriuretic peptide" or "CNP" means the human protein (UniProt No. P23582) encoded by the NPPC gene that is cleaved to the 22 amino acid peptide C-type natriuretic peptide (CNP), having the sequence GLSKGCFGLKLDRIGSMSGLGC, as well as species and synthetic variations thereof, having at least a portion of the biological activity of the native peptide. CNP is a selective agonist for the B-type natriuretic receptor (NPRB) and is reported to be a potent stimulator of endochondral bone growth. CNP binds to its receptor, initiates intracellular signals & ultimately inhibit the overactive FGFR3 pathway. Use of CNP is indicated for achondroplasia, a common form of skeletal dysplasia or short-limbed dwarfism, and human disorders caused by FGFR3 mutations, including syndromes affecting skeletal development; e.g., hypochondroplasia [HCH], ACH, thanatophoric dysplasia [TD]), skin (epidermal nevi, seborrhaeic keratosis, acanthosis nigricans), and cancer (multiple myeloma [MM], prostate and bladder carcinoma, seminoma) (Foldynova-Trantirkova S. Hum Mutat. (2012) 33:29). The half-life of CNP-22 is reported to be 2.6 min, being rapidly metabolized by neutral endopeptidase & cleared by a clearance receptor (Prickett T., 2004, Clinical Science, 106:535), thereby limiting its utility.

[00278] "Luteinizing hormone-releasing hormone" or "LHRH" means the human protein (UniProt No. P01148) encoded by the *GNRH1* gene that is processed in the preoptic anterior hypothalamus from a 92-amino acid preprohormone into the linear decapeptide end-product having the sequence pyroGlu-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-NH2, , as well as species and synthetic variations thereof, having at least a portion of the biological activity of the native peptide. LHRH plays a pivotal role in the regulation of the pituitary/gonadal axis, and thus reproduction. LHRH exerts its effects through binding to high-affinity receptors on the pituitary gonadotroph cells and subsequent release of FSH and LH. LHRH is found in organs outside of the hypothalamus and pituitary, and because a high percentage of certain cancer tissues have LHRH binding sites and because sex steroids have been implicated in the development of breast and prostate cancers, hormonal therapy with LHRH agonists are approved or are considered for the treatment of sex-steroid-dependent conditions such as estrogen-dependent breast cancer, ovarian cancer, endometrial cancer, bladder cancer and androgen-dependent prostate carcinoma. Because the half-life is reported to be less than 4 minutes, (Redding TW, et al. The Half-life,

Metabolism and Excretion of Tritiated Luteinizing Hormone-Releasing Hormone (LH-RH) in Man. J Clin Endocrinol. Metab. (1973) 37:626-631), its utility as a therapeutic is limited.

[00279] "Cilengitide" means the synthetic cyclic RGD pentapeptide having the sequence Arg-Gly-Asp-Dphe-NmeVal or the chemical name 2-[(2S,5R,8S,11S)-5-benzyl-11-{3-[(diaminomethylidene)amino]propyl}-7-methyl-3,6,9,12,15-pentaoxo-8-(propan-2-yl)-1,4,7,10,13-pentaazacyclopentadecan-2-yl]acetic acid (CAS No. 188968-51-6). Cilengitide is selective for αv integrins, which are important in angiogenesis (forming new blood vessels). The binding of such ligands activates the integrins to regulate tumor cell invasion, migration, proliferation, survival & angiogenesis. Hence, the use of cilengitide is under investigation for the treatment of glioblastoma by inhibiting angiogenesis (Burke P, et al. Cilengitide targeting of αvβ3 integrin receptor synergizes with radioimmunotherapy to increase efficacy and apoptosis in breast cancer xenografts". Cancer Res (2002) 62(15): 4263–4272). Because cilengitide has a short half-life of 3-5 h, and poor solubility limiting the maximum drug concentration to 15mg/mL (O'Donnell PH. A phase I study of continuous infusion cilengitide in patients with solid tumors. Invest New Drugs (2012) 30:604), its utility as a therapeutic is limited.

[00280] "Growth hormone releasing hormone" or "GHRH" (also known as growth-hormone-releasing factor, GRF, GHRF, somatoliberin or somatocrinin" means the 44-amino acid peptide hormone produced in the arcuate nucleus of the hypothalamus having the sequence YADAIFTNSYRKVLGQLSARKLLQDIMSRQQGESNQERGARARL, as well as species and synthetic variations thereof, having at least a portion of the biological activity of the native peptide, including the biologically active 1-29 amino acid truncation peptide YADAIFTNSYRKVLGQLSARKLLQDIMSR. GHRH is released from neurosecretory nerve terminals and is carried by the hypothalamo-hypophyseal portal system to the anterior pituitary gland where it acts on GHRH receptor to stimulate pulsatile growth hormone release. The GHRH analog tesamorelin is a drug approved for the treatment of lipodystrophy in HIV patients under highly active antiretroviral therapy, and is also considered for use in cachexia, abdominal obesity in growth-hormone deficient patients, muscle wasting related to certain chronic diseases, mild cognitive impairment, and growth hormone replacement in growth hormone deficient patients. Because the half-life is reported to be less than 15 minutes, (Chapman IM. J Endocrinol (1991) 128:369-374), its utility as a therapeutic is limited.

[00281] "Peptide YY" and "PYY" mean human peptide YY polypeptide (UniProt No. P10082), synthetic versions and species and non-natural sequence variants having at least a portion of the biological activity of mature PYY. As used herein, "PYY" includes both major forms of the human full length, 36 amino acid peptide, PYY_{1-36} and the predominant circulating form PYY_{3-36} ("PYY3-36") which have the PP fold structural motif. PYY3-36 has the sequence IKPEAPGEDASPEELNRYYASLRHYLNLVTRQRY-NH2. PYY is produced by specialized

endocrine cells (L-cells) in the gut after a person eats and inhibits gastric motility and increases water and electrolyte absorption in the colon. PYY may also suppress pancreatic secretion. The naturally occurring PYY3-36 is a nonselective Y_1, Y_2, & Y_5 agonist. PPY-containing fusion proteins of the invention may find particular use in the treatment of diabetes for glucose regulation, insulin-resistance disorders, and obesity. Analogs of PYY have been prepared, as described in U.S. Pat. Nos. 5,604,203, 5,574,010 and 7,166,575. Because the half-life is reported to be less than 1 h, (Addison ML. A role for metalloendopeptidases in the breakdown of the gut hormone, PYY 3-36. Endocrinology (2011) 152(12):4630-4640) and is typically administered by the intranasal route three times daily, its utility as a therapeutic is limited.

[00282] "Leptin" means the naturally occurring leptin (UnitProt No. P41159) encoded by the *Ob(Lep)* gene, synthetic versions and species and non-natural sequence variants having at least a portion of the biological activity of the mature leptin. Leptin has the sequence VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVY QQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYST EVVALSRLQGSLQDMLWQLDLSPGC, and has a disulfide bridge between residues 97 and 147. Leptin plays a key role in regulating energy intake and energy expenditure, including appetite, metabolism, and body weight. Leptin-containing polypeptides of the invention may find particular use in the treatment of diabetes for glucose regulation, insulin-resistance disorders, obesity, congenital/acquired lipodystrophy, HAART-induced lipodystrophy, hypothalamic amenorrhea. Leptin has been cloned, as described in U.S. Pat. No. 7,112,659, and leptin analogs and fragments in U.S. Pat. No. 5,521,283, U.S. Pat. No. 5,532,336, PCT/US96/22308 and PCT/US96/01471. Because the commercially available form, metreleptin has a half-life reported to be 8-30 min (Klein S., et al. Adipose tissue leptin production and plasma leptin kinetics in humans. Diabetes (1996) 45:984–987) and the majority of current leptin therapies require 1x-2x/day dosing, its utility as a therapeutic is limited.

[00283] "Pramlintide" means the synthetic amylin mimetic having the sequence KCNTATCATNRLANFLVHSSNNFGPILPPTNVGSNTY-NH2, and sequence variants having at least a portion of the biological activity of pramlintide or native amylin. The pramlintide has a sequence wherein amino acids from the rat amylin sequence are substituted for amino acids in the human amylin sequence. Amylin is a 37aa peptide secreted by pancreatic b-cells that is co-released with insulin in pulsatile fashion, typically in a molar ratio of 100 insulin to 1 amylin. Amylin functions to inhibit gastric emptying, glucagon secretion, promote satiety & meal termination (Kong MF, et al. Infusion of pramlintide, a human amylin analogue, delays gastric emptying in men with IDDM. Diabetologia. (1997) 40:82–88). Pramlintide is used as an adjunct to insulin therapy in T1D and T2D and shows improvement in glycemic control and reduction in insulin requirements, and also demonstrate modest reduction in body weight (Neary MT,

Batterham RL. Gut hormones: Implications for the treatment of obesity. Pharmacology & Therapeutics (2009)124:44-56). Because pramlintide has a half-life reported to be 20 min (McQueen, J. Pramlintide acetate. Am. J. Health-System Pharmacy (2005) 22:2363-2372) and requires 2x-3x/day dosing, its utility as a therapeutic is limited.

[00284] "Oxytocin" means the mammalian hormone peptide (UniProt No. P01178) having the sequence CYIQNCPLG-NH2 and a disulfide bridge between residues 1 and 6, and synthetic versions, such as pitocin. Oxytocin acts primarily as a neuromodulator in the brain, having a structure very similar to that of vasopressin, which are the only known hormones released by the human posterior pituitary gland to act at a distance. Oxytocin has uterine-contracting properties mediated by specific, high-affinity oxytocin receptors expressed in the mammary gland and the uterus; hence its role in parturition and lactation. Oxytocin-containing polypeptides of the invention may find particular use in the treatment of autism, fragile X syndrome, chronic daily headache, and male infertility.

[00285] "Relaxin" means the protein hormone that is a heterodimer of two peptide chains of 24 & 29 amino acids linked by disulfide bridges created from the 185 amino acid precursor protein (UniProt No. P04090); the B chain having the sequence DSWMEEVIKLCGRELVRAQIAICGMSTWS and the A chain having the sequence QLYSALANKCCHVGCTKRSLARFC, with the disulfide bridges between B10-A10 and B23-A24, and includes synthetic and recombinant versions. Relaxin is produced by the corpus luteum during the menstrual cycle and pregnancy in women and by the prostate in men. Relaxin orchestrates many of the maternal physiological responses to pregnancy, acts as a systemic and renal vasodilator, is a cardioprotective & antifibrotic agent. Relaxin binds to relaxin receptor (GPCR), increases cAMP & activates PKC, PI3K & endothelin type B receptor resulting in increased nitric oxide production, and also activates MAPK, which may play a role in relaxin induced VEGF expression. Relaxin-containing polypeptides of the invention may find particular use in the treatment of acute decompensated heart failure (ADHF). Because the reported half-life of relaxin in humans is less than 10min (Dschietzig T, et al. Intravenous recombinant human relaxin in compensated heart failure: a safety, tolerability, and pharmacodynamic trial. J Card Fail. 2009;15:182–190), the utility of the unmodified protein as a therapeutic is limited.

[00286] "Cenderitide" and "CD-NP" means a human C-type natriuretic peptide-(32-53)-peptide (CNP-22) with eastern green mamba (Dendroaspis angusticeps) natriuretic peptide-(24-38)-peptide having the sequence GLSKGCFGLKLDRIGSMSGLGCPSLRDPRPNAPSTSA, with disulfide bridges between residues 6 and 22. The chimeric peptide has vasoprotective and RAAS suppressing actions via activation of the receptors guanylyl cyclase (GC)-A and GC-B, and may potentiate renal enhancement and cardiac unloading while having minimal hypotensive effects. Accordingly, it may have use in treatment of cardiorenal disease such as acute decompensated

heart failure (ADHF) and acute myocardial infarction (AMI), particularly during the "post-acute" treatment period.

[00287] "Peginesatide" or "hematide" is a peptide composed of two synthetic 21 amino-acid peptides having the sequence GlyGlyLeuTyrAlaCysHisMetGlyProIleThr1NalValCysGlnProLeuArgSarLys that are linked at lysine with a branched polyethylene glycol. Peginesatide is a novel analog of erythropoietin that has erythropoietic properties and is being developed for medical use as a treatment for anemia due to chronic kidney disease (CKD) in patients not on dialysis.

[00288] "Oxyntomodulin" or "OXM" means human oxyntomodulin, sythetic versions and sequence variants thereof having at least a portion of the biological activity of mature oxyntomodulin. Oxyntomodulin is a 37 amino acid peptide having the sequence HSQGTFTSDYSKYLDSRRAQDFVQWLMNTKRNRNNIA, is produced postprandially from intestinal L-cells in the colon and contains the 29 amino acid sequence of glucagon followed by an 8 amino acid carboxyterminal extension. Oxyntomodulin is an agonist at both the glucagon receptor and the GLP-1R, with its anorectic effect probably mediated via the latter receptor. OXM has been found to suppress appetite. OXM-containing polypeptides of the invention may find particular use in the treatment of diabetes for glucose regulation, insulin-resistance disorders, obesity, and can be used as a weight loss treatment. As native oxyntomodulin has been reported to have a half-life of ~12 min in human plasma (measured with a cross-reacting glucagon assay; Schjoldager BT. Oxyntomodulin: a potential hormone from the distal gut. Pharmacokinetics and effects on gastric acid and insulin secretion in man. Eur J Clin Invest. (1988) 18(5):499-503.), the utility of the unmodified protein as a therapeutic is limited.

[00289] "POT4" or "APL-1" means the synthetic cyclic peptide having the sequence H-Ile-[Cys-Val-Val-Gln-Asp-Trp-Gly-His-His-Arg-Cys]-Thr-NH2. POT4 is a more potent C3 complement inhibitor than compstatin, which inhibits the cleavage of native C3 to its active fragments C3a and C3b, and has extended circulating in vivo half-life of 8 hours. It is considered for use to prevent inflammation, damage and upregulation of angiogenic factors like VEGF in diseases like age-related macular degeneration (AMD), paroxysmal nocturnal hemoglobinuria (PNH), asthma and COPD.

[00290] "Interferon-lambda", "IFN- λ", interleukin-29" and "IL-29" means the human interleukin (UniProt No. Q8IU54 (20-200)) encoded by the *IL29* gene having the sequence GPVPTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALEESLKLKNWSCSSPVFPGNWDL RLLQVRERPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHHILSQLQACIQPQPTAG PRPRGRLHHWLHRLQEAPKKESAGCLEASVTFNLFRLLTRDLKYVADGNLCLRTSTHPE ST, recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of mature IL-29. A type III interferon, IL-29 signals through a heterodimer

receptor complex (IL-10R2 & IL-28Rα receptor chains) distinct from type I IFN (IFNAR1/IFNAR2 receptor complex), and plays an important role in anti-viral immunity. Notably, the IL-29 receptor is highly expressed on hepatocytes, the primarysite of HCV infection, but is not signicantly expressed on immune or bone marrow cells. Pegylated versions have an estimated half-life of 50-70 h.

[00291] "Interferon-beta" or "IFN-ß" means the human protein encoded by the *IFNB1* gene having the sequence MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTI YEMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSS LHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of mature IFN-ß. IFN-ß is produced by various cell types including fibroblasts & macrophages, and mediates antiviral, antiproliferative & immunomodulatory activities in response to viral infection & other biological inducers. The binding of IFN-ß to specific receptors on the surface of human cells initiates a cascade of intracellular events that leads to the expression of numerous interferon-induced gene products such as 2', 5'-oligoadenylate synthetase, ß2-microglobulin, and neopterin. These gene products are routinely used as biomarkers in clinical setting. IFN-ß is used in treatment of various forms of multiple sclerosis (MS), including eclapse remitting MS, secondary progressive MS, primary progressive MS, juvenile onset MS, and clinically isolated syndromes suggestive of MS. Commercially-available forms of IFN-ß have reported half-lives of 4 to 67 h and require frequent dosing, such that their utility as a therapeutic is limited.

[00292] "C-peptide" means the human pancreatic protein having the sequence EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native C-peptide. C-peptide is the middle segment of proinsulin that is between the N-terminal B-chain and the C-terminal A-chain, and is cleaved from preproinsulin as mature insulin is formed and secreted. Cirulating C-peptide binds to a receptor that is likely G-protein-coupled, and the signal activates Ca2+-dependent intracellular signaling pathways such as MAPK, PLCγ, and PKC, leading to upregulation of a range of transcription factors as well as eNOS and Na+K+ATPase activities. C-peptide is considered for use in diabetic complications and diabetic nephropathy. Since the reported half-life is about 30 minutes (Matthews DR. The half-life of endogenous insulin and C-peptide in man assessed by somatostatin suppression. Clin Endocrinol (Oxf). (1985) 23(1):71-79), the utility of the unmodified protein as a therapeutic is limited.

[00293] "Ghrelin" means the human hormone having the sequence GSSFLSPEHQRVQQRKESKKPPAKLQPR, truncated versions, recombinant and synthetic

versions and sequence variants thereof having at least a portion of the biological activity of native ghrelin, including the native, processed 27 or 28 amino acid sequence and homologous sequences. Ghrelin induces satiation, or species and non-natural sequence variants having at least a portion of the biological activity of mature ghrelin, including the native, processed 27 or 28 amino acid sequence and homologous sequences. Ghrelin is produced mainly by P/D1 cells lining the fundus of the human stomach and epsilon cells of the pancreas that stimulates hunger, and is considered the counterpart hormone to leptin. Ghrelin levels increase before meals and decrease after meals, and can result in increased food intake and increase fat mass by an action exerted at the level of the hypothalamus. Ghrelin also stimulates the release of growth hormone. Ghrelin is acylated at a serine residue by n-octanoic acid; this acylation is essential for binding to the GHS1a receptor and for the agonist activity and the GH-releasing capacity of ghrelin. Ghrelin-containing polypeptides of the invention may find particular use as agonists; e.g., to selectively stimulate motility of the GI tract in gastrointestinal motility disorder, to accelerate gastric emptying, or to stimulate the release of growth hormone. The invention also contemplates unacylated forms and sequence variants of ghrelin, which act as antagonists. Ghrelin analogs with sequence substitutions or truncated variants, such as described in U.S. Pat. No. 7,385,026, may find particular use as fusion partners to XTEN for use as antagonists for improved glucose homeostasis, treatment of insulin resistance and treatment of obesity, cancen cachexia, post-operative ileus, bowel disorders, and gastrointestinal disorders. The isolation and characterization of ghrelin has been reported (Kojima M, *et al.*, Ghrelin is a growth-hormone-releasing acylated peptide from stomach. Nature. 1999;402(6762):656-660) and synthetic analogs have been prepared by peptide synthesis, as described in U.S. Pat. No. 6,967,237. As ghrelin has a reported terminal half-life of 10-30 min (Akamizu T, et al. Pharmacokinetics, safety, and endocrine and appetite effects of ghrelin administration in young healthy subjects. Eur J. Endocrinology (2004)150(4):447–455), the utility of the unmodified protein as a therapeutic is limited, and analogs with, at position 3, the native serine amino acid with an octyl side group instead of the native octanoyl side group may confer added resistant to proteases.

[00294] "Follistatin," also known as "activin-binding protein" or "FSH-suppressing protein (FSP)," means the protein that, in humans, is encoded by the *FST* gene. As used herein, "follistatin" includes homologs, species variants, sequence variants and fragments thereof. The mature protein form in humans has 315 amino acids, is referred to as FS-315 and has been cloned (US Pat Nos. 5,041,538 and 5,182,375). Follistatin contains two potential N-glycosylation sites, Asn95 and Asn259, however it has been demonstrated that mutation at these sites followed by testing of the recombinant product for their ability to inhibit FSH secretion and to bind activin resulted in each mutant having a similar property as the non-mutated recombinant hFS-315, suggesting that glycosylation of the follistatin molecule has no effect in these functions (Inouye,

S., et al. Site-specific mutagenesis of human follistatin. BBRC (1991) 179(1):352–358). Porcine follistatin is disclosed in Ueno et al., PNAS:USA 84:8282-8286 (1987) and bovine follistatin is disclosed in Robertson et al., Biochem. Biophys. Res. Commun. 149:744-749 (1987). As bone morphogenetic proteins and growth/differentiation factors such as activin and myostatin have the ability to induce the growth, formation, differentiation and maintenance of various tissues, including bone, cartilage, tendon/ligament, muscle, neural, and various organs, their neutralization by follistatin and follistatin agonists have therapeutic value (U.S. Pat. Nos. 5,545,616, 5,041,538, and AU9675056). As follistatin administered to a subject is rapidly eliminated from the circulation, with a terminal half-life of just over 2 hours in rats (Kogure K , et al. Intravenous administration of follistatin: delivery to the liver and effect on liver regeneration after partial hepatectomy. Hepatology. (1996) 24(2):361-366), the utility of the unmodified protein as a therapeutic is limited.

[00295] "Vasoactive intestinal peptide" and "VIP" means the 28 amino acid peptide hormone (UniProt No. P01282 (125-152)) encoded by the *VIP* gene residues having the sequence HSDAVFTDNYTRLRKQMAVKKYLNSILN-NH2 and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native VIP. The VIP peptide is produced in many tissues, including the gut, pancreas and suprachiasmatic nuclei of the hypothalamus in the brain. VIP stimulates contractility in the heart, causes vasodilation, increases glycogenolysis, lowers arterial blood pressure and relaxes the smooth muscle of trachea, stomach and gall bladder. Changes in concentration are associated with myocardial fibrosis, heart failure, cardiomyopathy and pulmonary hypertension, and its deficiency in the respiratory system is considered to be a pathogenetic factor in pulmonary disease (Said SI, 2007, Circulation, 115: 1260; Said SI, 2008, Ann N Y Acad Sci, 1144:148; Petkov V et.al., 2003, J Clin Invest, 111:1339). VIP is considered for use in treating resistant hypertension, primary pulmonary arterial hypertension (PAH), asthma, COPD, diabetes, erectile dysfunction, and female sexual dysfunction. As its half-life is reported to be approximately 1 minute (Domschke S, et al. Vasoactive intestinal peptide in man: pharmacokinetics, metabolic and circulatory effects. Gut (1978) 19:1049–1053), the utility of the unmodified protein as a therapeutic is limited.

[00296] "Fuzeon" means the 36 amino acid peptide derived from the gp41 of HIV, a viral protein involved in fusion of HIV to CD4+ T cells, having the sequence YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the binding activity of native gp41. Fuzeon and multimers thereof or conjugates with related peptides are used or are being considered for use in treating resistant forms of HIV infection. As fuzeon has a half-life of 3.8h in patients, requiring frequent injection administrations, its utility is limited.

[00297] "KAI-4169" means the peptide agonist of the human cell surface calcium-sensing receptor (CaSR) under development by KAI Pharma for the treatment of secondary hyperparathyroidism (SHPT) in kidney disease patients and and bone disorder (CKD-MBD) patients.

[00298] "Pasireotide" means the a somatostatin analog having the chemical name [(3S,6S,9S,12R,15S,18S,20R)-9-(4-aminobutyl)-3-benzyl-12-(1H-indol-3-ylmethyl)-2,5,8,11,14,17-hexaoxo-15-phenyl-6-[(4-phenylmethoxyphenyl)methyl]-1,4,7,10,13,16-hexazabicyclo[16.3.0]henicosan-20-yl] N-(2-aminoethyl)carbamate used for the treatment of Cushing's disease. Pasireotide is a multi-receptor somatostatin analogue with high binding affinity for somatostatin-R-subtypes R1, 2, 3 & 5 that suppresses growth hormone, IGF-1 and adrenocorticotropic hormone secretion. In addition to treatment of Cushing's Disease, it is also considered for use in acromegaly, neuroendocrine disease, liver disease, symptomatic polycystic liver disease, neuroendocrine tumor, lympangioleiomyomatosis, congenital hyperinsulinism, recurrent or progressive meningioma, and other endocrine disorders. As a commercially-available form has a reported half-life of 12 to 17 h (Petersenn, S. et al. Tolerability and Dose Proportional Pharmacokinetics of Pasireotide Administered as a Single Dose or Two Divided Doses in Healthy Male Volunteers: A Single-Center, Open-Label, Ascending-Dose Study. Clinical Therapeutics (2012) 34:677-688), its utility is limited.

[00299] "Irisin" means the clevage product of the protein encoded by the FNDC5 gene having the sequence DSPSAPVNVTVRHLKANSAVVSWDVLEDEVVIGFAISQQKKDVRMLRFIQEVNTTTRSC ALWDLEEDTEYIVHVQAISIQGQSPASEPVLFKTPREAEKMASKNKDEVTMKE, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native irisin. Irisin mediates beneficial effects of muscular exercise, and induces browning of white adipose tissue by up-regulating UCP1 expression through activation of the nuclear receptor PPARA. Mildly increased irisin levels have been shown to result in increased energy expenditure, reduced body weight and improved diet-induced insulin resistance (Bostrom P, 2012, Nature, 481:463). Irisin is considered for use in treating obesity, diabetes, and metabolic disorders.

[00300] "TXA127" and "PanCyte" are analogs of angiotensin (1-7), with TXA127 having the sequence NRVYIHP and PanCyte is an cyclic analog linking the 4th and 7th residues with dAla and Ala, respectively, with the result that it is more resistant to degradation and has a longer half-life. The analogs bind to MAS receptor and stimulate early hematopoietic precursor cells in bone marrow, and also have vasodilation, anti-trophic, antifibrotic, natriuresis, anti-inflammatory, anti-thrombotic effects. The compounds are considered for use in acceleration of platelet recovery following stem cell transplant for patients with hematological cancers such as acute

myelogenous leukemia (AML), myelodysplastic syndrome (MDS), acute lymphocytic leukemia (ALL), chronic myelogenous leukemia (CML), chronic lymphocytic leukemia (CLL), Hodgkin's lymphoma (HL), or non-Hodgkin's lymphoma (NHL), and multiple myeloma, and use in treating pulmonary fibrosis, acute lung injury, pulmonary arterial hypertension, and fibrosis of the kidney and liver.

[00301] "Interleukin-7" and "IL-7" means the human interleukin (UniProt No. P13232 (26-177)) encoded by the *IL7* gene having the sequence DCDIEGKDGKQYESVLMVSIDQLLDSMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRA ARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSLEENKS LKEQKKLNDLCFLKRLLQEIKTCWNKILMGTKEH, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native IL-7. IL-7 IL-7 stimulates the differentiation of multipotent (pluripotent) hematopoietic stem cells into lymphoid progenitor cells, including expansion of CD4/CD8 T cells. IL-7 limits the production of suppressor regulatory T cells and T cell anergy through TGF-B antagonism, and supports production of central memory T cells. IL-7 is considered for use in treating lymphopenia in HIV, oncology, transplant, HBV and HCV infection, as well as treating minimal residual disease or advanced tumors, and may have roles in immune reconstitution or enhancement of immunotherapy. As the reported half-life of IL-7 in humans is approximately 10 h (Sportès, C. et al. Phase I Study of Recombinant Human Interleukin-7 Administration in Subjects with Refractory Malignancy. Clin Cancer Res 2010;16:727-735), its utility in unmodified form is limited.

[00302] "Fibroblast growth factor 18" or "FGF-18" means the human protein (UniProt No. O76093(28-207)) encoded by the *FGF18* gene, having the sequence EENVDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQVLGRRISARGEDGDKYAQL LVETDTFGSQVRIKGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAK YSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQPELQKPFKYTTVTKRSRRIRP THPA and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native FGF-18. FGF-18 is a protein member of the fibroblast growth factor (FGF) family. FGF family members possess broad mitogenic and cell survival activities, and are involved in a variety of biological processes, including embryonic development, cell growth, morphogenesis, tissue repair, tumor growth, and invasion. It has been shown in vitro that this protein is able to induce neurite outgrowth in PC12 cells. FGF-18 stimulates the proliferation of chondrocyte & osteoblasts (cells that produce and maintain bone and cartilage) and its use is considered for the repair and generation of the cartilage, for example in the knee joints (Ellsworth JL. Fibroblast growth factor-18 is a trophic factor for mature chondrocytes and their progenitors. Osteoarthritis Cartilage (2002) 10:308-320).

[00303] "Alpha-Melanocyte Stimulating Hormone" or "α-MSH" is the 13-amino acid peptide generated as a proteolyic cleavage product from ACTH (1-13), which is in turn a cleavage product of proopiomelanocortin (POMC), having the sequence N-Ac-SYSMGFRWGLPV, and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native α-MSH. Alpha-MSH is a non-selective agonist of the melanocortin receptors MC1, MC3, MC4 & MC5 but not MC2 (which is exclusive for ACTH). Alpha-MSH stimulates melanocytes to produce & release melanin which has a photo-protective effect; it signals the brain, which has effects on appetite and sexual arousal. It is considered for use in treating erythropoietic protoporphyria (EPP, intolerant to sun), nonsegmental vitilligo (skin discoloration), actinic keratosis (AK, solar keratosis, precursor to skin cancer), polymorphous light eruption (PLE/PMLE), post-surgery kidney damage, erectile dysfunction, and sexual dysfunction. Because its half-life is mere seconds, its utility in unmodified form is limited.

[00304] "Endostatin" means the naturally-occurring 20-kDa C-terminal fragment derived from type XVIII collageh (UniProt. No. P39060(1572-1754)) having the sequence HSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYS IVRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSV WHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSF MTASK, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native endostatin. Endostatin is an angiogenesis inhibitor and may interfere with the pro-angiogenic action of growth factors such as basic fibroblast growth factor (bFGF/FGF-2) and VEGF. It is considered for use in certain cancers. Because its half-life is 13 h (Thomas, JP et al. Phase I Pharmacokinetic and Pharmacodynamic Study of Recombinant Human Endostatin in Patients With Advanced Solid Tumors. J. Clin. Oncol. (2003) 21:223-231), its utility in unmodified form is limited.

[00305] "Humanin" means the peptide (UniProt No. Q8IVG9(1-24)) encoded by the *MT-RNR2* gene, having the sequence MAPRGFSCLLLLTSEIDLPVKRRA, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native humanin. Humanin has a role in neuro-protection against cell death associated with Alzheimer's disease (AD), AD-specific insults, prion induced apoptosis & chemically induced neuronal damage (Hashimoto, Y, A rescue factor abolishing neuronal cell death by a wide spectrum of familial Alzheimer's disease genes and Aβ. PNAS (2001) 98:6336-6341). More recently, humanin was found to help improve insulin action and lower blood glucose levels (Muzumdar RH, Humanin: A Novel Central Regulator of Peripheral Insulin Action. PLoS One (2009) 4:e6334). Humanin s considered for use in treating Alzheimer's disease, diabetes, and vascular & cardiovascular diseases.

[00306] "Glucagon" means the human glucagon glucose regulating peptide having the sequence HSQGTFTSDYSKYLDSRRAQDFVQWLMNT, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native glucagon. The term "glucagon" as used herein also includes peptide mimetics of glucagon. Native glucagon is produced by the pancreas, released when blood glucose levels start to fall too low, causing the liver to convert stored glycogen into glucose and release it into the bloodstream. While the action of glucagon is opposite that of insulin, which signals the body's cells to take in glucose from the blood, glucagon also stimulates the release of insulin, so that newly-available glucose in the bloodstream can be taken up and used by insulin-dependent tissues. Glucagon-containing polypeptides of the invention may find particular use in increasing blood glucose levels in individuals with extant hepatic glycogen stores and maintaining glucose homeostasis in diabetes. Glucagon has been cloned, as disclosed in U.S. Pat. No. 4,826,763.

[00307] "Glucagon-like protein-1" or "GLP-1" means human glucagon like peptide-1 and sequence variants thereof having at least a portion of the biological activity of native GLP-1. The term "GLP-1" includes human GLP-1(1-37) having the sequence HDEFERHAEGTFTSDVSSTLEGQAALEFIAWLVKGRG, GLP-1(7-37), and GLP-1(7-36)amide. GLP-1 stimulates insulin secretion, but only during periods of hyperglycemia. The safety of GLP-1 compared to insulin is enhanced by this property and by the observation that the amount of insulin secreted is proportional to the magnitude of the hyperglycemia. The biological half-life of GLP-1(7-37)OH is a mere 3 to 5 minutes (U.S. Pat. No. 5,118,666). GLP-1-containing polypeptides of the invention may find particular use in the treatment of diabetes and insulin-resistance disorders for glucose regulation. GLP-1 has been cloned and derivatives prepared, as described in U.S. Pat. No. 5,118,666.

[00308] "Glucagon-like protein-2" or "GLP-2" means, collectively herein, human glucagon like peptide-2 having the sequence HADGSFSDEMNTILDNLAARDFINWLIQTKITD, species homologs of human GLP-2, and non-natural sequence variants having at least a portion of the biological activity of mature GLP-2 including variants such as, but not limited to, a variant with glycine substituted for alanine at position 2 of the mature sequence resulting in HGDGSFSDEMNTILDNLAARDFINWLIQTKITD ("2G") as well as Val, Glu, Lys, Arg, Leu or Ile substituted for alanine at position 2. GLP-2 or sequence variants have been isolated, synthesized, characterized, or cloned, as described in U.S. Patent or Application Nos. 5,789,379; 5,834,428; 5,990,077; 5,994,500; 6,184,201; 7,186,683; 7,563,770; 20020025933; and 20030162703.

[00309] "Insulin" means human insulin or a homolog, species variants, or sequence variants thereof that includes, but is not limited to, the mature human insulin protein composed of 51 amino acids with a molecular weight of 5808 Da and the proinsulin precursor of 110 amino

acids. The precursor protein is processed to mature insulin that has an A-chain with sequence GIVEQCCTSICSLYQLENYCN and a B-chain with sequence FVNQHLCGSHLVEALYLVCGERGFFYTPKT bound together by disulfide bonds.

[00310] "Factor XIII A chain", "FXIIIA" or "F13A" means the coagulation protein (UniProt No. P00488(2-732)) having the sequence SETSRTAFGGRRAVPPNNSNAAEDDLPTVELQGVVPRGVNLQEFLNVTSVHLFKERWDT NKVDHHTDKYENNKLIVRRGQSFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYIP VPIVSELQSGKWGAKIVMREDRSVRLSIQSSPKCIVGKFRMYVAVWTPYGVLRTSRNPE TDTYILFNPWCEDDAVYLDNEKEREEYVLNDIGVIFYGEVNDIKTRSWSYGQFEDGILDT CLYVMDRAQMDLSGRGNPIKVSRVGSAMVNAKDDEGVLVGSWDNIYAYGVPPSAWT GSVDILLEYRSSENPVRYGQCWVFAGVFNTFLRCLGIPARIVTNYFSAHDNDANLQMDIF LEEDGNVNSKLTKDSVWNYHCWNEAWMTRPDLPVGFGGWQAVDSTPQENSDGMYRC GPASVQAIKHGHVCFQFDAPFVFAEVNSDLIYITAKKDGTHVVENVDATHIGKLIVTKQI GGDGMMDITDTYKFQEGQEEERLALETALMYGAKKPLNTEGVMKSRSNVDMDFEVEN AVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVTLEPLSFKKEAV LIQAGEYMGQLLEQASLHFFVTARINETRDVLAKQKSTVLTIPEIIIKVRGTQVVGSDMT VTVQFTNPLKETLRNVWVHLDGPGVTRPMKKMFREIRPNSTVQWEEVCRPWVSGHRK LIASMSSDSLRHVYGELDVQIQRRPSM, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native FXIIIA. Factor XIII is the last enzyme in the coagulation cascade and is responsible for cross-linking fibrin molecules to each other in a newly formed blood clot. By forming intermolecular covalent bonds between fibrin monomers and by cross-linking alpha-2 antiplasmin, fibrinogen, fibronectin, collagen, and other proteins to enhance the mechanical strength of the fibrin clot, protect from proteolytic degradation, and provide stability to the extracellular matrix. Plasma FXIII circulates as a heterotetramer composed of 2 A subunits and 2 B subunits noncovalently linked together and bound to fibrinogen. The B subunit, which appears to stabilize the structure of the A subunit and to protect the A subunit from proteolysis, is normally present in excess in plasma as free FXIII-B subunit. Most patients with FXIII deficiency have mutations in the FXIII-A subunit; few cases of patients with FXIII-B subunit mutations have been reported (Mikkola, H, 1996, Semin Thromb Hemost, 22:393; Ichinose A, 1996, Semin Thromb Hemost, 22:385). FXIIIA is used or is considered for use in treating hemophilia and related coagulopathies, congenital FXIII deficiency, and acquired FXIII deficiency due to chronic liver disease, inflammatory bowel disease, and post- surgery bleeding.

[00311] "Factor X" or "FX" means the coagulation protein (UniProt No. P00742(2-488)) having the sequence GRPLHLVLLSASLAGLLLLGESLFIRREQANNILARVTRANSFLEEMKKGHLERECMEET

CSYEEAREVFEDSDKTNEFWNKYKDGDQCETSPCQNQGKCKDGLGEYTCTCLEGFEGK NCELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTLE RRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNLTRIVG GQECKDGECPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTEQE EGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMT QKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDA CQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGIYTKVTAFLKWIDRSMKTRGLP KAKSHAPEVITSSPLK, and recombinant and synthetic versions and sequence variants thereof having at least a portion of the biological activity of native FX. Factor X is activated into factor Xa by both factor IX (with its cofactor, factor VIII, to make a complex known as intrinsic Xase) and factor VII with its cofactor, tissue factor (to make a complex known as extrinsic Xase). Factor X is the first member of the final common (or thrombin) pathway. Factor X is used to treat factor X deficiency, hemophilia A & B using bypass strategies due to FVIII and FIX patients developing inhibitory antibodies to FVIII and FIX replacement therapies), emergency treatment of patients with hemorrhages due to oral anticoagulants overdose or unknown causes of critical bleeding, and patients who develop acquired FX deficiency caused by lack of vitamin K, amyloidosis, severe liver disease & use of anticoagulants (e.g. warfarin). While the half-life of mature factor X is 40-45h, the plasma half-life of activated factor X (Fxa) is <1-2 min ((Bunce MW, 2008, Blood, 117:290), making its utility in unmodified form limited, being rapidly inactivated by anti-thrombin III & TFP1.

4. Nucleic acids as payloads

[00312] The invention also contemplates the use of nucleic acids as payloads in the XTEN conjugates. In one embodiment, the invention provides XTEN-payload conjugates wherein the payload is selected from the group consisting of aptamers, antisense oligonucleotides, ribozyme nucleic acids, RNA interference nucleic acids, and antigene nucleic acids. Such nucleic acids used as therapeutics are know in the art (Edwin Jarald, Nucleic acid drugs: a novel approach. African Journal of Biotechnology Vol. 3 (12):662-666, 2004; Joanna B. Opalinska. Nucleic-acid therapeutics: basic principles and recent applications. Nature Reviews Drug Discovery 1:503-514, 2002).

IV). XTEN-CROSS-LINKER AND XTEN-PAYLOAD CONJUGATES AND METHODS OF MAKING SUCH CONJUGATES

[00313] The present invention relates in part to highly purified preparations of XTEN-cross-linker conjugate compositions useful as conjugation partners to which payloads are conjugated, as described herein. The invention also relates to highly purified preparations of payloads linked to one or more XTEN using the XTEN-cross-linker conjugation partners. The present invention encompasses compositions and methods of making the XTEN-payload conjugates formed by

linking of any of the herein described XTEN with a payload, as well as reactive compositions and methods of making the compositions formed by conjugating XTEN with a cross-linker or other chemical methods described herein. It is specifically intended that the terms "XTEN-payload" and "XTEN-cross-linker" encompass the linked reaction products remaining after the conjugation of the reactant conjugation partners, including the reaction products of cross-linkers, click-chemistry reactants, or other methods described herein.

[00314] In some embodiments, the XTEN utilized to create the subject conjugates comprise XTEN selected from any one of the sequences in Table 2, Table 3, and Tables 22-25, which may be linked to the payload component directly or via cross-linkers disclosed herein. In other embodiments, the one or more XTEN utilized to create the subject conjugates individually comprise an XTEN sequence having at least about 80% sequence identity, or alternatively 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity compared to an XTEN selected from Tables 2, 3, and 22-25 or a fragment thereof, when optimally aligned with a sequence of comparable length. In one embodiment, the subject conjugates are multimeric in that they comprise a first and a second XTEN sequence, wherein the XTEN are the same or they are different and wherein each individually comprises an XTEN sequence having at least about 80% sequence identity, or alternatively 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity compared to an XTEN selected from Tables 2, 3, and 22-25 or a fragment thereof, when optimally aligned with a sequence of comparable length. In another embodiment, the subject conjugates are multimeric in that they comprise a first, a second, and a third XTEN sequence, wherein the XTEN are the same or they are different and wherein each individually comprises an XTEN sequence having at least about 80% sequence identity, or alternatively 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity compared to an XTEN selected from Tables 2, 3, 22-25 or a fragment thereof, when optimally aligned with a sequence of comparable length. In yet another embodiment, the subject conjugates are multimeric in that they comprise 3, 4, 5, 6 or more XTEN sequences, wherein the XTEN are the same or they are different and wherein each individually comprises an XTEN sequence having at least about 80% sequence identity, or alternatively 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity compared to an XTEN selected from Tables 2, 3, and 22-25 or a fragment thereof. In the multimeric conjugates, the cumulative length of the residues in the XTEN sequences is greater than about 200 to about 3000 or about 400 to about 1000 amino acid residues, and the XTEN can be identical or they can be different in sequence or in length. As used herein, cumulative length

is intended to encompass the total length, in amino acid residues, when more than one XTEN is incorporated into the conjugate.

[00315] In one aspect, the invention provides compositions of XTEN covalently linked to a small molecule payload drug, resulting in an XTEN-drug conjugate ("XTEN-D"). In another aspect, the invention provides compositions of XTEN covalently linked to a payload biologically active protein (which encompasses peptides or polypeptides), resulting in an XTEN-peptide/polypeptide conjugate ("XTEN-P"). In another aspect, the invention provides compositions of one or more XTEN recombinantly linked to a payload peptide or polypeptide, resulting in an XTEN-peptide/polypeptide recombinant fusion protein ("XTEN-PR"). In another aspect, the invention provides compositions of one or more XTEN linked to payloads of one or more drugs and one or more proteins that can be biologically active or can be targeting moieties. In particular, the invention provides isolated XTEN-D, XTEN-P, XTEN-PR, and XTEN-D-P compositions useful in the treatment of a condition for which the administration of a payload drug and/or protein is known in the art to be useful in the treatment, amelioration or prevention of a disease or condition in a subject. The XTEN-D conjugates generally comprise one or more of the following components: 1) XTEN; 2) cross-linker; and 3) payload to which the XTEN is chemically conjugated either directly or by use of a cross-linker, such as commercially-available cross-linkers described herein, or by use of click-chemistry reactants, or in some cases, may be created by conjugation between reactive groups in the XTEN and payload without the use of a linker as described herein. The XTEN-P generally comprise one or more of the following components: 1) XTEN; 2) cross-linker; and 3) biologically active protein payload, and are also generally created by conjugation with the use of a cross-linker or click-chemistry reactants. The XTEN-PR conjugates generally comprises one or more of the following components: 1) one or more XTEN; 2) a spacer sequence and 3) payload. The XTEN-D-P generally comprise one or more of the following components: 1) XTEN; 2) optional linker; 3) biologically active protein; and 4) drug, wherein the payloads are generally created by conjugation with the use of a cross-linker or click-chemistry reactants, as described above. However, in some cases of foregoing types of compositions, the composition can be created without the use of a cross-linker provided the components are otherwise chemically reactive.

[00316] The conjugation of XTEN to payloads confers several advantages on the resulting compositions compared to the payloads not linked to XTEN. As described more fully below, non-limiting examples of the enhanced properties include increases in the overall solubility and metabolic stability, reduced susceptibility to proteolysis in circulation, reduced immunogenicity, reduced rate of absorption when administered subcutaneously or intramuscularly, reduced clearance by the kidney, enhanced interactions with substrate, reduced toxicity, targeted delivery of payload, and enhanced pharmacokinetic properties. Enhanced pharmacokinetic properties of

the conjugates compared to payload not linked to XTEN include longer terminal half-life (e.g., two-fold, three-fold, four-fold or more), increased area under the curve (AUC) (e.g., 25%, 50%, 100% or more), lower volume of distribution, slower absorption after subcutaneous or intramuscular injection (an advantage compared to commercially-available forms of payload that must be administered by a similar route) such that the Cmax is lower, which, in turn, results in reductions in adverse effects of the payload that, collectively, results in an increased period of time that a conjugation composition administered to a subject provides therapeutic activity. In some embodiments, the conjugation compositions comprise cleavage sequences (described more fully, below) that permits sustained release of active payload, such that the administered XTEN-payload acts as a depot when subcutaneously or intramuscularly administered. It is specifically contemplated that XTEN-payload conjugates can exhibit one or more or any combination of the improved properties disclosed herein. As a result of these enhanced properties, the XTEN-payload conjugates permit less frequent dosing, more tailored dosing, and/or reduced toxicity compared to payload not linked to XTEN and administered in a comparable fashion. Such XTEN-payload conjugates have utility to treat certain conditions known in the art to be affected, ameliorated, or prevented by administration of the payload to a subject in need thereof., as described herein.

1. Cross-linker and azide/alkyne click-chemistry reactants for conjugation

[00317] In another aspect, the invention relates to XTEN conjugated to cross-linkers, resulting in XTEN-cross-linker conjugates that can be utilized to prepare XTEN–payload conjugation compositions. In particular, the herein-described XTEN-cross-linker conjugate partners are useful for conjugation to payload agents or surfaces bearing at least one thiol, amino, carboxyl, aldehyde or alcohol or any other reactive group available and suitable, as known in the art, for reaction between the components described herein.

[00318] In another aspect, the invention relates to methods of making conjugates of XTEN-cross-linker reactants and XTEN-click-chemistry azide/alkyne reactants, resulting in conjugates that can be utilized to prepare the subject XTEN–payload compositions. In particular, the herein-described methods for making XTEN-cross-linkers and XTEN-azide/alkyne reactants are useful wherein the payload agent or a reaction surface bears at least one thiol, amino, carboxyl, aldehyde, alkene, alkyne, heterocycle, alcohol, or other reactive group available for reaction.

[00319] Exemplary embodiments of XTEN have been described above, including preparations of substantially homogeneous XTEN. The invention provides XTEN that further serve as a platform to which payloads can be conjugated, such that they serve as a "carrier", conferring certain desirable pharmacokinetic, chemical and pharmaceutical properties to the compositions, amongst other properties described below. In other embodiments, the invention provides polynucleotides that encode XTEN that can be linked to genes encoding peptide or polypeptide

payloads that can be incorporated into expression vectors and incorporated into suitable hosts for the expression and recovery of the subject XTEN-payload recombinant fusion proteins.

[00320] In some embodiments, the XTEN components as described herein, above, are engineered to incorporate a defined number of reactive amino acid residues that can be reacted with cross-linking agents or can further contain reactive groups that can be used to conjugate to payloads. In one embodiment, the invention provides cysteine-engineered XTEN wherein the cysteine, each of which contains a reactive thiol group, are conjugated to a cross-linker, resulting in an XTEN-cross-linker conjugate. In another embodiment, invention provides lysine-engineered XTEN wherein lysine, each of which contains a positively charged hydrophilic ε-amino group, are conjugated to a cross-linker, resulting in an XTEN-cross-linker conjugate. In the embodiments of cysteine-engineered XTEN, each comprises about 1 to about 100 cysteine amino acids, or from 1 to about 50 cysteine amino acids, or from 1 to about 40 cysteine amino acids, or from 1 to about 20 cysteine amino acids, or from 1 to about 10 cysteine amino acids, or from 1 to about 5 cysteine amino acids, or 9 cysteines, or 3 cysteines, or a single cysteine amino acid that is available for conjugation. In the embodiments of lysine-engineered XTEN, each comprises about 1 to about 100 lysine amino acids, or from 1 to about 50 lysine amino acids, or from 1 to about 40 lysine engineered amino acids, or from 1 to about 20 lysine engineered amino acids, or from 1 to about 10 lysine engineered amino acids, or from 1 to about 5 lysine engineered amino acids, or 9 cysteines, or 3 cysteines, or a single lysine that is available for conjugation. In another embodiment, the engineered XTEN comprises both cysteine and lysine residues of the foregoing ranges or numbers.

[00321] Generally, XTEN cysteine thiol groups are more reactive, i.e., more nucleophilic, towards electrophilic conjugation reagents than amine or hydroxyl groups. In addition, cysteine residues are generally found in smaller numbers in a given protein; thus are less likely to result in multiple conjugations within the same protein. Cysteine residues have been introduced into proteins by genetic engineering techniques to form covalent attachments to ligands or to form new intramolecular disulfide bonds (Better et al (1994) J. Biol. Chem. 13:9644-9650; Bernhard et al (1994) Bioconjugate Chem. 5:126-132; Greenwood et al (1994) Therapeutic Immunology 1:247-255; Tu et al (1999) Proc. Natl. Acad. Sci USA 96:4862-4867; Kanno et al (2000) J. of Biotechnology, 76:207-214; Chmura et al (2001) Proc. Nat. Acad. Sci. USA 98(15):8480-8484; U.S. Pat. No. 6,248,564).

[00322] In one embodiment, the invention provides an isolated composition comprising a cysteine-engineered XTEN conjugated to a cross-linker, wherein the cross-linker is selected from sulfhydryl-reactive homobifunctional or heterobifunctional cross-linkers. In another embodiment, the invention provides an isolated composition comprising a lysine-engineered XTEN conjugated by a cross-linker, wherein the cross-linker is selected from amine-reactive

homobifunctional or heterobifunctional cross-linkers. Cross-linking is the process of chemically linking two or more molecules by a covalent bond. The process is also called conjugation or bioconjugation with reference to its use with proteins and other biomolecules. For example, proteins can be modified to alter N- and C-termini, and amino acid side chains on proteins and peptides in order to block or expose reactive binding sites, inactivate functions, or change functional groups to create new targets for cross-linking

[00323] In one aspect, the invention provides methods for the site-specific conjugation to XTEN polymer, accomplished using chemically-active amino acid residues or their derivatives (e.g., the N-terminal α-amine group, the ε-amine group of lysine, the thiol group of cysteine, the C-terminal carboxyl group, carboxyl groups of glutamic acid and aspartic acid. Functional groups suitable for reactions with primary α- and ε-amino groups are chlorocyanurates, dichlorotreazines, trezylates, benzotriazole carbonates, p-nitrophenyl carbonates, trichlorophenyl carbonates, aldehydes, mixed anhydrides, carbonylimidazoles, imidoesters, N-hydroxysuccinimide esters, N-hydroxysulfosuccinimide esters (Harris, J. M., Herati, R. S. *Polym. Prepr.* (*Am. Chem. Soc., Div. Polym. Chem*), 32(1), 154-155 (1991); Herman, S., et al. *Macromol. Chem. Phys.* 195, 203-209 (1994); Roberts, M. J. et. al. *Advanced Drug Delivery Reviews,* 54, 459-476 (2002)). N-hydroxysuccinimide esters (NHS-esters and their water soluble analogs sulfo-NHS-esters) are commonly used for protein conjugation (see FIG. 2). NHS-esters yield stable amide products upon reaction with primary amines with relatively efficient coupling at physiological pH. The conjugation reactions are typically performed in 50-200 mM phosphate, bicarbonate/carbonate, HEPES or borate buffers (pH between 7 and 9) at 4°C to room temperature from 0.5 to 2 hrs. NHS-esters are usually used at two- to 50-fold molar excess to protein. Typically, the concentration of the reagent can vary from 0.1-10 mM, while the optimal protein concentration is 50-100 μM.

[00324] In another method, given that XTEN polypeptides possess only a single N-terminal α-amino group, the XTEN can be engineered to contain additional ε-amino group(s) of intentionally incorporated lysine residues; exemplary sequences of which are provided in Table 3. The α-and ε-amino groups have different pKa values: approximately 7.6 to 8.0 for the α-amino group of the N-terminal amino acid, and approximately 10-10.5 for the ε-amino group of lysine. Such a significant difference in pKa values can be used for selective modification of amino groups. Deprotonation of all primary amines occurs at pH above pH 8.0. In this environment, the nucleophilic properties of different amines determine their reactivity. When deprotonated, the more nucleophilic ε-amino groups of lysines are generally more reactive toward electrophiles than α-amino groups. On the other hand, at a lower pH (for example pH 6), the more acidic α-amino groups are generally more deprotonated than ε-amino groups, and the order of reactivity is inverted. For example, the FDA-approved drug Neulasta (pegfilgranstim) is

granulocyte colony-stimulating factor (G-CSF) modified by covalent attachment of 20 kDa PEG-aldehyde. Specific modification of the protein's N-terminal amino acid was accomplished by exploiting the lower pKa of α-amino group as compared to ε-amino groups of internal lysines (Molineaux, G. *Curr. Pharm. Des.* 10, 1235-1244 (2004), US Patent 5,824,784).

[00325] The XTEN polypeptides comprising cysteine residues can be genetically engineered using recombinant methods described herein (see, e.g., Examples) or by standard methods known in the art. Conjugation to thiol groups can be carried using highly specific reactions, leading to the formation of single conjugate species joined by cross-linking agents. Functional groups suitable for reactions with cysteine thiol-groups are N-maleimides, haloacetyls, and pyridyl disulfides. The maleimide group reacts specifically with sulfhydryl groups when the pH of the reaction mixture is between pH 6.5 and 7.5, forming a stable thioether linkage that is not reversible (see FIG. 3). At neutral pH, maleimides react with sulfhydryls 1,000-fold faster than with amines, but when the pH is raised to greater than 8.5, the reaction favors primary amines. Maleimides do not react with tyrosines, histidines or methionines. For reaction solutions, thiols must be excluded from reaction buffers used with maleimides as they will compete for coupling sites. Excess maleimides in the reaction can be quenched at the end of a reaction by adding free thiols, while EDTA can be included in the coupling buffer to minimize oxidation of sulfhydryls.

[00326] In another embodiment, the invention contemplates use of haloacetyl reagents that are useful for cross-linking sulfhydryls groups of XTEN or payloads to prepare the subject conjugates. The most commonly used haloacetyl reagents contain an iodoacetyl group that reacts with sulfhydryl groups at physiological pH. The reaction of the iodoacetyl group with a sulfhydryl proceeds by nucleophilic substitution of iodine with a thiol producing a stable thioether linkage (see FIG. 4). Using a slight excess of the iodoacetyl group over the number of sulfhydryl groups at pH 8.3 ensures sulfhydryl selectivity. If a large excess of iodoacetyl group is used, the iodoacetyl group can react with other amino acids. Imidazoles can react with iodoacetyl groups at pH 6.9-7.0, but the incubation must proceed for longer than one week. Histidyl side chains and amino groups react in the unprotonated form with iodoacetyl groups above pH 5 and pH 7, respectively. In another embodiment, cross-linkers useful for sulfhydryls groups are pyridyl disulfides. Pyridyl disulfides react with sulfhydryl groups over a broad pH range (the optimal pH is 4-5) to form disulfide bonds linking XTEN to payloads (see FIG. 5). As a disulfide, conjugates prepared using these reagents are cleavable. During the reaction, a disulfide exchange occurs between the molecule's –SH group and the 2-pyridyldithiol group. As a result, pyridine-2-thione is released. These reagents can be used as crosslinkers and to introduce sulfhydryl groups into proteins. The disulfide exchange can be performed at physiological pH, although the reaction rate is slower.

[00327] The XTEN-payload conjugates comprising active synthetic peptides or polypeptides can be prepared using chemically active amino acid residues or their derivatives; e.g., the N-terminal α-amino group, the ε-amino group of lysine, a thiol group of cysteine, the carboxyl group of the C-terminal amino acid, a carboxyl group of aspartic acid or glutamic acid. Each peptide contains N-terminal α- amino group regardless of a primary amino acid sequence. If necessary, N-terminal α-amino group can be left protected/blocked upon chemical synthesis of the active peptide/polypeptide. The synthetic peptide/polypeptide may contain additional ε-amino group(s) of lysine that can be either natural or specifically substituted for conjugation. As described above, α- and ε-amino groups can be selectively modified at different pH. Another approach to selectively modify either α- or ε-amino group in a synthetic peptide is a reversible protection of amino groups with Di-*tert*-butyl dicarbonate (BOC_2). For example, selective BOC protection of vapreotide peptide (a synthetic somatostatin analog) has been achieved by modification at pH 6 (α-group protected) or pH 8.5 (ε-group protected). The remaining free amino group was then specifically modified by PEG-N-hydroxysuccinimide or PEG-aldehyde. Finally, BOC protection was removed by acidic treatment to yield mono-modified peptides (Morpurgo, M. et al. Selective Alkylation and Acylation of α and ε Amino Groups with PEG in a Somatostatin Analogue: Tailored Chemistry for Optimized Bioconjugates. *Bioconjugate Chem.* 2002. 13:1238-1243).

[00328] Since cysteines are generally less abundant in natural peptide and protein sequences than lysines, the use of cysteines as a site for conjugation reduces the likelihood of multiple conjugations to XTEN-cross-linker molecules in a reaction. It also reduces the likelihood of peptide/protein deactivation upon conjugation. Moreoever, conjugation to cysteine sites can often be carried out in a well-defined manner, leading to the formation of single species XTEN polymer-peptide or XTEN polymer–polypeptide conjugates. In some cases cysteine may be absent in the amino acid sequence of the peptide to be conjugated. In such a case, cysteine residue can be added to the N- or C-terminus of the peptide either recombinantly or synthetically using standard methods. Alternatively, a selected amino acid can be chemically or genetically modified to cysteine. As one example, serine modification to cysteine is considered a conservative mutation. Another approach to introduce a thiol group in cysteine-lacking peptides is chemical modification of the lysine ε-amino group using thiolating reagents such as 2-iminothiolane (Traut's reagent), SATA (N-succinimidyl S-acetylthioacetate), SATP (N-succinimidyl S-acetylthiopropionate), SAT-PEO_4-Ac (N-Succinimidyl S-acetyl(thiotetraethylene glycol)), SPDP (*N*-Succinimidyl 3-(2-pyridyldithio)propionate), LC-SPDP (Succinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate) (described more fully, below). Once a unique thiol group is introduced in the peptide, it can be selectively modified by compounds containing sufhydryl- reactive such as N-maleimides, haloacetyls, and pyridyl disulfides, as described above.

[00329] The conjugation between the XTEN polypeptide and a peptide, protein or small molecule drug payload may be achieved by a variety of linkage chemistries, including commercially available zero-length, homo- or hetero-bifunctional, and multifunctional cross-linker compounds, according to methods known and available in the art, such as those described, for example, in R. F. Taylor (1991) "Protein immobilization. Fundamentals and Applications", Marcel Dekker Inc., N.Y.; G. T. Hermanson et al. (1992) "Immobilized Affinity Ligand Techniques", Academic Press, San Diego; G. T. Hermanson (2008) "Bioconjugate Techniques", 2nd. ed. Elsevier, Inc., S. S. Wong (1991) "Chemistry of Protein Conjugation and Crosslinking", CRC Press, Boca Raton. Suitable cross-linking agents for use in preparing the conjugates of the disclosure are commercially-available from companies like Sigma-Aldrich, Thermo Fisher Scientific (Pierce Protein Research Products), Invitrogen, ProteoChem, G-Biosciences. Preferred embodiments of cross-linkers comprise a thiol-reactive functional group or an amino-reactive functional group. A list of exemplary cross-linkers is provided in Table 13.

Table 13: Exemplary cross-linkers

Cross-linker
maleimides, haloacetyls, pyridyl disulfides, haloacetyls, pyridyl disulfides, ABH (*p*-Azidobenzoyl hydrazide), AMAS (*N*-(α-Maleimidoacetoxy)-succinimide ester), ANB-NOS (*N*-5-Azido-2-nitrobenzyloxy-succinimide), APDP (*N*-(4-[*p*-Azidosalicylamido]butyl)-3'-(2'-pyridyldithio) propionamide), ASBA (4-(*p*-Azidosalicylamido)-butylamine), BASED (*Bis* (β-[4-azidosalicylamido]ethyl) disulfide), BMB (1,4-*Bis*-Maleimidobutane), BMDB (1,4 Bismaleimidyl-2,3-dihydroxybutane), BMH (*Bis*-Maleimidohexane), BMOE (*Bis*-Maleimidoethane), BMPH (*N*-(β-Maleimidopropionic acid)hydrazide), BMPS (*N*-(β-Maleimidopropyloxy)succinimide ester), $BM(PEG)_2$ (1,8-*Bis*-Maleimidodiethylene-glycol), $BM(PEG)_3$ (1,11-*Bis*-Maleimidotriethyleneglycol), BS^2G (*Bis* (sulfosuccinimidyl)glutarate), BS^3 (Sulfo-DSS) (*Bis* (sulfosuccinimidyl)suberate), $BS[PEG]_5$ (*Bis* (NHS)PEG5), $BS(PEG)_9$ (*Bis* (NHS)PEG9), BSOCOES (Bis(2-[succinimidoxycarbonyloxy]ethyl)sulfone), C6-SANH (C6-Succinimidyl 4-hydrazinonicotinate acetone hydrazone), C6-SFB (C6-Succinimidyl 4-formylbenzoate), DCC (*N,N*-Dicyclohexylcarbodiimide), DFDNB (1-5-Difluoro-2,4-dinitrobenzene), DMA (Dimethyl adipimidate), DMP (Dimethyl pimelimidate), DMS (Dimethyl suberimidate), DPDPB (1,4-Di-(3'-[2'pyridyldithio]propionamido) butane), DSG (Disuccinimidyl glutarate), DSP (Dithiobis(succimidylpropionate), Lomant's Reagent), DSS (Disuccinimidyl suberate), DST (Disuccinimidyl tartarate), DTBP (Dimethyl 3,3'-dithiobispropionimidate), DTME (Dithiobis-maleimidoethane), DTSSP (Sulfo-DSP) (3,3'-Dithiobis (sulfosuccinimidylpropionate)), EDC (1-Ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride), EGS (Ethylene glycol *bis*(succinimidylsuccinate)), EMCA (*N*-ε-Maleimidocaproic acid), EMCH (*N*-(ε-Maleimidocaproic acid)hydrazide), EMCS (*N*-(ε-Maleimidocaproyloxy)succinimide ester), GMBS (*N*-(γ-Maleimidobutyryloxy)succinimide ester), KMUA (*N*-κ-Maleimidoundecanoic acid), KMUH (*N*-(κ-Maleimidoundecanoic acid)hydrazide), LC-SDA (NHS-LC-Diazirine), LC-SMCC (Succinimidyl 4-(*N*-maleimidomethyl) cyclohexane-1-carboxy-(6-amidocaproate)), LC-SPDP (Succinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), MBS (*m*-Maleimidobenzoyl-*N*-hydroxysuccinimide ester), MPBH (4-(4-N-Maleimidophenyl)-butyric acid hydrazide), NHS-ASA (*N*-Hydroxysuccinimidyl-4-azidosalicylic acid), PDPH (3-(2-Pyridyldithio)propionylhydrazide), PMPI (*N*-(*p*-Maleimidophenyl)isocyanate), SADP (Succinimidyl (4-azidophenyl dithio) propionate), SAED (Succimidyl 2-[7-azido-4-methylcoumarin-3-acetamido]ethyl-1,3'-dithiopropionate), SAND (Succinimidyl-2-(m-azido-*o*-nitrobenzamido)ethyl 1,3'-dithiopropionate), SANH (Succinimidyl 4-hydrazinonicotinate acetone hydrazone), SANPAH

Cross-linker
(*N*-Succinimidyl 6-(4'-azido-2'-nitrophenylamino)hexanoate), SASD (Succinimidyl-2-(p-azidosalycylamido)ethyl-1,3-dithiopropionate), SBAP (Succinimdyl 3-(bromoacetamido)propionate), SDA (NHS-Diazirine), SDAD (NHS-SS-Diazirine), SFAD (Succinimidyl(perfluoroazidobenzamido)ethyl 1,3'-dithiopropionate), SFB (Succinimidyl 4-formylbenzoate), SHTH (Succinimidyl 4-hydrazidoterephthalate), SIA (*N*-succinimidyl iodoacetate), SIAB (*N*-Succinimidyl(4-iodoacetyl)aminobenzoate), SMPB (Succinimidyl 4-(p-maleimidophenyl) butyrate), SMCC (Succinimidyl 4-(*N*-maleimido-methyl)cyclohexane-1-carboxylate), SM[PEG]$_2$ (NHS-PEG2-Maliemide), SM[PEG]$_4$ (NHS-PEG4-Maliemide), SM(PEG)$_6$ (NHS-PEG6-Maleimide), SM[PEG]$_8$ (NHS-PEG8-Maliemide), SM[PEG]$_{12}$ (NHS-PEG12-Maliemide), SM(PEG)$_{24}$ (NHS-PEG24-Maleimide), SMPB (Succinimidyl 4-(*p*-maleimido-phenyl)butyrate), SMPH (Succinimidyl-6-(β-maleimidopropionamido)hexanoate), SMPT (4-Succinimidyloxycarbonyl-methyl-α-(2-pyridyldithio)toluene), SPB (Succinimidyl-(4-psoralen-8-yloxy)butyrate), SPDP (*N*-Succinimidyl 3-(2-pyridyldithio)propionate), Sulfo-DST (Sulfodisuccinimidyl tartrate), Sulfo-EGS (Ethylene glycol bis (sulfo-succinimidyl succinate)), Sulfo-EMCS (*N*-(ε-Maleimidocaproyloxy)sulfosuccinimide ester), Sulfo-GMBS (*N*-(γ-Maleimidobutryloxy)sulfosuccinimide ester), Sulfo-HSAB (*N*-Hydroxysulfosuccinimidyl-4-azidobenzoate), Sulfo-KMUS (*N*-(κ-Maleimidoundecanoyloxy)sulfosuccinimide ester), Sulfo-LC-SDA (Sulfo-NHS-LC-Diazirine), Sulfo-LC-SMPT (Sulfosuccinimidyl 6-(α-methyl-α-[2-pyridyldithio]-toluamido)hexanoate), Sulfo-LC-SPDP (Sulfosuccinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), Sulfo-MBS (*m*-Maleimidobenzoyl-*N*-hydroxysulfosuccinimide ester), Sulfo-NHS-LC-ASA (Sulfosuccinimidyl(4-azido-salicylamido) hexanoate), Sulfo-SADP (Sulfosuccinimidyl (4-azidophenyl dithio) propionate), Sulfo-SAED (Sulfosuccimidyl 2-[7-azido-4-methylcoumarin-3-acetamido]ethyl-1,3'-dithiopropionate), Sulfo-SAND (Sulfosuccinimidyl-2-(m-azido-*o*-nitrobenzamido)ethyl 1,3'-dithiopropionate), Sulfo-SANPAH (Sulfosuccinimidyl 6-(4'-azido-2'-nitrophenylamino)hexanoate), Sulfo-SASD (Sulfosuccinimidyl-2-(p-azidosalycylamido)ethyl-1,3-dithiopropionate), Sulfo-SDA (Sulfo-NHS-Diazirine), Sulfo-SDAD (Sulfo-NHS-SS-Diazirine), Sulfo-SFAD (Sulfosuccinimidyl(perfluoroazidobenzamido)ethyl 1,3'-dithiopropionate), Sulfo-SIAB (Sulfosuccinimidyl(4-iodo-acetyl)aminobenzoate), Sulfo-SMCC (Sulfosuccinimidyl 4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate), Sulfo-SMPB (Sulfosuccinimidyl 4-(*p*-maleimidophenyl)butyrate), THPP (β-(Tris[hydroxymethyl]phosphine)propionic acid (betaine)), TMEA (*Tris*-(2-Maleimidoethyl)amine), TSAT (*Tris*-(succinimidyl aminotriacetate)), 3-propargyloxypropanoic acid,NHS ester, acetylene-PEG-NHS ester, dibenzylcyclooctyne, (DBCO)-NHS ester, DBCO-PEG-NHS ester, cyclooctyne (COT)-NHS ester, COT-PEG-NHS ester, COT-PEG-pentafluorophenyl (PFP) ester, BCOT-NHS ester, BCOT-PEG-NHS ester, BCOT-PEG-pentafluorophenyl (PFP) ester, Acetylene-PEG4-maleimide, DBCO-maleimide, COT-maleimide, BCOT-maleimide, 3-azide-propionic acid, NHS ester, 6-azide-hexanoic acid, NHS ester, 3-azide-propionic acid, PFP ester, 6-azide-hexanoic acid, PFP ester, azide-PEG-NHS ester, azide-PEG-PFP ester, azide-PEG-maleimide, N-(5-Aminopentyl)maleimide, aminopentyl-maleimide

[00330] Non-limiting examples of cross-linkers are ABH (*p*-Azidobenzoyl hydrazide), AMAS (*N*-(α-Maleimidoacetoxy)-succinimide ester), ANB-NOS (*N*-5-Azido-2-nitrobenzyloxy-succinimide), APDP (*N*-(4-[*p*-Azidosalicylamido]butyl)-3'-(2'-pyridyldithio) propionamide), ASBA (4-(*p*-Azidosalicylamido)-butylamine), BASED (*Bis* (β-[4-azidosalicylamido]ethyl) disulfide), BMB (1,4-*Bis*-Maleimidobutane), BMDB (1,4 Bismaleimidyl-2,3-dihydroxybutane), BMH (*Bis*-Maleimidohexane), BMOE (*Bis*-Maleimidoethane), BMPH (*N*-(β-Maleimidopropionic acid)hydrazide), BMPS (*N*-(β-Maleimidopropyloxy)succinimide ester), BM(PEG)$_2$ (1,8-*Bis*-Maleimidodiethylene-glycol), BM(PEG)$_3$ (1,11-*Bis*-

Maleimidotriethyleneglycol), BS^2G (*Bis* (sulfosuccinimidyl)glutarate), BS^3 (Sulfo-DSS) (*Bis* (sulfosuccinimidyl)suberate), $BS[PEG]_5$ (*Bis* (NHS)PEG5), $BS(PEG)_9$ (*Bis* (NHS)PEG9), BSOCOES (Bis(2-[succinimidoxycarbonyloxy]ethyl)sulfone), C6-SANH (C6-Succinimidyl 4-hydrazinonicotinate acetone hydrazone), C6-SFB (C6-Succinimidyl 4-formylbenzoate), DCC (*N,N*-Dicyclohexylcarbodiimide), DFDNB (1-5-Difluoro-2,4-dinitrobenzene), DMA (Dimethyl adipimidate), DMP (Dimethyl pimelimidate), DMS (Dimethyl suberimidate), DPDPB (1,4-Di-(3'-[2'pyridyldithio]propionamido) butane), DSG (Disuccinimidyl glutarate), DSP (Dithiobis(succimidylpropionate), Lomant's Reagent), DSS (Disuccinimidyl suberate), DST (Disuccinimidyl tartarate), DTBP (Dimethyl 3,3'-dithiobispropionimidate), DTME (Dithiobis-maleimidoethane), DTSSP (Sulfo-DSP) (3,3'-Dithiobis (sulfosuccinimidylpropionate)), EDC (1-Ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride), EGS (Ethylene glycol *bis*(succinimidylsuccinate)), EMCA (*N*-ε-Maleimidocaproic acid), EMCH (*N*-(ε-Maleimidocaproic acid)hydrazide), EMCS (*N*-(ε-Maleimidocaproyloxy)succinimide ester), GMBS (*N*-(γ-Maleimidobutyryloxy)succinimide ester), KMUA (*N*-κ-Maleimidoundecanoic acid), KMUH (*N*-(κ-Maleimidoundecanoic acid)hydrazide), LC-SDA (NHS-LC-Diazirine), LC-SMCC (Succinimidyl 4-(*N*-maleimidomethyl) cyclohexane-1-carboxy-(6-amidocaproate)), LC-SPDP (Succinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), MBS (*m*-Maleimidobenzoyl-*N*-hydroxysuccinimide ester), MPBH (4-(4-N-Maleimidophenyl)-butyric acid hydrazide), NHS-ASA (*N*-Hydroxysuccinimidyl-4-azidosalicylic acid), PDPH (3-(2-Pyridyldithio)propionylhydrazide), PMPI (*N*-(*p*-Maleimidophenyl)isocyanate), SADP (Succinimidyl (4-azidophenyl dithio) propionate), SAED (Succimidyl 2-[7-azido-4-methylcoumarin-3-acetamido]ethyl-1,3'-dithiopropionate), SAND (Succinimidyl-2-(m-azido-*o*-nitrobenzamido)ethyl 1,3'-dithiopropionate), SANH (Succinimidyl 4-hydrazinonicotinate acetone hydrazone), SANPAH (*N*-Succinimidyl 6-(4'-azido-2'-nitrophenylamino)hexanoate), SASD (Succinimidyl-2-(p-azidosalycylamido)ethyl-1,3-dithiopropionate), SBAP (Succinimdyl 3-(bromoacetamido)propionate), SDA (NHS-Diazirine), SDAD (NHS-SS-Diazirine), SFAD (Succinimidyl(perfluoroazidobenzamido)ethyl 1,3'-dithiopropionate), SFB (Succinimidyl 4-formylbenzoate), SHTH (Succinimidyl 4-hydrazidoterephthalate), SIA (*N*-succinimidyl iodoacetate), SIAB (*N*-Succinimidyl(4-iodoacetyl)aminobenzoate), SMPB (Succinimidyl 4-(p-maleimidophenyl) butyrate), SMCC (Succinimidyl 4-(*N*-maleimido-methyl)cyclohexane-1-carboxylate), $SM[PEG]_2$ (NHS-PEG2-Maliemide), $SM[PEG]_4$ (NHS-PEG4-Maliemide), $SM(PEG)_6$ (NHS-PEG6-Maleimide), $SM[PEG]_8$ (NHS-PEG8-Maliemide), $SM[PEG]_{12}$ (NHS-PEG12-Maliemide), $SM(PEG)_{24}$ (NHS-PEG24-Maleimide), SMPB (Succinimidyl 4-(*p*-maleimido-phenyl)butyrate), SMPH (Succinimidyl-6-(β-maleimidopropionamido)hexanoate), SMPT (4-Succinimidyloxycarbonyl-methyl-α-(2-pyridyldithio)toluene), SPB (Succinimidyl-(4-psoralen-8-yloxy)butyrate), SPDP (*N*-Succinimidyl 3-(2-pyridyldithio)propionate), Sulfo-DST

(Sulfodisuccinimidyl tartrate), Sulfo-EGS (Ethylene glycol bis (sulfo-succinimidyl succinate)), Sulfo-EMCS (*N*-(ε-Maleimidocaproyloxy)sulfosuccinimide ester), Sulfo-GMBS (*N*-(γ-Maleimidobutryloxy)sulfosuccinimide ester), Sulfo-HSAB (*N*-Hydroxysulfosuccinimidyl-4-azidobenzoate), Sulfo-KMUS (*N*-(κ-Maleimidoundecanoyloxy)sulfosuccinimide ester), Sulfo-LC-SDA (Sulfo-NHS-LC-Diazirine), Sulfo-LC-SMPT (Sulfosuccinimidyl 6-(α-methyl-α-[2-pyridyldithio]-toluamido)hexanoate), Sulfo-LC-SPDP (Sulfosuccinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), Sulfo-MBS (*m*-Maleimidobenzoyl-*N*-hydroxysulfosuccinimide ester), Sulfo-NHS-LC-ASA (Sulfosuccinimidyl(4-azido-salicylamido) hexanoate), Sulfo-SADP (Sulfosuccinimidyl (4-azidophenyl dithio) propionate), Sulfo-SAED (Sulfosuccimidyl 2-[7-azido-4-methylcoumarin-3-acetamido]ethyl-1,3'-dithiopropionate), Sulfo-SAND (Sulfosuccinimidyl-2-(m-azido-*o*-nitrobenzamido)ethyl 1,3'-dithiopropionate), Sulfo-SANPAH (Sulfosuccinimidyl 6-(4'-azido-2'-nitrophenylamino)hexanoate), Sulfo-SASD (Sulfosuccinimidyl-2-(p-azidosalycylamido)ethyl-1,3-dithiopropionate), Sulfo-SDA (Sulfo-NHS-Diazirine), Sulfo-SDAD (Sulfo-NHS-SS-Diazirine), Sulfo-SFAD (Sulfosuccinimidyl(perfluoroazidobenzamido)ethyl 1,3'-dithiopropionate), Sulfo-SIAB (Sulfosuccinimidyl(4-iodo-acetyl)aminobenzoate), Sulfo-SMCC (Sulfosuccinimidyl 4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate), Sulfo-SMPB (Sulfosuccinimidyl 4-(*p*-maleimidophenyl)butyrate), THPP (β-(Tris[hydroxymethyl]phosphine)propionic acid (betaine)), TMEA (*Tris*-(2-Maleimidoethyl)amine), TSAT (*Tris*-(succinimidyl aminotriacetate)).

[00331] In some embodiments, XTEN-payload conjugates using cross-linking reagents introduce non-natural spacer arms. However, in cases where a native peptide bond is preferred, the invention provides that a reaction can be carried out using zero-length cross-linkers that act via activation of a carboxylate group. In the embodiments thereof, in order to achieve reaction selectivity, the first polypeptide has to contain only a free C-terminal carboxyl group while all lysine, glutamic acid and aspartic acid side chains are protected and the second peptide/protein N-terminal α-amine has to be the only available unprotected amino group (requiring that any lysines, asparagines or glutamines be protected). In such cases, use of XTEN AG family sequences of Table 2 that are without glutamic acid as the first polypeptide in the XTEN-payload or XTEN-cross-linker is preferred. Accordingly, in one embodiment, the invention provides XTEN-cross-linker and XTEN-payload comprising AG XTEN sequences wherein the compositions are conjugated to payloads using a zero-length cross-linkers. Exemplary zero-length cross-linkers utilized in the embodiment include but are not limited to DCC (N,N-Dicyclohexylcarbodiimide) and EDC (1-Ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride) wherein the cross-linikers are used to directly conjugate carboxyl functional groups of one molecule (such as a payload) to the primary amine of another molecule, such as a payload with that functional group (see FIG. 6). Sulfo-NHS (N-hydroxysulfosuccinimide) and

NHS (N-hydroxysuccinimide) are used as catalysts for conjugation, increasing reaction efficiency (Grabarek Z, Gergely J. Zero-length crosslinking procedure with the use of active esters. (1990) Anal. Biochem. 185(1), 131-135). EDC reacts with carboxylic acid group and activates the carboxyl group to form an active O-acylisourea intermediate, allowing it to be coupled to the amino group in the reaction mixture. The O-acylisourea intermediate is unstable in aqueous solutions, making it ineffective in two-step conjugation procedures without increasing the stability of the intermediate using N-hydroxysuccinimide. This intermediate reacts with a primary amine to form an amide derivative. The crosslinking reaction is usually performed between pH 4.5 to 5 and requires only a few minutes for many applications. However, the yield of the reaction is similar at pH from 4.5 to 7.5. The hydrolysis of EDC is a competing reaction during coupling and is dependent on temperature, pH and buffer composition. 4-Morpholinoethanesulfonic acid (MES) is an effective carbodiimide reaction buffer. Phosphate buffers reduce the reaction efficiency of the EDC, but increasing the amount of EDC can compensate for the reduced efficiency. Tris, glycine and acetate buffers may not be used as conjugation buffers.

[00332] The invention also provides compositions in which three XTENs are linked by trivalent cross-linkers, resulting in trimeric XTEN-cross-linker conjugates. Trimeric cross-linkers can be created by connecting a symmetric trivalent core such as tertiary amine, trisubstituted methane or 1,3,5-trisubstituted benzene or asymmetric trivalent molecule such a LysLys dipeptide or a GluGlu dipeptide or a AspAsp dipeptide or a CysCysCys tripeptide by spacers with various reactive side groups described in Table 14, using standard conjugation techniques. In one embodiment, the invention provides compositions in which three XTENs are covalently linked by a trivalent cross-linker selected from the group consisting of thiol-reactive Tris-(2-Maleimidoethyl)amine (TMEA), amine-reactive Tris-(succimimidyl aminotricetate) (TSAT) and the cross-linkers set forth in Table 14.

Table 14: Trivalent Cross-linkers

Trivalent Cross-linker*			
Trivalent Core	**Group 1**	**Group 2**	**Group 3**
Tertiary amine Trisubstituted methane 1,3,5-trisubstituted benzene LysLys GluGluGlu AspAspAsp CysCysCys	Azide	Azide	Azide
	Alkyne	Alkyne	Alkyne
	NHS	NHS	NHS
	Maleimide	Maleimide	Maleimide
	Iodoacetyl	Iodoacetyl	Iodoacetyl
	Azide	NHS	NHS
	Azide	Azide	NHS
	Azide	Iodoacetyl	Iodoacetyl
	Azide	Azide	Iodoacetyl
	Alkyne	NHS	NHS

Trivalent Cross-linker*			
	Alkyne	Alkyne	NHS
	Alkyne	Iodoacetyl	Iodoacetyl
	Alkyne	Alkyne	Iodoacetyl
	Alkyne	Maleimide	Maleimide
	Alkyne	Alkyne	Maleimide
	NHS	Maleimide	Maleimide
	NHS	NHS	Maleimide
	NHS	Alkyne	Maleimide

* One of the trivalent core + any one of Group 1 + any one of Group 2 + any one of Group 3

[00333] In other embodiments, XTEN and payloads can be conjugated using a broad group of cross-linkers, including those consisting of a spacer arm (linear or branched) and two or more reactive ends that are capable of attaching to specific functional groups (e.g., primary amines, sulfhydryls, etc.) on proteins or other molecules. Linear cross-linkers can be homobifunctional or heterobifunctional. Homobifunctional cross-linkers have two identical reactive groups which are used to cross-link proteins in one step reaction procedure. Non-limiting examples of amine-reactive homobifunctional cross-linkers are BS2G (Bis (sulfosuccinimidyl)glutarate), BS3 (Sulfo-DSS) (Bis (sulfosuccinimidyl)suberate), BS[PEG]5 (Bis (NHS)PEG5), BS(PEG)9 (Bis (NHS)PEG9), BSOCOES (Bis(2-[succinimidoxycarbonyloxy]ethyl)sulfone), DFDNB (1-5-Difluoro-2,4-dinitrobenzene), DMA (Dimethyl adipimidate), DMP (Dimethyl pimelimidate), DMS (Dimethyl suberimidate), DSG (Disuccinimidyl glutarate), DSP (Dithiobis(succimidylpropionate) (Lomant's Reagent), DSS (Disuccinimidyl suberate), DST (Disuccinimidyl tartarate), DTBP (Dimethyl 3,3'-dithiobispropionimidate), DTSSP (Sulfo-DSP) (3,3'-Dithiobis (sulfosuccinimidylpropionate)), EGS (Ethylene glycol bis(succinimidylsuccinate)), Sulfo-EGS (Ethylene glycol bis (sulfo-succinimidyl succinate)).

[00334] Additionally, examples of homobifunctional cross-linkers employed in the compositions and in the methods to create the XTEN-payload and/or XTEN-cross-linker compositions are sulfhydryl–reactive agents such as BMB (1,4-Bis-Maleimidobutane), BMH (Bis-Maleimidohexane), BMDB (1,4 Bismaleimidyl-2,3-dihydroxybutane), BMOE (Bis-Maleimidoethane), BM(PEG)2 (1,8-Bis-Maleimidodiethylene-glycol), BM(PEG)3 (1,11-Bis-Maleimidotriethyleneglycol), DPDPB (1,4-Di-(3'-[2'pyridyldithio]propionamido) butane), DTME (Dithiobis-maleimidoethane).

[00335] For the creation of XTEN-cross-linker conjugates for subsequent conjugation to payloads, as well as the creation of XTEN-payload conjugates, heterobifunctional cross-linkers are preferred as the sequential reactions can be controlled. As heterobifunctional cross-linkers possess two different reactive groups, their use in the compositions allows for sequential two-step conjugation. A heterobifunctional reagent is reacted with a first protein using the more labile group. In one embodiment, the conjugation of the heterobifunctional cross-linker to a

reactive group in an XTEN results in an XTEN-cross-linker conjugate. After completing the reaction and removing excess unreacted cross-linker, the modified protein (such as the XTEN-cross-linker) can be added to the payload which interacts with a second reactive group of the cross-linker, resulting in an XTEN-payload conjugate. Most commonly used heterobifunctional cross-linkers contain an amine-reactive group at one end and a sulfhydryl–reactive group at the other end. Accordingly, these cross-linkers are suitable for use with cysteine- or lysine-engineered XTEN, or with the alpha-amino group of the N-terminus of the XTEN. Non-limiting examples of heterobifunctional cross-linkers are AMAS (*N*-(α-Maleimidoacetoxy)-succinimide ester), BMPS (*N*-(β-Maleimidopropyloxy)succinimide ester), EMCS (*N*-(ε-Maleimidocaproyloxy)succinimide ester), GMBS (*N*-(γ-Maleimidobutyryloxy)succinimide ester), LC-SMCC (Succinimidyl 4-(*N*-maleimidomethyl) cyclohexane-1-carboxy-(6-amidocaproate)), LC-SPDP (Succinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), MBS (*m*-Maleimidobenzoyl-*N*-hydroxysuccinimide ester), SBAP (Succinimdyl 3-(bromoacetamido)propionate), SIA (*N*-succinimidyl iodoacetate), SIAB (*N*-Succinimidyl(4-iodoacetyl)aminobenzoate), SMPB (Succinimidyl 4-(p-maleimidophenyl) butyrate), SMCC (Succinimidyl 4-(*N*-maleimido-methyl)cyclohexane-1-carboxylate), SM[PEG]$_2$ (NHS-PEG2-Maliemide), SM[PEG]$_4$ (NHS-PEG4-Maliemide), SM(PEG)$_6$ (NHS-PEG6-Maleimide), SM[PEG]$_8$ (NHS-PEG8-Maliemide), SM[PEG]$_{12}$ (NHS-PEG12-Maliemide), SM(PEG)$_{24}$ (NHS-PEG24-Maleimide), SMPB (Succinimidyl 4-(*p*-maleimido-phenyl)butyrate), SMPH (Succinimidyl-6-(β-maleimidopropionamido)hexanoate), SMPT (4-Succinimidyloxycarbonyl-methyl-α-(2-pyridyldithio)toluene), SPDP (*N*-Succinimidyl 3-(2-pyridyldithio)propionate), Sulfo-EMCS (*N*-(ε-Maleimidocaproyloxy)sulfosuccinimide ester), Sulfo-GMBS (*N*-(γ-Maleimidobutryloxy)sulfosuccinimide ester), Sulfo-KMUS (*N*-(κ-Maleimidoundecanoyloxy)sulfosuccinimide ester), Sulfo-LC-SMPT (Sulfosuccinimidyl 6-(α-methyl-α-[2-pyridyldithio]-toluamido)hexanoate), Sulfo-LC-SPDP (Sulfosuccinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), Sulfo-MBS (*m*-Maleimidobenzoyl-*N*-hydroxysulfosuccinimide ester), Sulfo-SIAB (Sulfosuccinimidyl(4-iodo-acetyl)aminobenzoate), Sulfo-SMCC (Sulfosuccinimidyl 4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate), Sulfo-SMPB (Sulfosuccinimidyl 4-(*p*-maleimidophenyl)butyrate). An example of a heterobifunctional cross-linker that allows covalent conjugation of amine- and sulfhydryl-containing molecules is Sulfo-SMCC (SulfoSulfosuccinimidyl 4-(*N*-maleimidomethyl)cyclohexane-1-carboxylate). Sulfo-SMCC is a water soluble analog of SMCC that can be prepared in aqueous buffers up to 10 mM concentration. The cyclohexane ring in the spacer arm of this cross-linker decreases the rate of hydrolysis of the maleimide group compared to similar reagents not containing this ring. This feature enables XTEN that have been maleimide-activated with SMCC or Sulfo-SMCC to be lyophilized and stored for later conjugation to a sulfhydryl-containing molecule. Thus, in one

embodiment, the invention provides an XTEN-cross-linker having an XTEN having at least about 80% sequence identity, or at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity, or is identical to a sequence or a fragment of a sequence selected from of Table 3, when optimally aligned, wherein XTEN-cross-linker has one or more cross-linkers of sulfo-SMCC linked to the α-amino group of the XTEN or the ε-amine of a lysine-engineered XTEN. In another embodiment, the invention provides an XTEN-cross-linker having an XTEN having at least about 80% sequence identity, or at least about 90%, or about 91%, or about 92%, or about 93%, or about 94%, or about 95%, or about 96%, or about 97%, or about 98%, or about 99% sequence identity, or is identical to a sequence or a fragment of a sequence selected from of Table 2, when optimally aligned., wherein the XTEN-cross-linker has one sulfo-SMCC linked to the amino group of the N-terminus of the XTEN. The foregoing described heterobifunctional cross-linkers conjugate two molecules via a single amine and a single cysteine. A special type of cross-linker was developed for site-specific conjugation to disulfide bridges in proteins (Balan S. et al. Site-specific PEGylation of protein disulfide bonds using a three-carbon bridge. (2007) Bioconjugate Chem. 18, 61-76; Brocchini S. et al. Disulfide bridge based PEGylation of proteins. (2008) Advanced Drug Delivery Reviews 60, 3-12). First, the linker is synthesized as an amine-specific 4-[2,2-bis[*p*-tolylsulfonyl)methyl]acetyl) benzoic acid–NHS ester. This molecule can be covalently attached to the amino group of XTEN yielding XTEN-Bis(sulfone). Incubation of the latter molecule in 50 mM sodium phosphate buffer, pH 7.8, will result in elimination of toluene sulfinic acid to generate XTEN-α,β-unsaturated β'-monosulfone. The resulting molecule will react with a disulfide bridge-containing payload protein in a site-specific manner. In a first step the disulfide bridge is converted into two thiols by reduction. In a second step, the XTEN-monosulfone bis-alkylates two cysteines resulting in a chemically-stable three-carbon bridge. The same α,β-unsaturated β'-monosulfone can be used not only for conjugation to two thiol groups derived from a disulfide bridge but also for conjugation to polyhistidine tags (Cong Y. et al. Site-specific PEGylation at histidine tags. (2012) Bioconjugate Chem. 23, 248-263).

[00336] Conjugation using XTEN-cross-linker compositions with the sulfo-SMCC is usually performed in a two-step process. In one embodiment, the amine-containing protein is prepared in conjugation buffer of, e.g., phosphate-buffered saline (PBS = 100mM sodium phosphate, 150mM sodium chloride, pH 7.2) or a comparable amine- and sulfhydryl-free buffer at pH 6.5-7.5. The addition of EDTA to 1-5mM helps to chelate divalent metals, thereby reducing disulfide formation in the sulfhydryl-containing protein. The concentration of the amine-containing protein determines the cross-linker molar excess to be used. In general, in protein samples of < 1mg/ml utilize an 40-80-fold molar excess, protein samples of 1-4mg/ml utilize a 20-fold molar excess, and protein samples of 5-10mg/ml utilize a 5- to 10-fold molar excess of the cross-linker.

The reaction mixture (amine-containing protein and cross-linker) is incubated for 30 minutes at room temperature or 2 hours at 4°C and then the excess cross-linker is removed using a desalting column equilibrated with conjugation buffer. In the case of preparing a XTEN-cross-linker, the composition would be held at that point. In embodiments wherein the XTEN-cross-linker is conjugated to a payload, the sulfhydryl-containing payload and the XTEN-cross-linker conjugate are mixed in a molar ratio corresponding to that desired for the final conjugate (taking into account the number of expected cross-linkers conjugated to one or more amino groups per molecule of the XTEN) and consistent with the single sulfhydryl group that exists on the payload. The reaction mixture is incubated at room temperature for 30 minutes or 2 hours at 4°C. Conjugation efficiency can be estimated by SDS-PAGE followed by protein staining or by appropriate analytical chromatography technique such as reverse phase HPLC or cation/anion exchange chromatography.

[00337] In one embodiment, the invention provides XTEN-cross-linker conjugate compositions created using cross-linkers that are multivalent, resulting in compositions that have 2, 3, 4, 5, 6 or more XTEN. In another embodiment, the invention provides XTEN-cross-linker-payload conjugate compositions created using cross-linkers that are multivalent, resulting in compositions that have 2, 3, 4, 5, 6 or more XTEN linked to 1, 2, 3, 4, 5, 6 or more different payloads. Non-limiting examples of multivalent trifunctional cross-linkers are "Y-shaped" sulfhydryl-reactive TMEA (*Tris*-(2-Maleimidoethyl)amine) and amine-reactive TSAT (*Tris*-(succimimidyl aminotricetate). Any combination of reactive moieties can be designed using a scaffold polymer, either linear or branched, for multivalent compositions. Examples are shown in FIG. 7, wherein the constructs can have any combination of homo- or heterofunctional reactive groups. Of particular interest are trimeric configurations, shown schematically in FIGS 21-23 and 97-105, and tetrameric configurations, shown in FIGS. 21 and 105-106. Not to be bound by a particular theory, a conjugate composition having three XTEN linked by a trifunctional linker (with payloads linked, in turn to XTEN via incorporated lysine or cysteine residues) can utilize proportionally shorter XTEN for each "arm" of the construct compared to a monovalent XTEN-payload composition wherein the same number of payloads are linked to the incorporated cysteine or lysine or N-terminal amino residues of each XTEN, and the resulting trimeric XTEN-payload composition will have a comparable apparent molecular weight and hydrodynamic radius as the monomeric XTEN-payload composition, yet will have lower viscosity, aiding administration of the composition to the subject through small-bore needles, and will provide equal or better potency from the payloads due to reduced steric hindrance and increased flexibility of the composition compared to the monomeric XTEN-payload composition having an equivalent number of XTEN amino acids.

[00338] In one embodiment, the invention provides a composition comprising three XTEN linked by a trivalent cross-linker wherein a solution containing approximately 100 mg/ml of protein of the composition has a viscosity that is at least about 5 cP, or about 6 cP, or about 7 cP, or about 8 cP, or about 9 cP, or about 10 cP lower than the corresponding linear XTEN of equal molecular weight and concentration. In another embodiment, the invetion provides a composition comprising four XTEN linked by a tetravalent cross-linker wherein a solution containing approximately 100 mg/ml of protein of the composition has a viscosity that is at least about 5 cP, or about 6 cP, or about 7 cP, or about 8 cP, or about 9 cP, or about 10 cP lower than the corresponding linear XTEN of equal molecular weight and concentration.

[00339] Methods to make such compositions using the multivalent cross-linkers can employ similar reaction conditions as described herein, above, while an exemplary method and supporting data are provided in the Examples, below. Additionally, multivalent cross-linkers can be readily obtained by modification of lysine oligomers. For instance, the peptide Lys-Lys comprises three amino groups, one alpha-amino group and two epsilon amino groups at each Lys residue. These amino groups can be converted into many other reactive groups by reacting them with Bifunctional cross-linkers which have one amine-reactive group. For example the reaction of Lys-Lys with DBCO-NHS cross-linker yields a product that carries three DBCO groups. The reaction of Lys-Lys with NMal-NHS cross linker yields product that carries three NMal groups. In similar way one can obtain tetravalent cross-linkers based on Lys-Lys-Lys and higher valency cross-linkers by using longer lysine peptides.

[00340] Cross-linkers can be classified as either "homobifunctional" or "heterobifunctional" wherein homobifunctional cross-linkers have two or more identical reactive groups and are used in one-step reaction procedures to randomly link or polymerize molecules containing like functional groups, and heterobifunctional cross-linkers possess different reactive groups that allow for either single-step conjugation of molecules that have the respective target functional groups or allow for sequential (two-step) conjugations that minimize undesirable polymerization or self-conjugation. In a preferred embodiment, where XTEN-cross-linkers are prepared and isolated as compositions for subsequent reaction, the XTEN-cross-linker is linked to a heterbifunctional cross-linker and has at least one reactive group available for subsequent reaction.

[00341] In one embodiment, the invention provides XTEN-cross-linkers and XTEN-payloads that are conjugated utilizing cleavable cross-linkers with disulfide bonds. Typically, the cleavage is effected by disulfide bond reducing agents such as β-mercaptoethanol, DTT, TCEP, however it is specifically contemplated that such compositions would be cleavable endogenously in a slow-release fashion by conditions with endogenous reducing agents (such as cysteine and glutathione). The following are non-limiting examples of such cross-linkers: APDP (*N*-(4-[*p*-

Azidosalicylamido]butyl)-3'-(2'-pyridyldithio) propionamide), BASED (*Bis* (β-[4-azidosalicylamido]ethyl) disulfide), DPDPB (1,4-Di-(3'-[2'pyridyldithio]propionamido) butane), DSP (Dithiobis(succimidylpropionate) (Lomant's Reagent), DTBP (Dimethyl 3,3'-dithiobispropionimidate), DTME (Dithiobis-maleimidoethane), DTSSP (Sulfo-DSP) (3,3'-Dithiobis (sulfosuccinimidylpropionate)), LC-SPDP (Succinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), PDPH (3-(2-Pyridyldithio)propionylhydrazide), SDAD (NHS-SS-Diazirine), SMPT (4-Succinimidyloxycarbonyl-methyl-α-(2-pyridyldithio)toluene), SPDP (*N*-Succinimidyl 3-(2-pyridyldithio)propionate), Sulfo-LC-SMPT (Sulfosuccinimidyl 6-(α-methyl-α-[2-pyridyldithio]-toluamido)hexanoate), Sulfo-LC-SPDP (Sulfosuccinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate), Sulfo-SAED (Sulfosuccimidyl 2-[7-azido-4-methylcoumarin-3-acetamido]ethyl-1,3'-dithiopropionate), Sulfo-SAND (Sulfosuccinimidyl-2-(m-azido-*o*-nitrobenzamido)ethyl 1,3'-dithiopropionate), Sulfo-SDAD (Sulfo-NHS-SS-Diazirine), Sulfo-SFAD (Sulfosuccinimidyl(perfluoroazidobenzamido)ethyl 1,3'-dithiopropionate. In another embodiment, XTEN-payload conjugates comprising BSOCOES (Bis(2-[succinimidoxycarbonyloxy]ethyl)sulfone) can be cleaved under alkaline conditions. In another embodiment, XTEN-payload conjugates comprising DST (Disuccinimidyl tartarate) and BMDB (1,4 Bismaleimidyl-2,3-dihydroxybutane) can be cleaved by periodate oxidation. EGS (Ethylene glycol *bis*(succinimidylsuccinate)) and Sulfo-EGS (Ethylene glycol bis (sulfo-succinimidyl succinate)) are cleaved by hydroxylamine but would be expected to be cleaved endogenously such that the active payload would be released from the conjugate.

[00342] In general, the conjugation reagents described above assume that a cross-linker is reactive with the otherwise stable and inert groups such as amines, sulfhydryls and carboxyls. In other embodiments, the invention provides a different approach of conjugation based on separate modifications of the XTEN and payload with two functional groups which are stable and inactive toward biopolymers in general yet highly reactive toward each other. Several orthogonal reactions have been grouped under the concept of click chemistry, which provides XTEN-azide/alkyne reactants that have good stability properties and are therefor particularly suited as reagents for subsequent conjugation with payloads in a separate reaction (Kolb H.C., Finn M.G., Sharpless K.B. Click chemistry: diverse chemical function from a few good reactions. (2001) *Angew. Chem. Int. Ed. Engl.* 40(11), 2004-2021). Generally, click chemistry is used as a reaction concept which embraces reactions involving (1) alkyne-azide; (2) "ene"-thiol, and (3) aldehyde-hydrazide, and the invention contemplates use of all three. One example is the Huisgen 1,3-dipolar cycloaddition of alkynes to azides to form 1,4-disubsituted-1,2,3-triazoles, shown in FIG. 8. Azide and alkyne moieties can be introduced into peptide/protein or drug payloads or into XTEN by chemical modification of N-terminal α-amino groups, ε-amino groups of lysine, and sulfhydryl groups of cysteine. Table 15 provides non-limiting examples of click chemistry

reactants contemplated for use in the making of the conjugate compositions, wherein one component of the intended conjugate (and XTEN or a payload) is reacted with a reactant 1 of the Table and the second component (a payload or an XTEN) is reacted with a azide reactant 2 of the Table. For example, one molecule is modified with an alkyne moiety using an amine-reactive alkyne, such as 3-propargyloxypropanoic acid, NHS ester, acetylene-PEG4-NHS ester, dibenzylcyclooctyne (DBCO)-NHS ester, DBCO-PEG4-NHS ester, cyclooctyne (COT)-PEG2-NHS ester, COT-PEG3-NHS ester, COT-PEG4-NHS ester, COT-PEG2-pentafluorophenyl (PFP) ester, COT-PEG3-PFP ester, COT-PEG4-PFP ester, BCOT-PEG2-NHS ester, BCOT-PEG3-NHS ester, BCOT-PEG4-NHS ester, BCOT-PEG2-PFP ester, BCOT-PEG3-PFP ester, BCOT-PEG4-PFP ester. Alternatively, the molecule is modified with a sulfhydryl-reactive alkyne such as acetylene-PEG4-Maleimide, DBCO-Maleimide, or DBCO-PEG4-Maleimide. The second molecule is modified with azide-PEG2-NHS ester, azide-PEG3-NHS ester , azide-PEG4-NHS ester , azide-PEG2-PFP ester, azide-PEG3-PFP ester , azide-PEG4-PFP ester or azide-PEG4-Maleimide. The azide and alkyne moieties can be used interchangeably; they are biologically unique, stable and inert towards biological molecules and aqueous environments. When mixed, the azide and alkyne reactants form an irreversible covalent bond without any side reactions (Moses J.E. and Moorhouse A.D. The growing applications of click chemistry. (2007) Chem. Soc. Rev. 36, 1249–1262; Breinbauer R. and Köhn M. Azide-alkyne coupling: a powerful reaction for bioconjugate chemistry. (2003) ChemBioChem 4(11), 1147–1149; Rostovtsev V.V., Green L.G., Fokin V.V., Sharpless K.B. A stepwise Huisgen cycloaddition process: copper(I)-catalyzed regioselective "ligation" of azides and terminal alkynes.(2002) Angew Chem Int Ed Engl. 41(14), 2596-2599). In one embodiment, the invention provides a conjugate comprising a first XTEN conjugated to a second XTEN wherein the first XTEN is linked to a alkyne reactant 1 from Table 15, the second XTEN is linked to a azide reactant 2 from Table 15, and then the first XTEN and the second XTEN are linked under conditions effective to react the alkyne reactant 1 and the azide reactant 2, resulting in the XTEN-XTEN conjugate. In another embodiment, the invention provides a conjugate comprising a first XTEN conjugated to a payload wherein the XTEN is linked to a alkyne reactant 1 from Table 15, the payload is linked to a azide reactant 2 from Table 15, and then the XTEN and the payload are linked under conditions effective to react the alkyne reactant 1 and the azide reactant 2, resulting in the XTEN-payload conjugate. In another embodiment, the invention provides a conjugate comprising a first XTEN conjugated to a payload wherein the XTEN is linked to a azide reactant 2 from Table 15, the payload is linked to a alkyne reactant 1 from Table 15, and then the XTEN and the payload are linked under conditions effective to react the alkyne reactant 1 and the azide reactant 2, resulting in the XTEN-payload conjugate. In the foregoing embodiments, the conditions to effect the reactions are those described herein or are reaction conditions known in the art for the conjugation of such

reactants. The invention also contemplates the various combinations of the foregoing conjugates; e.g., an XTEN-XTEN conjugate in which the XTEN are linked by click chemistry reactants and in which one XTEN further comprises one or more molecules of a payload conjugated to the XTEN using click chemistry, an XTEN-XTEN conjugate in which the XTEN are linked by click chemistry reactants in which one XTEN further comprises one or more molecules of a first payload conjugated to the XTEN using click chemistry and the second XTEN further comprises one or more molecules of a second payload conjugated to the XTEN using click chemistry. Additional variations on these combinations will be readily apparent to those of ordinary skill in the art.

Table 15: Alkyne and Azide Click-chemistry Reactants

Alkyne Reactant 1	Attached to:	Azide Reactant 2	Attached to:
3-propargyloxypropanoic acid, NHS ester*	Amine	3-azide-propionic acid, NHS ester*	Amine
acetylene-(oxyethyl)$_n$-NHS ester*, where n is 1-10	Amine	6-azide-hexanoic acid, NHS ester*	Amine
dibenzylcyclooctyne (DBCO)-NHS ester*	Amine	3-azide-propionic acid, PFP ester	Amine
DBCO-(oxyethyl)$_n$- NHS ester*, where n is 1-10	Amine	6-azide-hexanoic acid, PFP ester	Amine
cyclooctyne (COT)-NHS ester*	Amine	azide-(oxyethyl)$_n$NHS ester*, where n is 1-10	Amine
COT-(oxyethyl)$_n$- NHS ester*, where n is 1-10	Amine	azide-(oxyethyl)$_n$- PFP ester, where n is 1-10	Amine
COT-(oxyethyl)$_n$-pentafluorophenyl (PFP) ester, where n is 1-10	Amine	1-azido-3,6,9,12-tetraoxapentadecan-15-oic acid N-hydroxysuccinimide ester	Amine
BCOT-NHS ester*	Amine	azide-(oxyethyl)$_n$- maleimide, where n is 1-10	Thiol
BCOT-(oxyethyl)$_n$- NHS ester*, where n is 1-10	Amine		
BCOT-(oxyethyl)$_n$-pentafluorophenyl (PFP) ester, where n is 1-10	Amine		
6-(11,12-didehydrodibenzo[b,f]azocin-5(6H)-yl)-6-oxohexanoic acid N-hydroxysulfosuccinimide ester	Amine		
ccetylene-(oxyethyl)$_n$-maleimide, where n is 1-10	Thiol		
DBCO-maleimide	Thiol		
COT-maleimide	Thiol		
BCOT-maleimide	Thiol		

*could be either NHS ester or sulfo-NHS ester

[00343] In some embodiments, the XTEN-XTEN conjugates and the XTEN-payload conjugates are conjugated using thio-ene based click chemistry that proceeds by free radical reaction, termed thiol-ene reaction, or anionic reaction, termed thiol Michael addition (see FIG. 9) (Hoyle C. E. and Bowman C.N. Thiol-ene click chemistry. (2010) *Angew. Chem. Int. Ed.* 49, 1540-1573). It particular, is believed that thiol Michael addition is better suited for XTEN-payload conjugates wherein the payload is a protein (Pounder R. J. et. al. Metal free thiol-maleimide 'Click' reaction as a mild functionalisation strategy for degradable polymers. (2008) *Chem Commun (Camb).* 41, 5158-5160). As at least one molecule needs to contain a free thiol group, a cysteine-engineered XTEN can be utilized if the payload does not contain cysteine. Alternatively, the thiol group can be introduced by chemical modification of N-terminal α-amino group or the lysine ε-amino groups of either the XTEN or the payload peptide/protein using thiolating reagents such as 2-iminothiolane (Traut's reagent), SATA (N-succinimidyl S-acetylthioacetate), SATP (N-succinimidyl S-acetylthiopropionate), SAT-PEO_4-Ac (N-Succinimidyl S-acetyl(thiotetraethylene glycol)), SPDP (*N*-Succinimidyl 3-(2-pyridyldithio)propionate), LC-SPDP (Succinimidyl 6-(3'-[2-pyridyldithio]propionamido)hexanoate). Such methods are known in the art (Carlsson J. et al. (1978) *Biochem. J.* 173, 723-737; Wang D. et al. (1997) *Bioconjug. Chem.* 8, 878-884; Traut R.R. et al. (1973) *Biochemistry* 12(17), 3266-3273; Duncan, R.J.S. et.al. (1983) *Anal. Biochem.* 132. 68-73; U.S. Pat. No. 5,708,146). The second component of thiol-Michael addition reaction requires a reagent with electron-deficient carbon-carbon double bond, such as in (meth)acrylates, maleimides, α,β-unsaturated ketones, fumarate esters, acrylonitrile, cinnamates, and crotonates. The N-maleimides are commonly used as sulfhydryl-reactive functionalities and can be introduced into the payload protein or the XTEN molecule via N-terminal α-amino group or Lys ε-amino group modification using commercially available heterobifunctional cross-linkers such as AMAS (*N*-(α-Maleimidoacetoxy)-succinimide ester), BMPS (*N*-(β-Maleimidopropyloxy)succinimide ester) and others described above. The resulting two molecules containing free thiol and maleimide moieties, respectively, form a stable covalent bond under mild conditions, resulting in a XTEN-payload linked by maleimide.

[00344] In other embodiments, XTEN-XTEN conjugates and XTEN-payload conjugates are created utilizing click chemistry based on reactions between hydrazides and aldehydes, such as described by Ganguly et al. and as shown in FIG. 10 (Ganguly T. et al. The hydrazide/hydrazone click reaction as a biomolecule labeling strategy for M(CO)3 (M = Re, 99mTc) radiopharmaceuticals. (2011) *Chem. Commun.* 47, 12846-12848). For example, an XTEN can be modified to have a hydrazine or hydrazide that is mixed with a payload having an aldehyde group to yield the desired XTEN-payload conjugate. In one embodiment, the invention provides XTEN with at least one hydrazine or hydrazide introduced in either the α–N-terminal amino group or, alternatively one or more lysine ε-amino groups are modified to provide an XTEN

suitable as a reagent for conjugation to a target payload as it is considered to be stable. The resulting bis-arylhydrazones formed from aromatic hydrazines and aromatic aldehydes are stable to 92°C and a wide range of pH values from 2.0-10.0 (Solulink, Inc., Protein-Protein Conjugation Kit, Technical Manual, Catalog # S-9010-1). The leaving group in the reaction is water and no reducing agents (e.g., sodium cyanoborohydride) are required to stabilize the bond. Molecules modified with either hydrazine/hydrazide or aldehyde moieties have good stability in aqueous environments and remain active without special handling requirements. The amino group(s) of the XTEN molecule are modified by NHS-ester/hydrazide, such as SANH (succinimidyl 4-hydrazinonicotinate acetone hydrazone), C6-SANH (C6-Succinimidyl 4-hydrazinonicotinate acetone hydrazone), SHTH (Succinimidyl 4-hydrazidoterephthalate hydrocholoride). In a typical reaction, a protein is prepared as 1-5 mg/ml solution in modification buffer (100 mM Phosphate, 150 mM NaCl, pH 7.4) and the modifying agent is added in a 5- to 20-fold molar excess and the reaction is carried out for 2 hrs at room temperature. Separately, the payload molecule is modified with NHS-ester/aldehyde SFB (succinimidyl 4-formylbenzoate) or C6-SFB (C6-Succinimidyl 4-formylbenzoate) under similar conditions. Both modified molecules are then desalted into conjugation buffer (100 mM phosphate, 150 mM NaCl, pH 6.0). The resulting components are mixed together using 1 mole equivalent of a limiting protein and 1.5-2 mole equivalents of a protein that can be used in abundance. A catalyst buffer of 100 mM aniline in 100 mM phosphate, 150 mM NaCl, pH 6.0 is added to adjust the final concentration of aniline to 10 mM and the reaction is carried out for 2 hrs at room temperature.

[00345] In another embodiment, the XTEN-payload conjugate can be produced by reaction between an aldehyde and primary amino group followed by reduction of the formed Schiff base with sodium borohydride or cyanoborohydride. As a first step in the method, an XTEN molecule, such as XTEN with a primary α-amino group or Lys-containing XTEN with an ε-amino group, is modified by NHS-ester/aldehyde SFB (succinimidyl 4-formylbenzoate), C6-SFB (C6-succinimidyl 4-formylbenzoate) or SFPA (succinimidyl 4-formylphenoxyacetate) using typical amine-NHS chemistry in an amine-free coupling buffer such as 0.1M sodium phosphate, 0.15M NaCl, pH 7.2. The resulting modified aldehyde-XTEN can either be held at this point as an XTEN-cross-linker composition or can be used as a reagent to create an XTEN-payload conjugate. To make the XTEN-payload, the modified aldehyde-XTEN is mixed with a payload with a reactive amino-group and a mild reducing agent such as 20-100 mM sodium cyanoborohydride. The reaction mixture is incubated up to 6 hours at room temperature or overnight at 4°C. Unreacted aldehyde groups are then blocked with 50-500 mM Tris•HCl, pH 7.4 and 20-100 mM sodium cyanoborohydride, permitting separation of the conjugated purified XTEN-payload.

[00346] In other embodiments, the invention provides XTEN-payload conjugates comprising peptides or protein payloads wherein the payload is conjugated via chemical ligation based on the reactivity of the peptide/protein C-terminal acyl azide of the payload. As an example, when the peptide or protein is produced using solid-phase peptide synthesis (SPPS) with hydroxymethylbenzoic acid (HMBA) resin, the final peptide can be cleaved from the resin by a variety of nucleophilic reagents to give access to peptides with diverse C-terminal functionalities. In one embodiment, the method includes hydrazinolysis of the peptidyl/protein resins to yield peptide or protein hydrazides. Nitrosation of resulting acyl hydrazides with sodium nitrite or *tert*-butyl nitrite in dilute hydrochloric acid then results in formation of acyl azides. The resulting carbonyl azide (or acyl azide) is an activated carboxylate group (esters) that can react with a primary amine of an XTEN to form a stable amide bond, resulting in the XTEN-payload conjugate. In alternative embodiments, the primary amine could be the α-amine of the XTEN N-terminus or one or more ε-amine of engineered lysine residues in the XTEN sequence. In the conjugation reaction, the azide function is the leaving group, shown in FIG. 11. The conjugation reaction with the amine groups occurs by attack of the nucleophile at the electron-deficient carbonyl group (Meienhofer, J. (1979) The Peptides: Analysis, Synthesis, Biology. Vol. 1, Academic Press: N.Y.; ten Kortenaar P. B. W. et. al. Semisynthesis of horse heart cytochrome c analogues from two or three fragments. (1985) *Proc. Natl. Acad. Sci. USA* 82, 8279-8283)

[00347] In yet other embodiments, the invention provides XTEN-cross-linker and XTEN-payload conjugates in which the conjugation is performed by orthogonal protein ligation in which an initial chemoselective capture is followed by an intramolecular acyl rearrangement, as shown in FIG. 12. The chemoselective capture requires a nucleophile or electrophile proximally placed at an N-terminal amine and another compatible electrophile or nucleophile also proximally located at a C-terminal carboxylic ester. In the embodiment, it is specifically contemplated that the XTEN can serve as either Protein1 or Protein2 in FIG. 12. Thus, in alternative embodiments, the XTEN can be reacted with appropriate reagents to produce the thioester on the C-terminus or introduce a cysteine on the N-terminus to produce alternative XTEN-cross-linker compositions. In using the foregoing XTEN-cross-linker conjugates to make the XTEN-payload, the chemoselective capture of the nucleophile and electrophile pair forming an ester or a thioester brings the N-terminal amino group and C-terminal ester of the respective reactants into such a close proximity to permit a spontaneous intramolecular acyl transfer to form an amide bond. Most orthogonal ligation reactions do not require protection of side-chain groups and take place under mild conditions that are compatible with biological environments (Tam J. P., Xu J., Eom K. D. Methods and strategies of peptide ligation. (2001) *Biopolymers (Peptide Science)* 60, 194-205).

[00348] In another embodiment, the conjugates can be created by a method reaction known as Native Chemical Ligation (NCL) involving a C-terminal thioester as an electrophile and N-terminal cysteine as a nucleophile. The result of this reaction is a native amide bond at the ligation site of the XTEN-payload conjugate (Dawson P. E., Muir T. W., Clark-Lewis I., Kent S. B. Synthesis of proteins by native chemical ligation. (1994) *Science* 266, 776-779; Tam J. P.; Lu Y.-A.; Liu C. F.; Shao, J. Peptide synthesis using unprotected peptides through orthogonal coupling methods. (1995) *Proc. Natl. Acad. Sci. USA,* 92, 12485–12489; Johnson, E.C.B.; Kent, S.B.H. J. Insights into the mechanism and catalysis of the native chemical ligation reaction. (2006) *J. Am. Chem. Soc.* 128, 6640-6646; Kent S. B. (2009) Total chemical synthesis of proteins. (2009) *Chem. Soc. Rev.* 38:338–351). The first amino acid of the C-terminal component in NCL reaction (shown as Protein2 in FIG. 12) is cysteine. Such a protein can be XTEN with cysteine in the first position or any other protein prepared by conventional recombinant protein biosynthesis, including a peptide/protein payload. The N-terminal component (shown as Payload in FIG. 13) is prepared as C-terminal thioester by chemical synthesis. Examples of thioester synthesis methods are known and available in the art, such as those described, for example, in Li X., Kawakami T., Aimoto S., Direct preparation of peptide thioesters using an Fmoc solid-phase method. (1998) *Tetrahedron Lett.,* 39, 8660-8672); Ingenito R., Bianchi E., Fattori D., Pessi A. Solid-phase synthesis of peptide C-terminal thioesters by Fmoc/tBu chemistry. (1999) *J. Am. Chem. Soc.,* 121, 11369-11374); Sewing A., Hilvert D. Fmoc-compatible solid-phase peptide synthesis of long C-terminal peptide thioesters. (2001) *Angew. Chem. Int. Ed.* 40, 3395-3398; Brask J., Albericio F., Jensen K. J. ,Fmoc solid-phase synthesis of peptide thioesters by masking as trithioorthoesters. (2003) *Org. Lett.,* 2003, 5, 2951-2953; Ollivier N., Behr J.-B., El-Mahdi O., Blanpain A., Melnyk O. Fmoc-solid-phase synthesis of peptide thioesters using an intramolecular N, S-acyl shift. (2005) *Org. Lett.,* 7, 2647-2650. Usually, α-alkylthioesters are preferred because of ease of preparation and storage. However, because they are rather unreactive, the ligation reaction is catalyzed by *in situ* transthioesterification with thiol additives, with the most common thiol catalysts being 2-mercaptoethanesulfonate (MESNa) or 4-mercaptophenylacetic acid (MPAA). Chemical conjugation is typically complete in few hours and with high yields. While all 20 natural amino acids are suitable as the last residue of N-terminal component, the highest ligation rates were reported for glycine and histidine, making XTEN particularly suited for this reaction as the exemplary XTEN of Table 2 are nearly all glycine N-terminal polypeptides (Hackeng T.M. et al. Protein synthesis by native chemical ligation: expanded scope by using straightforward methodology. (1999) *Proc. Natl. Acad. Sci. USA* 96, 10068-10073). In other embodiments of this conjugation method, orthogonal ligation reactions include: (1) C-terminal thioacid with N-terminal BrAla or N-terminal aziridine (Tam J. P.; Lu Y.-A.; Liu C. F.; Shao, J. Peptide synthesis

using unprotected peptides through orthogonal coupling methods. (1995) *Proc. Natl. Acad. Sci. USA*, 92, 12485–12489); (2) C-terminal thioacid with N-terminal Cys-perthioester (Liu, C. F., Rao, C., Tam, J. P. (1996) *Tetrahedron Lett.,* 37, 933–936); (3) C-terminal thioester with N-terminal Homocysteine (Tam J.P., Yu Q. Methionine ligation strategy in the biomimetic synthesis of parathyroid hormones. (1998) *Biopolymers* 46(5), 319-327); and (4) C-terminal thioacid and N-terminal His (Zhang L., Tam J. P. (1997) *Tetrahedron. Lett.* 38, 3–6). In the method, the preparation of C-terminal thioesters by chemical synthesis constrains the size of N-terminal component in NCL reaction. However, use of expressed protein ligation (EPL) methodology overcomes size limitations of peptide α-thioester imposed by the need of chemical synthesis (Muir T. W.; Sondhi D.; Cole P. A. Expressed protein ligation: a general method for protein engineering. (1998) *Proc. Natl. Acad. Sci. USA* 95, 6705-6710; Muir T.W. Semisynthesis of proteins by expressed protein ligation. (2003) *Annu. Rev. Biochem.* 72, 249–289). The EPL method is based on protein splicing, the process in which a protein undergoes an intramolecular rearrangement resulting in the extrusion of an internal sequence (intein) and the joining of the lateral sequences (exteins). The latter process involves a formation of ester or thioester intermediates. In practicing the invention, the commercially available *Escherichia coli* protein expression vectors allows one to produce proteins of interest, such as XTEN, expressed in frame fused with an intein-chitin binding domain (CBD) sequence. In the method, the fused protein undergoes an N-S shift when the side chain of the first cysteine residue of the intein portion of the precursor protein nucleophilically attacks the peptide bond of the residue immediately upstream (that is, for example, the final residue of XTEN) to form a linear thioester intermediate, as shown in FIG. 13. The chemical ligation step is initiated by incubating the protein with thiophenol (or other thiol catalysts such as MESNa and MPAA) and a cysteine-containing synthetic peptide or protein. This results in the *in situ* generation of a highly reactive phenyl α-thioester derivative of, for example, the XTEN protein that then rapidly ligates with the synthetic peptide/protein payload to result in the desired XTEN-payload conjugate. In another embodiment, an XTEN-thioester intermediate can be cleaved by 50 mM 2-mercaptoethanesulfonic acid (MESNa) in 20 mM Na-HEPES, pH 8.5, 50–1000 mM NaCl, and 1 mM EDTA (optional) and the resulting MESNa-tagged protein can be purified and stored -80°C in 5 mM Bis Tris, pH 6.5, 250 mM NaCl until use as an XTEN-cross-linker conjugate for NCL reaction as the N-terminal component in the above described conjugation. The C-terminal component can be a payload with either a natural or synthetic peptide/protein with an N-terminal cysteine.

[00349] In yet other embodiments, the invention provides XTEN-cross-linker and XTEN-payload conjugates in which the conjugation between the XTEN and payload is performed by traceless Staudinger ligation, like Native Chemical Ligation (NCL), resulting in a native amide

bond at the ligation site. In an advantage to the method, a cysteine is not required at the ligation juncture (Saxon, E.; Armstrong, C.R.; Bertozzi, C.R. A "traceless" Staudinger ligation for the chemoselective synthesis of amide bonds. (2000) *Org. Lett.* 2, 21412143; Nilsson, B.L.; Kiessling, L.L.; Raines, R.T. Staudinger ligation: a peptide from a thioester and azide. (2000) *Org. Lett.* 2, 1939-1941). Instead, an N-terminal Protein 1 is prepared as a C-terminal thioester using diphenylphosphinemethanethiol (see FIG. 14), while a C-terminal Protein 2 is prepared as an N-terminal azide that can be generated via a diazo-transfer reaction (Cavender C. J.; Shiner V. J., Jr. (1972) *J. Org. Chem.* 22, 3567–3569; Lundquist J. T., IV, Pelletier J. C. Improved solid-phase peptide synthesis method utilizing alpha-azide-protected amino acids. (2001) *Org. Lett.* 3, 781–783). A phosphine residue reacts with the azide of Protein2 to form an iminophosphorane after elimination of nitrogen (Staudinger reaction). The resulting iminophosphorane with its highly nucleophilic nitrogen atom can also be regarded as an aza-ylide. The nucleophilic nitrogen atom of the aza-ylide then attacks the carbonyl group of Protein1, cleaving the thioester. It is specifically intended that either XTEN or the payload can be either Protein1 or Protein2 in this reaction. Hydrolysis of the rearranged XTEN-payload product finally produces a native amide and liberates phosphine component as phosphine(V) oxide. Bis(*p*-dimethylaminoethylphenyl)phosphinomethanethiol, a water-soluble variant of diphenylphosphinemethanethiol, mediates the rapid ligation of equimolar substrates in water (Tam, A.; Soellner, M.B.; Raines, R.T. Water-soluble phosphinothiols for traceless Staudinger ligation and integration with Expressed Protein Ligation. (2007) *J. Am. Chem. Soc.,* 129, 1142111-430).

[00350] In another embodiment, the invention provides XTEN-payload conjugates prepared by enzymatic ligation. Transglutaminases are enzymes that catalyze the formation of an isopeptide bond between the γ-carboxamide group of glutamine of a payload peptide or protein and the ε-amino group of a lysine in a lysine-engineered XTEN, thereby creating inter- or intramolecular cross-links between the XTEN and payload (see FIG. 15), resulting in the composition (Lorand L, Conrad S.M. Transglutaminases.(1984) Mol. Cell Biochem. 58(1-2), 9-35). Non-limiting examples of enzymes that have been successfully used for ligations are factor XIIIa (Schense J.C., Hubbell J.A. Cross-linking exogenous bifunctional peptides into fibrin gels with factor XIIIa. (1999) *Bioconjug. Chem.* 10(1):75-81) and tissue transglutaminase (Collier J.H., Messersmith P.B. Enzymatic modification of self-assembled peptide structures with tissue transglutaminase. (2003) *Bioconjug. Chem.* 14(4), 748-755; Davis N. E., Karfeld-Sulzer L. S., Ding S., Barron A. E. Synthesis and characterization of a new class of cationic protein polymers for multivalent display and biomaterial applications. (2009) *Biomacromolecules* 10 (5), 1125-1134). The glutamine substrate sequence GQQQL is known to have high specificity toward tissue transglutaminase (Hu B.H., Messersmith P.B. Rational design of transglutaminase

substrate peptides for rapid enzymatic formation of hydrogels.(2003) *J. Am. Chem. Soc.* 125(47), 14298-14299). Tissue transglutaminase sequence specificity was less stringent for an acyl acceptor (lysine) than for acyl donor (glutamine) (Greenberg C. S., Birckbichler P. J., Rice R. H. Transglutaminases: multifunctional cross-linking enzymes that stabilize tissues. (1991) *FASEB J.* 1991, 5, 3071–3077).

[00351] In an alternative embodiment of an enzymatically-created XTEN-payload composition, the sortase A transpeptidase enzyme from *Staphylococcus aureus* is used to catalyze the cleavage of a short 5-amino acid recognition sequence LPXTG between the threonine and glycine residues of Protein1, and subsequently transfers the acyl-fragment to an N-terminal oligoglycine nucleophile of Protein1 (see FIG. 16). By functionalizing the Protein2 to contain the oligoglycine, it is possible to enzymatically conjugate the two proteins in a site-specific fashion to result in the desired XTEN-payload composition. The (poly)peptide bearing the sortase recognition site (LPXTG) can be readily made using standard molecular biology cloning protocols. It is convenient to introduce glutamic acid in the X position of the recognition site, as this residue is commonly found in natural substrates of sortase A (Boekhorst J., de Been M.W., Kleerebezem M., Siezen R. J. Genome-wide detection and analysis of cell wall-bound proteins with LPxTG-like sorting motifs. (2005) *J. Bacteriol.* 187, 4928-4934). A high level of transacylation can be achieved by placing the sortase cleavage site both at the C-terminus of the substrate (Popp M.W., Antos J.M., Grotenbreg G.M., Spooner E., Ploegh H.L. Sortagging: A versatile method for protein labeling. (2007) *Nat. Chem. Biol.* 311,707-708) and in flexible loops (Popp M.W., Artavanis-Tsakonas K., Ploegh H.L. Substrate filtering by the active-site crossover loop in UCHL3 revealed by sortagging and gain-of-function mutations. (2009) *J. Biol. Chem.* 284(6), 3593-3602). For proteins labeled at the C-terminus, it is important that the glycine in the minimal LPETG tag is not placed at the C-terminus; it must be in a peptide linkage with at least one further C-terminal amino acid. In addition, better linkage is achieved by adding an extra glycine to the C-terminus of the cleavage site to yield LPETGG (Pritz S., Wolf Y., Kraetke O., Klose J., Bienert M., Beyermann M. Synthesis of biologically active peptide nucleic acid-peptide conjugates by sortase-mediated ligation. (2007) *J. Org. Chem.* 72, 3909-3912; Tanaka T., Yamamoto T., Tsukiji S., Nagamune T. Site-specific protein modification on living cells catalyzed by sortase. (2008) *Chembiochem* 95, 802-807). Nucleophiles compatible with sortase-mediated transpeptidation have the single structural requirement of a stretch of glycine residues with a free amino terminus. Successful transpeptidation can be achieved with nucleophiles containing anywhere from one to five glycines; however, in a preferred embodiment, a maximum reaction rate is obtained when two or three glycines are present.

[00352] While the various embodiments of conjugation chemistry have been described in terms of protein-protein conjugations, it is specifically intended that in practicing the invention, the

payload moiety of the XTEN-payload conjugates can be a small molecule drug in those conjugation methods applicable to functional groups like amines, sulfhydryls, carboxyl that are present in the target small molecule drugs. It will be understood by one of ordinary skill in the art that one can apply even more broad chemical techniques compared to protein and peptides whose functionalities are usually limited to amino, sulfhydryl and carboxyl groups. Drug payloads can be conjugated to the XTEN through functional groups including, but not limited to, primary amino groups, aminoxy, hydrazide, hydroxyl, thiol, thiolate, succinate (SUC), succinimidyl succinate (SS), succinimidyl propionate (SPA), succinimidyl butanoate (SBA), succinimidyl carboxymethylate (SCM), benzotriazole carbonate (BTC), N-hydroxysuccinimide (NHS), p-nitrophenyl carbonate (NPC). Other suitable reactive functional groups of drug molecule payloads include acetal, aldehydes (e.g., acetaldehyde, propionaldehyde, and butyraldehyde), aldehyde hydrate, alkenyl, acrylate, methacrylate, acrylamide, active sulfone, acid halide, isocyanate, isothiocyanate, maleimide, vinylsulfone, dithiopyridine, vinylpyridine, iodoacetamide, epoxide, glyoxal, dione, mesylate, tosylate, and tresylate.

[00353] In another embodiment, the drug payloads can also be conjugated to XTEN-cross-linker conjugates using a heterocycle ring system in which one or more ring atoms is a heteroatom, e.g. a nitrogen, an oxygen, a phosphorus or a sulfur atom. The heterocycle group comprises at least 1 to as many as 20 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S. In the embodiment, the heterocycle may be a monocycle having 3 to 7 ring members (2 to 6 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S) or a bicycle having 7 to 10 ring members (4 to 9 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S), for example: a bicyclo [4,5], [5,5], [5,6], or [6,6] system. Heterocycles are described in Paquette, Leo A. "Principles of Modern Heterocyclic Chemistry", W. A. Benjamin, New York, (1968); "The Chemistry of Heterocyclic Compounds, A series of Monographs" (John Wiley & Sons, New York, 1950 to present), in particular Volumes 13, 14, 16, 19, and 28. Non-limiting examples of heterocycles that may be found in drugs suitable for conjugation include pyridyl, dihydroypyridyl, tetrahydropyridyl (piperidyl), thiazolyl, tetrahydrothiophenyl, sulfur oxidized tetrahydrothiophenyl, pyrimidinyl, furanyl, thienyl, pyrrolyl, pyrazolyl, imidazolyl, tetrazolyl, benzofuranyl, thianaphthalenyl, indolyl, indolenyl, quinolinyl, isoquinolinyl, benzimidazolyl, piperidinyl, 4-piperidonyl, pyrrolidinyl, 2-pyrrolidonyl, pyrrolinyl, tetrahydrofuranyl, bis-tetrahydrofuranyl, tetrahydropyranyl, bis-tetrahydropyranyl, tetrahydroquinolinyl, tetrahydroisoquinolinyl, decahydroquinolinyl, octahydroisoquinolinyl, azocinyl, triazinyl, 6H-1,2,5-thiadiazinyl, 2H,6H-1,5,2-dithiazinyl, thienyl, thianthrenyl, pyranyl, isobenzofuranyl, chromenyl, xanthenyl, phenoxathinyl, 2H-pyrrolyl, isothiazolyl, isoxazolyl, pyrazinyl, pyridazinyl, indolizinyl, isoindolyl, 3H-indolyl, 1H-indazolyl, purinyl, 4H-quinolizinyl, phthalazinyl, naphthyridinyl, quinoxalinyl, quinazolinyl, cinnolinyl, pteridinyl, 4Ah-carbazolyl,

carbazolyl, β-carbolinyl, phenanthridinyl, acridinyl, pyrimidinyl, phenanthrolinyl, phenazinyl, phenothiazinyl, furazanyl, phenoxazinyl, isochromanyl, chromanyl, imidazolidinyl, imidazolinyl, pyrazolidinyl, pyrazolinyl, piperazinyl, indolinyl, isoindolinyl, quinuclidinyl, morpholinyl, oxazolidinyl, benzotriazolyl, benzisoxazolyl, oxindolyl, benzoxazolinyl, and isatinoyl.

[00354] In some embodiments of the XTEN-payload conjugates with drugs as the payload, the drug molecules are attached to lysine- or cysteine engineered XTEN (such as the sequences of Table 3) by cross-linkers having two reactive sites for binding to the drug and the XTEN. Preferred cross-inker groups are those that are relatively stable to hydrolysis in the circulation, are biodegradable and are nontoxic when cleaved from the conjugate. In addition, the use of cross-linkers can provide the potential for conjugates with an even greater flexibility between the drug and the XTEN, or provide sufficient space between the drug and the XTEN such that the XTEN does not interfere with the binding between the pharmacophore and its binding site. In one embodiment, a cross-linker has a reactive site that has an electrophilic group that is reactive to a nucleophilic group present on an XTEN. Preferred nucleophiles include thiol, thiolate, and primary amine. The heteroatom of the nucleophilic group of a lysine- or cysteine-engineered XTEN is reactive to an electrophilic group on a cross-linker and forms a covalent bond to the cross-linker unit, resulting in an XTEN-cross-linker conjugate. Useful electrophilic groups for cross-linkers include, but are not limited to, maleimide and haloacetamide groups, and provide a convenient site for attachment to the XTEN. In another embodiment, a cross-linker has a reactive site that has a nucleophilic group that is reactive to an electrophilic group present on a drug such that a conjugation can occur between the XTEN-cross-linker and the payload drug, resulting in an XTEN-drug conjugate. Useful electrophilic groups on a drug include, but are not limited to, hydroxyl, thiol, aldehyde, alkene, alkane, azide and ketone carbonyl groups. The heteroatom of a nucleophilic group of a cross-linker can react with an electrophilic group on a drug and form a covalent bond. Useful nucleophilic groups on a cross-linker include, but are not limited to, hydrazide, oxime, amino, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide. The electrophilic group on a drug provides a convenient site for attachment to a cross-inker.

[00355] In a particular embodiment, the conjugation of drugs to the lysine epsilon amino group of a subject lysine-engineered XTEN makes use of a reactive drug-N-hydroxylsuccinimide reactant, or esters such as drug-succinimidyl propionate, or drug-succinimidyl butanoate or other drug-succinimide conjugates. Alternatively, lysine residues of the subject lysine-engineered XTEN may be used to introduce free sulfhydryl groups through reaction with 2-iminothiolane. Alternatively, targeting substance lysines of subject lysine-engineered XTEN may may be linked to a heterobifunctional reagent having a free hydrazide or aldehyde group available for conjugation with an active drug agent. Reactive esters can conjugate at physiological pH, but

less reactive derivatives typically require higher pH values. Low temperatures may also be employed if a labile protein payload is being used. Under low temperature conditions, a longer reaction time may be used for the conjugation reaction.

[00356] In another particular embodiment, the invention provides XTEN-payload conjugates with an amino group conjugation with lysine residues of a subject lysine-engineered XTEN wherein the conjugation is facilitated by the difference between the pKa values of the α-amino group of the N-terminal amino acid (approximately 7.6 to 8.0) and pKa of the ε-amino group of lysine (approximately 10). Conjugation of the terminal amino group often employs reactive drug-aldehydes (such as drug-propionaldehyde or drug-butylaldehyde), which are more selective for amines and thus are less likely to react with, for example, the imidazole group of histidine. In addition, amino residues are reacted with succinic or other carboxylic acid anhydrides, or with N,N′-Disuccinimidyl carbonate (DSC), N,N′-carbonyl diimidazole (CDI), or p-nitrophenyl chloroformate to yield the activated succinimidyl carbonate, imidazole carbamate or p-nitrophenyl carbonate, respectively. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Conjugation of a drug-aldehyde to the terminal amino group of a subject XTEN typically takes place in a suitable buffer performed at a pH which allows one to take advantage of the pKa differences between the ε-amino groups of the lysine residues and that of the α-amino group of the N-terminal residue of the protein. In the method of the embodiment, the reaction for coupling uses a pH in the range of from about pH 7 up to about 8. Useful methods for conjugation of the lysine epsilon amino group have been described in U.S. Pat. No. 4,904,584 and U.S. Pat. No. 6,048,720.

[00357] The person with ordinary skill in the art will be aware that the activation method and/or conjugation chemistry to be used in the creation of the XTEN-payload conjugates depends on the reactive groups of the XTEN polypeptide as well as the functional groups of the drug moiety (e.g., being amino, hydroxyl, carboxyl, aldehyde, sulfhydryl, alkene, alkane, azide, etc), the functional group of the drug-cross-linker reactant, or the functional group of the XTEN-cross-linker reactant. The drug conjugation may be directed towards conjugation to all available attachment groups on the engineered XTEN polypeptide such as the specific engineered attachment groups on the incorporated cysteine residues or lysine residues. In order to control the reactants such that the conjugation is directed to the appropriate reactive site, the invention contemplates the use of protective groups during the conjugation reaction. A "protecting group" is a moiety that prevents or blocks reaction of a particular chemically reactive functional group in a molecule under certain reaction conditions. The protecting group will vary depending upon the type of chemically reactive group being protected as well as the reaction conditions to be employed, as well as the presence of additional reactive groups in the molecule. Non-limiting examples of functional groups which may be protected include carboxylic acid groups, hydroxyl

groups, amino groups, thiol groups, and carbonyl groups. Representative protecting groups for carboxylic acids and hydroxyls include esters (such as a p-methoxybenzyl ester), amides and hydrazides; for amino groups, carbamates (such as tert-butoxycarbonyl) and amides; for hydroxyl groups, ethers and esters; for thiol groups, thioethers and thioesters; for carbonyl groups, acetals and ketals; and the like. Such protecting groups are well-known to those skilled in the art and are described, for example, in T. W. Greene and G. M. Wuts, *Protecting Groups in Organic Synthesis* , Third Edition, Wiley, New York, 1999, and references cited therein. The conjugation may be achieved in one step or in a stepwise manner (e.g., as described in WO 99/55377), such as through addition of a reaction intermediate cross-linker, using the cross-linkers disclosed herein or those known in the art to be useful for conjugation to cysteine or lysine residues of polypeptides to be linked to reactive functional groups on drug molecules.

[00358] In some embodiments of the invention, the method for conjugating a cross-linker to a cysteine-engineered XTEN may provide that the XTEN is pre-treated with a reducing agent, such as dithiothreitol (DTT) to reduce any cysteine disulfide residues to form highly nucleophilic cysteine thiol groups (—CH_2 SH). The reducing agent is subsequently removed by any conventional method, such as by desalting. The reduced XTEN thus reacts with drug-linker compounds, or cross-linker reagents, with electrophilic functional groups such as maleimide or α-halo carbonyl, according to, for example, the conjugation method of Klussman et al. (2004) *Bioconjugate Chemistry* 15(4), 765-773. Conjugation of a cross-linker or a drug to a cysteine residue typically takes place in a suitable buffer at pH 6-9 at temperatures varying from 4°C to 25°C for periods up to about 16 hours. Alternatively, the cysteine residues can be derivatized. Suitable derivatizing agents and methods are well known in the art. For example, cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as iodoacetic acid or iodoacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(4-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

[00359] In some instances, the conjugation is performed under conditions aiming at reacting as many of the available XTEN attachment groups as possible with drug or drug-linker molecules. This is achieved by means of a suitable molar excess of the drug in relation to the polypeptide. Typical molar ratios of activated drug or drug-linker molecules to polypeptide are up to about 1000-1, such as up to about 200-1 or up to about 100-1. In some cases, the ratio may be somewhat lower, however, such as up to about 50-1, 10-1 or 5-1. Equimolar ratios also may be used.

[00360] In the embodiments, the XTEN-payload conjugates of the disclosure retain at least a portion of the pharmacologic activity compared to the corresponding payload not linked to XTEN. In one embodiment, the XTEN-payload retains at least about 1%, or at least about 5%, or at least about 10%, or at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90%, or at least about 95% of the pharmacologic activity of the payload not linked to XTEN.

[00361] In one embodiment, XTEN-payload conjugates can be designed to release the payload in the body by unspecific or enzymatic hydrolysis of the linker, including disulfide bond reduction, pH-dependent release, or by exogenous or endogenous proteases, including the proteases of Table 9. Macromolecules can be taken up by the cell either through receptor-mediated endocytosis, adsorptive endocytosis or fluid phase endocytosis (Jain R.K. Transport of molecules across tumor vasculature. (1987) *Cancer Metastasis Rev.* 6(4), 559-593; Jain R.K. Transport of molecules, particles, and cells in solid tumors. (1999) *Ann. Rev. Biomed. Eng.* 1, 241-263; Mukherjee S., Ghosh R.N., Maxfield F.R. Endocytosis. (1997) *Physiol. Rev.* 77(3), 759-803). Upon cellular uptake of XTEN-payload, the payload can be released by low pH values in endosomes (pH 5.0 – 6.5) and lysosomes (pH 4.5 – 5.0), as well as by lysosomal enzymes (e.g., esterases and proteases). Example of acid-sensitive cross-linker is 6-maleimidodocaproyl hydrazone which can be coupled to thiol-bearing carriers. The hydrazone linker is rapidly cleaved at pH values < 5 allowing a release of the payload in the acidic pH of endosomes and lysosomes following internalization of the conjugate (Trail P.A. et al. Effect of linker variation on the stability, potency, and efficacy of carcinoma-reactive BR64-doxorubicin immunoconjugates. (1997) *Cancer Res.* 57(1), 100-105; Kratz F. et al. Acute and repeat-dose toxicity studies of the (6-maleimidocaproyl)hydrazone derivative of doxorubicin (DOXO-EMCH), an albumin-binding prodrug of the anticancer agent doxorubicin. (2007) *Hum. Exp. Toxicol.* 26(1), 19-35). Clinically approved mAb–drug conjugate, gemtuzumab ozogamicin (Mylotarg™) is a drug–antibody conjugate containing a humanized mAb P67.6 against CD33, linked chemically to the cytotoxic antibiotic agent calicheamicin. The linker between the antibody and the drug incorporates two labile bonds: a hydrazone and a sterically hindered disulfide. It has been shown that the acid-sensitive hydrazone bond is the actual cleavage site (Jaracz S., Chen J., Kuznetsova L.V., Ojima I. Recent advances in tumor-targeting anticancer drug conjugates. (2005) *Bioorg. Med. Chem.* 13(17), 5043-5054).

[00362] For those XTEN-payload conjugates in which the payload is linked by a disulfide bond, the payload can be released from XTEN by reduction of disulfide bond within the labile linker. For example, huN901–DM1 is a tumor-activated immunotherapeutic prodrug developed by ImmunoGen, Inc. for the treatment of small cell lung cancer. The prodrug consists of humanized

anti-CD56 mAb (huN901) conjugated with microtubule inhibitor maytansinoid DM1. An average of 3.5 – 3.9 molecules of DM1 are bound to each antibody via hindered disulfide bonds. Although the disulfide link is stable in blood, it is cleaved rapidly on entering the cell targeted by huM901, thus releasing active DM1 (Smith S.V. Technology evaluation: huN901-DM1, ImmunoGen. (2005) *Curr. Opin. Mol. Ther.* 7(4), 394-401). DM1 has been also coupled to Millennium Pharmaceuticals MLN-591, an anti-prostate-specific membrane antigen mAb. DM1 is linked to the antibody via a hindered disulfide bond that provides serum stability at the same time as allowing intracellular drug release on internalization (Henry M.D. et al. A prostate-specific membrane antigen-targeted monoclonal antibody-chemotherapeutic conjugate designed for the treatment of prostate cancer. (2004) *Cancer Res.* 64(21), 7995-8001).

[00363] Release of the payload from the carrier XTEN can be achieved by creating compositions using short cleavable peptides as linkers between the payload and XTEN. Example of the conjugate assessed clinically is doxorubicin–HPMA (N-(2-hydroxypropyl)methacrylamide) conjugate in which doxorubicin is linked through its amino sugar to the HPMA copolymer via a tetrapeptide spacer GlyPheLeuGly that is cleaved by lysosomal proteases, such as cathepsin B (Vasey P.A. et al. Phase I clinical and pharmacokinetic study of PK1 [N-(2-hydroxypropyl)methacrylamide copolymer doxorubicin]: first member of a new class of chemotherapeutic agents-drug-polymer conjugates. (1999) *Clin. Cancer Res.* 5(1), 83-94). Other examples of carrier-drug conjugates with peptide linkers that reached clinical stage of development are macromolecular platinum complexes. Two HPMA-based drug candidates consisted of a HPMA copolymer backbone to which the complexing aminomalonate platinum complexes were bound through cathepsin B-cleavable peptide spacer GlyPheLeuGly or tripeptide spacer GlyGlyGly (Rademaker-Lakhai J.M. et al. A Phase I and pharmacological study of the platinum polymer AP5280 given as an intravenous infusion once every 3 weeks in patients with solid tumors. (2004) *Clin. Cancer Res.* 10(10), 3386-3395; Sood P. et al. Synthesis and characterization of AP5346, a novel polymer-linked diaminocyclohexyl platinum chemotherapeutic agent. (2006) Bioconjugate Chem. 17(5), 1270-1279).

[00364] A highly selective method was developed to target prostate cancer via prostate-specific antigen (PSA) protease which is almost exclusively expressed in prostate tissue and prostate carcinomas. A novel albumin-binding prodrug of paclitaxel, EMC-ArgSerSerTyrTyrSerLeu-PABC-paclitaxel (EMC: ε-maleimidocaproyl; PABC: p-aminobenzyloxycarbonyl) was synthesized. This prodrug was water soluble and was bound to endogenous and exogenous albumin. Albumin-bound form of the prodrug was cleaved by PSA releasing the paclitaxel-dipeptide Ser-Leu-PABC-paclitaxel. Due to the incorporation of a PABC self-eliminating linker, this dipeptide was rapidly degraded to liberate paclitaxel as a final cleavage product (Elsadek B.

et al. Development of a novel prodrug of paclitaxel that is cleaved by prostate-specific antigen: an in vitro and in vivo evaluation study. (2010) *Eur. J. Cancer* 46(18), 3434-3444).

[00365] Self-immolative spacers have gained significant interest due to their utility in prodrug delivery systems. Several reports described linear self-eliminating systems or dendrimeric structures which can release all of their units through a domino-like chain fragmentation, initiated by a single cleavage event (Haba K. et al. Single-triggered trimeric prodrugs. (2005) *Angew. Chem., Int. Ed.* 44, 716-720; Shabat D. Self-immolative dendrimers as novel drug delivery platforms. (2006*) J. Polym. Sci., Part A: Polym. Chem.* 44, 1569-1578.Warnecke A., Kratz F. 2,4-Bis(hydroxymethyl)aniline as a building block for oligomers with self-eliminating and multiple release properties. (2008) *J. Org. Chem.* 73, 1546-1552; Sagi A. et al. Self-immolative polymers. (2008) *J. Am. Chem. Soc.* 130, 5434–5435). In one study, a self-immolative dendritic prodrug with four molecules of the anticancer agent camptothecin and two molecules of PEG5000 was designed and synthesized. The prodrug was effectively activated by penicillin-G-amidase under physiological conditions and free camptothecin was released to the reaction media to cause cell-growth inhibition (Gopin A. et al. Enzymatic activation of second-generation dendritic prodrugs: conjugation of self-immolative dendrimers with poly(ethylene glycol) via click chemistr y. (2006) *Bioconjugate Chem.* 17, 1432-1440). Incorporation of a specific enzymatic substrate, cleaved by a protease that is overexpressed in tumor cells, could generate highly efficient cancer-cell-specific dendritic prodrug activation systems. Non-limiting examples of spacer sequences that are cleavable by proteases are listed in Table 9.

[00366] In some embodiments, the invention provides XTEN-payload configurations, including dimeric, trimeric, tetrameric and higher order conjugates in which the payload is attched to the XTEN using a labile linker as described herein, above. In one embodiment of the foregoing, the composition further includes a targeting component to deliver the composition to a ligand or receptor on a targeted cell. In another embodiment, the invention provides conjugates in which one, two, three, or four XTEN-payload compositions are conjugated with labile linkers to antibodies or antibody fragments, providing soluble compositions for use in targeted therapy of clinical indications such as, but not limited to, various treatment of tumors and other cancers wherein the antibody provides the targeting component and then, when internalized within the target cell, the labile linker permits the XTEN-payload to disassociate from the composition and effect the intended activity (e.g, cytotoxicity in a tumor cell). Hence, the inventive compositions are a type of immunoconjugate.

[00367] The unstructured characteristics and uniform composition and charge of XTEN result in properties that can be exploited for purification of XTEN-payload conjugates following a conjugation reaction. Of particular utility is the capture of XTEN conjugates by ion exchange, which allows the removal of un-reacted payload and payload derivatives. Of particular utility is

the capture of conjugates by hydrophobic interaction chromatography (HIC). Due to their hydrophilic nature, most XTEN polypeptides show low binding to HIC resins, which facilitates the capture of XTEN-payload conjugates due to hydrophobic interactions between the payload and the column material, and their separation from un-conjugated XTEN that failed to conjugate to the payload during the conjugation process. The high purity of XTEN and XTEN-payload conjugates offers a significant benefit compared to most chemical or natural polymers, particularly pegylated payloads. Most chemical and natural poylmers are produced by random- or semi-random polymerization, which results in the generation of many homologs. Such polymers can be fractionated by various methods to increase fraction of the target entity in the product. However, even after enrichment most preparations of natural polymers and their payload conjugates contain less than 10% target entity. Examples of PEG conjugates with G-CSF have been described in [Bagal, D., et al. (2008) Anal Chem, 80: 2408-18]. This publication shows that even a PEG conjugate that is approved for therapeutic use contains more than 100 homologs that occur with a concentration of at least 10% of the target entity.

[00368] The complexity of random polymers, such as PEG, is a significant impediment for the monitoring and quality control during conjugation and purification. In contrast, XTEN purified by the methods described herein have high levels of purity and uniformity. In addition, the conjugates created as described herein routinely contain greater than about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the intended target and in the intended configuration, resulting in easy to interpret mass spectra and chromatograms.

2. Monomeric XTEN-cross-linker, and XTEN-payload Configurations

[00369] In another aspect, the invention provides XTEN-cross-linker conjugates and XTEN-payload conjugates with a single XTEN, wherein the conjugate is designed in different configurations. Exemplary configurations of such conjugates follow.

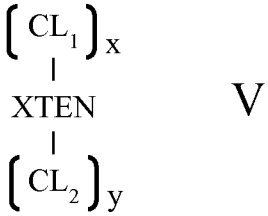
[00370] In one embodiment, the invention provides a conjugate having the configuration of formula IV:

$$\begin{array}{l}(CL_1)_x \\ | \\ XTEN\end{array} \qquad \text{IV}$$

wherein independently for each occurrence CL1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula IV, CL1 is

a cross-linker selected from Table 13. In another embodiment of the conjugate of formula IV, x has the foregoing ranges and a cross-linker of Table 13 is linked to each cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula IV, x has the foregoing ranges and a cross-linker is linked to a each lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula IV, x is 1 and a cross-linker of Table 13 is linked to the N-terminal amino group of the XTEN. It will be understood by one of skill in the art that the compositions of the foregoing embodiments comprising the cross-linker conjugated to an XTEN using the specified components represents the reaction product of the individual reactants and thus differs from the precise composition of the reactants. In another embodiment, the invention provides a preparation of the conjugate of formula IV in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[00371] In another embodiment, the invention provides a conjugate having the configuration of formula V:



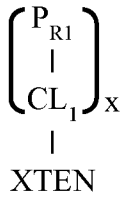
V

wherein independently for each occurrence CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y is ≥ 2; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula V, $CL_1$and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In one embodiment of the conjugate of formula V, x has the foregoing ranges and each CL_1 is linked to an epsilon amino group of each lysine of the XTEN and y has the foregoing ranges and each CL_2 is linked to a sulfur group of each cysteine of the XTEN. In another embodiment of the conjugate of formula V, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN and each CL_2 is linked to a cysteine sulfur group of the XTEN. It will be understood by one of skill in the art that the compositions of the foregoing embodiments comprising the cross-linker conjugated to an XTEN using the specified components represents

the reaction product of the reactants and thus differs from the precise composition of the reactants. In another embodiment, the invention provides a preparation of the conjugate of formula V in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[00372] In another aspect, the invention provides XTEN-payload conjugates having defined configurations. The invention takes advantage of the reactive XTEN-cross-linker conjugation partner compositions decribed herein to which reactive molecules of payloads can be joined by chemical reaction.

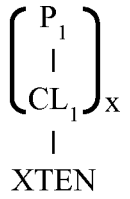
[00373] In one embodiment, the invention provides a conjugate having the configuration of formula VI:



VI

wherein independently for each occurrence P_{R1} is a single atom residue of a payload, wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 3, or is 2, or is 1; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula VI, the single atom residue of a payload is from a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21. In one embodiment of the conjugate of formula VI, $CL_1$is a cross-linker selected from Table 13. In one embodiment of the conjugate of formula VI, each cross-linker is linked to a cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula VI, each cross-linker is linked to an lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula VI, x is 1 and the cross-linker is linked to the N-terminal amino group of the XTEN. In another embodiment of the conjugate of formula VI, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment, the invention provides a preparation of the conjugate of formula VI in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[00374] In another embodiment, the invention provides a conjugate having the configuration of formula VII:



VII

wherein independently for each occurrence: P_1 is a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula VII, $CL_1$is a cross-linker selected from Table 13. In one embodiment of the conjugate of formula VII, each cross-linker is linked to a cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula VII, each cross-linker is linked to an lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula VII, x is 1 and the cross-linker is linked to the N-terminal amino group of the XTEN. In one embodiment, the conjugate of formula VII is selected from the group consisting of the conjugates set forth in Table 21. In another embodiment of the conjugate of formula VII, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. It will be understood by one of skill in the art that the compositions of the foregoing embodiments comprising the payload conjugated to an XTEN-cross-linker using the specified components represents the reaction product of the reactants and thus differs from the precise composition of the reactants. In another embodiment, the invention provides a preparation of the conjugate of formula VII in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[00375] In another embodiment, the invention provides a conjugate having the configuration of formula VIII:



VIII

wherein independently for each occurrence P_{R1} is a single atom residue of a payload, wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; P_{R2} is a single atom residue of a payload, wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y is $\geq$ 2; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula VIII, the single atom residue of a payload is from a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21. In one embodiment of the conjugate of formula VIII, CL_1 and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In one embodiment of the conjugate of formula VIII, each CL_1 is linked to an lysine epsilon amino group of the XTEN and each CL_2 is linked to a cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula VIII, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN and CL_2 is linked to either a cysteine sulfur or an lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula VIII, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula VIII, C_2 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment, the invention provides a preparation of the conjugate of formula VIII in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[00376] In another embodiment, the invention provides a conjugate having the configuration of formula IX:



IX

wherein independently for each occurrence P_1 is a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21; P_2 is a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21 and that is different from P_1; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y is $\geq$ 2; and XTEN is a sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula IX, the single atom residue of a payload is from a payload selected from the group consisting of the payloads set forth in Tables 11, 12, 18, 19, and 21. In one embodiment of the conjugate of formula IX, $CL_1$and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In one embodiment of the conjugate of formula IX, each CL_1 is linked to an lysine epsilon amino group of the XTEN and each CL_2 is linked to a cysteine sulfur of the XTEN. In another embodiment of the conjugate of formula IX, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN and CL_2 is linked to either a cysteine sulfur or an lysine epsilon amino group of the XTEN. In another embodiment of the conjugate of formula IX, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula IX, C_2 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In one embodiment, the conjugate of formula IX is selected from the group consisting of the conjugates set forth in Table 21. In another embodiment, the invention provides a preparation of the conjugate of formula IX in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

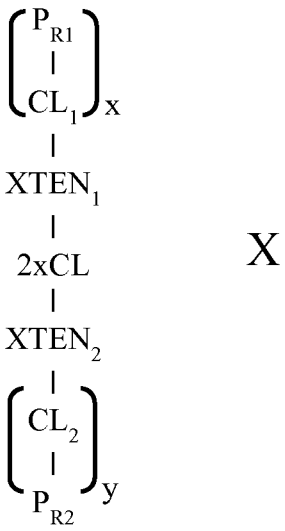
3. Dimeric, Trimeric, Tetrameric, and Multimeric Configurations of XTEN-cross-linkers and XTEN-payload conjugates

[00377] In one aspect, the invention provides conjugates wherein different numbers of XTEN or XTEN-payload conjugation partners are joined by linkers in a numerically-defined configuration; e.g., dimeric, trimeric, tetrameric, or multimeric. As used herein, "precursor" is intended to include components used as reactants in a conjugation reaction leading to an intermediate or final composition, and includes but is not limited to XTEN segments of any length (including the XTEN of Tables 2 and 3 or as depicted in the various formulae, above), XTEN-crosslinkers, XTEN-payload-crosslinker segments, payloads with reactive groups, linkers, and other such components described herein.

[00378] In some embodiments, the invention provides conjugates in which two XTEN or XTEN-payload precursor segments are linked by a divalent cross-linker, resulting in a divalent configuration, such as shown in FIG. 19C and FIG. 27B. In one embodiment of the divalent XTEN-payload conjugate, each XTEN-payload can be a monomeric fusion protein comprising a biologically active peptide or polypeptide, wherein each fusion protein precursor seqment is linked to the divalent linker by the alpha-amino group of the N-terminus, resulting in the divalent conjugate. In another embodiment of the divalent XTEN-payload conjugate, each XTEN-payload precursor segment is a monomeric fusion protein comprising a biologically active peptide or polypeptide, wherein each fusion protein is linked to the divalent linker at the C-terminus, resulting in the divalent conjugate. In another embodiment of the divalent XTEN-payload conjugate, each XTEN comprises one or more payloads (that can be a peptide, polypeptide or a drug) conjugated to the XTEN, wherein each XTEN precursor is linked to the other XTEN precursor comprising one or more second, different payload molecules by a divalent linker at the N-terminus, resulting in the divalent conjugate. In another embodiment of the divalent XTEN-payload conjugate, each XTEN comprises one or more payloads (that can be a peptide, polypeptide or a drug) conjugated to the XTEN, wherein each XTEN precursor is linked to the other XTEN precursor comprising one or more second, different payload molecules by a divalent linker by the carboxyl group or a modified group at the C-terminus (including, but not limited to XTEN modified by insertion of a cysteine at the C-terminus), resulting in the divalent conjugate. In the foregoing embodiments of the paragraph, as would be appreciated by one of ordinary skill in the art in light of the present disclosure, there are different approaches to create the precurors to be linked, such as conjugating a linker to a first precuror XTEN-payload and then effecting a second reaction to join the precursor to the reactive group of the terminus the second XTEN-payload precursor. Alterntiavely, one or both of the XTEN termini can be modified as precurors that can then be joined by click chemistry or by other methods described or illustrated herein, leaving few or no residual atoms to bridge the intersection of the XTEN. In

another embodiment, two XTEN-payload precuror sequences are linked by a disulfide bridge using cysteines or thiol groups introduced at or near the termini of the precursor XTEN-payload reactants, resulting in a divalent XTEN-payload conjugate. Exemplary configurations of such divalent conjugates follow.

[00379] In one embodiment, the invention provides a conjugate having the configuration of formula X

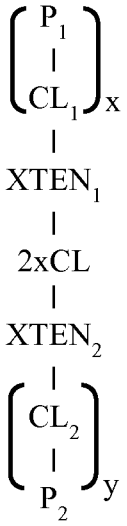


X

wherein independently for each occurrence P_{R1} is a single atom residue of a first payload wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; P_{R2} is a single atom residue of a second payload wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or 1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y is $\geq$ 2; 2xCL is alternatively a divalent cross-linker or the reaction product of a first and a second click chemistry reactant selected from Table 15; $XTEN_1$ is a polypeptide having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_2$ is a polypeptide having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula X, $CL_1$and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In another embodiment of the conjugate of formula

X, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN. In another embodiment of the conjugate of formula X, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula X, C_2 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula X, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a cysteine sulfur of $XTEN_2$. In another embodiment of the conjugate of formula X, each CL_1 is linked to a lysine epsilon amino group of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula X, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula X, $XTEN_1$ and $XTEN_2$ are identical. In another embodiment of the conjugate of formula X, $XTEN_1$ and $XTEN_2$ are different. In another embodiment, the invention provides a preparation of the conjugate of formula X in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the XTEN molecules of the preparation of the conjugate have identical sequence length.

[00380] In another embodiment, the invention provides a conjugate having the configuration of formula XI



XI

wherein independently for each occurrence P_1 is a first payload selected from the group of payloads set forth in Tables 11, 12, 18, 19, and 21; P_2 is a second payload selected from the group of payloads set forth in Tables 11, 12, 18, 19, and 21 and that is different from P_1; CL_1 is a cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL_2 is a cross-linker that is different from CL_1; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x +

y is ≥ 2; 2xCL is alternatively a divalent cross-linker or the reaction product of a first and a second click chemistry reactant selected from Table 15; $XTEN_1$ is a first substantially homogeneous XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_2$ is a first substantially homogeneous having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3. In one embodiment of the conjugate of formula XI, $CL_1$and CL_2 are each selected from the group of cross-linkers set forth in Table 13. In another embodiment of the conjugate of formula XI, x is 1 and CL_1 is linked to the N-terminal amino group of the XTEN. In another embodiment of the conjugate of formula XI, CL_1 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula XI, C_2 is the reaction product of a first and a second click chemistry reactant selected from Table 15. In another embodiment of the conjugate of formula XI, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a cysteine sulfur of $XTEN_2$. In another embodiment of the conjugate of formula XI, each CL_1 is linked to a lysine epsilon amino group of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula XI, each CL_1 is linked to a cysteine sulfur of the $XTEN_1$ and each CL_2 is linked to a lysine epsilon amino group of the $XTEN_2$. In another embodiment of the conjugate of formula XI, $XTEN_1$ and $XTEN_2$ are identical. In another embodiment of the conjugate of formula XI, $XTEN_1$ and $XTEN_2$ are different. In one embodiment, the conjugate of formula XI is selected from the group consisting of the conjugates set forth in Table 21. In another embodiment, the invention provides a preparation of the conjugate of formula XI in which at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95% of the respective $XTEN_1$ and $XTEN_2$ molecules of the preparation of the conjugate have identical sequence length.

[00381] In other embodiments, the invention provides XTEN-linker and XTEN-linker payload conjugates with a trimeric configuration, such as shown in FIGS. 21-23.

[00382] The invention provides trimeric conjugates in which three XTEN-cross-linker conjugates are linked by a trivalent linker, resulting in a trimeric XTEN-cross-linker configuration. In one embodiment, the invention provides a trimeric XTEN-crosslinker having the configuration of formula XII

$$(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)\text{-}(CL2)_y$$
$$|$$

$$(XTEN_3)\text{-}(CL3)_z \qquad XII$$

wherein independently for each occurrence 3xCL is the trivalent cross-linker, CL1 is the first cross-linker conjugated to XTEN1, CL2 is the second cross-linker conjugated to XTEN2, CL3 is the third cross-linker conjugated to XTEN3, x is an integer of 1 to about 10, y is an integer of 1 to about 10, z is an integer of 1 to about 10 with the proviso that x + y + z is > 3, $XTEN_1$ is the first XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_2$ is the second XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_3$ is the third XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, and $XTEN_3$ are the same or are different XTEN sequences. In one embodiment of the conjugate of formula XII, CL1, CL2, and CL3 are each selected from the group consisting of the cross-linkers set forth in Table 13, and are the same or are different. In one embodiment, the conjugate of formula XII further comprises a single atom residue of a first payload conjugated to each cross-linker of the first substantially homogeneous XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur, a single atom residue of a second payload conjugated to each cross-linker of the second substantially homogeneous XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur, and a single atom residue of a third payload conjugated to each cross-linker of the third substantially homogeneous XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

[00383] In another embodiment, the invention provides trimeric conjugates in which three XTEN-payload precursors are linked by a trivalent linker, resulting in a trimeric XTEN-payload configuration, such as shown in FIGS. 21 and 97-106. In one embodiment, the invention provides a trimeric XTEN-crosslinker having the configuration of formula XIII

$$\begin{array}{l} P_1\text{-}(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)\text{-}(CL2)_y\text{-}P_2 \\ \qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\quad | \\ \qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad\qquad (XTEN_3)\text{-}(CL3)_z\text{-}P_3 \end{array} \qquad XIII$$

wherein independently for each occurrence 3xCL is the trivalent cross-linker is selected from the group of trivalent cross-linkers set forth in Tables 13 and 14; P_1 is conjugated to each cross-linker

of the first XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, P2 is a second payload conjugated to each cross-linker of the second XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first payload, and P_3 is a third payload conjugated to each cross-linker of the third XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first or the second payload; CL_1 is the first cross-linker; x is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, orl to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; CL2 is a second cross-linker; y is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, or 1 to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1; and z is an integer from 1 to about 100, or 1 to about 50, or 1 to about 40, orl to about 20, or 1 to about 10, or 1 to about 5, or is 9, or is 3, or is 2, or is 1, with the proviso that x + y + z is $\geq$ 3; $XTEN_1$ is the first XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_2$ is the second XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; and $XTEN_3$ is the third XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, and $XTEN_3$ are the same or are different XTEN sequences. In some embodiments, the conjugate of formula XIII further comprises a first payload wherein the payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and at least one other of the payloads is a drug wherein the drug is selected from the group consisting of the drugs set forth in Table 11, Table 19, and Table 21. In one embodiment of the foregoing, the targeting moiety is LHRH or folate and the drug is selected from doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin.

. In another embodiment of the trimeric XTEN conjugate composition, the composition has the configuration of formula XIV:

$$(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)\text{-}(CL2)_y$$
$$|$$
$$(XTEN_3) \qquad \text{XIV}$$

wherein independently for each occurrence; 3xCL is the trivalent cross-linker; CL1 is the first cross-linker conjugated to $XTEN_1$; CL2 is the second cross-linker conjugated to $XTEN_2$; x is an integer of 1 to about 10; y is an integer of 1 to about 10 with the proviso that x + y is ≥ 2; $XTEN_1$ is the first XTEN; $XTEN_2$ is the second XTEN; and $XTEN_3$ is the third XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2. In one embodiment of the trimeric XTEN conjugate composition of formula XIV, the composition further comprises a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In another embodiment of the trimeric XTEN conjugate composition of formula XIV, the composition further comprises a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21; and a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21, wherein the payload is the same or is different from the first payload. In one embodiment of the foregoing, the first payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and the second payloads is a drug selected from the group consisting of the drugs set forth in Table 6, Table 18, and Table 21. In another embodiment of the foregoing, the first payload is a targeting moiety is selected from the group consisting of LHRH and folate, and the second payload is a drug is selected from the group consisting of doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. In one embodiment of the foregoing, the first payload is a drug selected from the group consisting of the drugs of Table 11 and the proteins of Table 12 and the second payload is different from the first payload and is selected from the group consisting of the drugs of Table 11 and the proteins of Table 12. In another embodiment of the foregoing, the first payload and the second payload are identical and are selected from the group consisting of the drugs of Table 11 and the proteins of Table 12. In another embodiment of the trimeric XTEN conjugate composition, the composition has the configuration of formula XV:

$$(CL1)_x\text{-}(XTEN_1)\text{-}3xCL\text{-}(XTEN_2)$$
$$|$$

$(XTEN_3)$ XV

wherein independently for each occurrence; 3xCL is the trivalent cross-linker; CL1 is the first cross-linker conjugated to $XTEN_1$; x is an integer of 1 to about 10; $XTEN_1$ is the first XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 3; $XTEN_2$ is the second XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2; and $XTEN_3$ is the third XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2. In one embodiment of the trimeric XTEN conjugate composition configured as formula XV, the composition further comprises a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur. In one embodiment of the trimeric XTEN conjugate composition configured as formula XV, the composition further comprises a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21.

[00384] In another embodiment of the trimeric XTEN-payload conjugate, each XTEN-payload can be a monomeric fusion protein comprising a biologically active peptide or polypeptide, wherein the fusion protein is linked to the trivalent linker at an amino group or a thiol group of the XTEN. In another embodiment of the trimeric XTEN-payload conjugate, each XTEN-payload can be a conjugate of a payload linked to the XTEN, which can be a biologically active peptide or polypeptide or a pharmacologically active small molecule or toxin, linked to the XTEN that, in turn, is linked to the trivalent linker at the N-terminus of the XTEN. In the foregoing XTEN-linker-payload embodiments hereinabove described in this paragraph, the three payloads can be identical or they can be different. In one embodiment of the trimeric XTEN-payload conjugate, the conjugate comprises at least one biologically active protein and at least one drug linked to different XTEN that, in turn, is linked to the trivalent linker at the N-terminus of the XTEN. In a particular embodiment of the foregoing configuration, the at least one biologically active protein is a targeting moiety and the at least one drug is a toxin including, but not limited to doxorubicin, paclitaxel, auristatin, monomethyl auristatin E, monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. Depending on the postion of the thiol or the epsilon amino group in the XTEN, one can control if the payload is interior to (as shown in FIG. 23B) or at the terminus of the cross-linked XTEN (as shown in FIG. 23A). In the foregoing embodiment, exemplarly, non-limiting targeting moieties include LHRH, folate, octreotide, pasireotide, bombesin, monocloncal antibodies, scFV, centryins, and the antibody fragments, scaffolds and mimetics of Table 17. Exemplary configurations of such trimeric conjugates follow.

[00385] The invention further provides XTEN-linker and XTEN-linker payload conjugates with a tetrameric configuration. In one embodiment, the invention provides conjugates in which four XTEN sequences are linked by a tetraravalent linker, resulting in a tetrarameric XTEN-crosslinker configuration, such as shown in FIG. 22D. Non-limiting examples of tetravalent linkers include a tetraravalent-thiol, a quadravalent-N-maleimide linker such as described in U.S. Pat. No. 7,524,821, or an antibody or antibody fragment with four reactive groups.

[00386] The invention provides conjugates in which four XTEN-cross-linker precursor sequences are linked by a tetrarvalent linker, resulting in a tetraravalent XTEN-cross-linker configuration. In one embodiment, the invention provides a tetrameric XTEN-crosslinker having the configuration of formula XVI

$$\begin{array}{c} (CL_1)_v\text{-}(XTEN_1)\text{-}4xCL\text{-}(XTEN_2)\text{-}(CL_2)_x \\ \qquad\qquad\quad / \quad \backslash \\ (CL_3)_y\text{-}(XTEN_3) \qquad (XTEN_4)\text{-}(CL_4)_z \end{array} \qquad \text{XVI}$$

wherein independently for each occurrence: 4xCL is the tetravalent cross-linker; CL_1 is the first cross-linker conjugated to $XTEN_1$; CL_2 is the second cross-linker conjugated to $XTEN_2$; CL_3 is the third cross-linker conjugated to $XTEN_3$; CL_4 is the fourth cross-linker conjugated to $XTEN_4$; v is an integer of 1 to about 10; x is an integer of 1 to about 10; y is an integer of 1 to about 10; z is an integer of 1 to about 10 with the proviso that $x + y + z$ is ≥ 4; $XTEN_1$ is the first XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_2$ is the second XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_3$ is the third XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, and $XTEN_3$ are the same or are different XTEN sequences; $XTEN_4$ is the fourth XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, $XTEN_3$ and $XTEN_4$ are the same or are different XTEN sequences.

[00387] The invention provides conjugates in which four XTEN-payload precursor sequences are linked by a tetrarvalent linker, resulting in a tetraravalent XTEN-payload configuration as shown in FIGS. 22C and 105. In one embodiment, the invention provides a tetrameric XTEN-payload having the configuration of formula XVII

$$P_1\text{-}(CL_1)_v\text{-}(XTEN_1)\text{-}4xCL\text{-}(XTEN_2)\text{-}(CL_2)_x\text{-}P_2$$
$$/ \quad \backslash$$
$$P_3\text{-}(CL_3)_y\text{-}(XTEN_3) \quad (XTEN_4)\text{-}(CL_4)_z\text{-}P_4 \qquad \text{XVII}$$

wherein independently for each occurrence: 4xCL is the tetravalent cross-linker; P_1 is conjugated to each cross-linker of the first XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, P2 is a second payload conjugated to each cross-linker of the second XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first payload, P_3 is a third payload conjugated to each cross-linker of the third XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first or the second payload; P_4 is a fourth payload conjugated to each cross-linker of the fourth XTEN and is selected from the group consisting of the payloads set forth in Tables 11, 12, 18 and 21, wherein the payload is the same or is different from the first, the second or the third payload; CL_1 is the first cross-linker conjugated to $XTEN_1$; CL_2 is the second cross-linker conjugated to $XTEN_2$; CL_3 is the third cross-linker conjugated to $XTEN_3$; CL_4 is the fourth cross-linker conjugated to $XTEN_4$; v is an integer of 1 to about 10; x is an integer of 1 to about 10; y is an integer of 1 to about 10; z is an integer of 1 to about 10 with the proviso that $x + y + z$ is ≥ 4; $XTEN_1$ is the first XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_2$ is the second XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3; $XTEN_3$ is the third XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, and $XTEN_3$ are the same or are different XTEN sequences; $XTEN_4$ is the fourth XTEN having at least 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about

94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Tables 2 and 3 wherein $XTEN_1$, $XTEN_2$, $XTEN_3$ and $XTEN_4$ are the same or are different XTEN sequences.

[00388] In another embodiment of the tetraravalent XTEN-payload conjugate, each XTEN-payload can be a monomeric fusion protein comprising a biologically active peptide or polypeptide, wherein the fusion protein is linked to the tetraravalent linker at an amino group or a thiol group of the XTEN. In another embodiment of the tetraravalent XTEN-payload conjugate, each XTEN-payload can be a conjugate of a payload, which can be a biologically active peptide or polypeptide or a pharmacologically active small molecule or toxin, linked to the XTEN that, in turn, is linked to the tetraravalent linker by the N-terminus of the XTEN. In the foregoing XTEN-linker-payload embodiments hereinabove described in this paragraph, the four payloads can be identical or they can be different. In a particular embodiment of the foregoing configuration, the at least one biologically active protein is a targeting moiety and the at least one drug is a toxin including, but not limited to doxorubicin, paclitaxel, auristatin, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin. Depending on the postion of the thiol or the epsilon amino group in the XTEN, one can control if the payload is interior to or at the terminus of the cross-linked XTEN.

4. Multivalent Configurations with Four or More XTEN-Payloads

[00389] Using XTEN of Table 3, compositions are contemplated containing four or more XTEN-payload molecules linked to the cysteine- or lysine-engineered backbone, resulting in a "comb" multivalent configuration, or linking multiple branched precurors to make a "dendrimer" configuration, as illustrated in FIG. 7. In one embodiment, the multivalent configuration conjugate is created by reacting a cysteine- or lysine-engineered XTEN with an XTEN-payload comprising a linker appropriate for reaction with the cysteine- or lysine-engineered XTEN (as illustrated in FIG. 24), resulting in the final product. In another embodiment, the multivalent configuration conjugate is created by reacting a cysteine- or lysine-engineered XTEN with linkers with an XTEN-payload comprising a cysteine or a primary or epsilon amino group appropriate for reaction with the linker linked to the cysteine- or lysine-engineered XTEN, resulting in the final product. In the embodiments, the valency of the final product is controlled by the number of reative groups incorporated into the XTEN, whether a reactive amino acid or linker. Additionally, it is contemplated that the final product can be designed to locate the payload either close to the XTEN termini, which improves interactions with its ligand, or close to the branch points to shield the payload and reduce the degree of interaction with the ligand.

5. Bispecific Payload Configurations on Monomer XTEN Backbone

[00390] In another aspect, the invention provides conjugates containing two different payload molecules linked to a single cysteine- and lysine-engineered XTEN backbone, as illustrated in FIG. 27A, resulting in a bivalent conjugate. In one embodiment, the bivalent configuration conjugate is created by reacting the engineered XTEN, such as those specifically provided in Table 3, with a first XTEN-payload comprising a linker appropriate for reaction with the cysteine-engineered XTEN, followed by a second reaction with a second XTEN-payload comprising a linker appropriate for reaction with the lysine-engineered XTEN, resulting in the final product. The number and location of payloads is controlled by the design of the engineered XTEN, with the placement of the reactive thiol or amino group being determinative. In one embodiment, the bivalent conjugate comprises a single molecule of a first payload and a single molecule of a second payload linked to the cysteine-lysine-engineered XTEN by linkers. In another embodiment, the bivalent conjugate comprises one, or two, or three, or four, or five molecules of a first payload and a single molecule of a second payload linked to the cysteine-lysine-engineered XTEN by linkers. In another embodiment, the bivalent conjugate comprises one, or two, or three, or four, or five molecules of a first payload and one, or two, or three, or four, or five molecules of a second payload linked to the cysteine-lysine-engineered XTEN by linkers.

[00391] In another embodiment, the bivalent configuration conjugate is created by reacting the cysteine- and lysine-engineered XTEN, such as those of Table 3, with a first linker appropriate for reaction with the cysteine-engineered XTEN, followed by a second reaction with a a linker appropriate for reaction with the lysine-engineered XTEN, then reacting the XTEN-crosslinker backbone with a first payload with a thiol reactive group capable of reacting with the first linker, followed by a reaction of a second payload with an amino group capable of reacting with the second cross-linker, resulting in the final product.

6. XTEN-cross-linker and XTEN-Payload Conjugates with Spacer and Release Groups

[00392] In another aspect, the invention provides XTEN-crosslinker and XTEN-payload conjugates configured with one or more spacers incorporated into or adjacent to the XTEN that are designed to incorporate or enhance a functionality or property to the composition, or as an aid in the assembly or manufacture of the compositions. Such properties include, but are not limited to, inclusion of a sequence capable of being proteolytically cleaved or a labile functional group to permit release of the payload, or a spacer can be introduced between an XTEN sequence and a payload component to decrease steric hindrance such that the payload component may interact appropriately with its target ligand.

[00393] In one embodiment, the one or more spacers are incorporated into the linkers of the subject conjugates. For spacers and methods of identifying desirable spacers, see, for example, George, *et al.* (2003) Protein Engineering 15:871–879, specifically incorporated by reference herein. In one embodiment, the spacer comprises one or more peptide sequences that are between 1–50 amino acid residues in length, or about 1–25 residues, or about 1-10 residues in length. Spacer sequences, exclusive of cleavage sites, can comprise any of the 20 natural L-amino acids, and will preferably have XTEN-like properties in that the majority of residues will be hydrophilic amino acids that are sterically unhindered. The spacer can be polyglycines or polyalanines, or is predominately a mixture of combinations of glycine, serine and alanine residues. In one embodiment, the spacer sequence is a sequence from Table 15. In another embodiment, the spacer sequence is GPEGPS.

[00394] In addition, spacer sequences are designed to avoid the introduction of T-cell epitopes which can, in part, be achieved by avoiding or limiting the number of hydrophobic amino acids utilized in the spacer; the determination of epitopes is described above and in the Examples.

[00395] In one embodiment, the spacer comprises a release group that permits the release of the payload from the conjugate. In another embodiment, the cross-linker comprises a release group that permits the release of the payload from the conjugate. The release group may be any labile group providing for such a releasable attachment. In one embodiment, the release group is a chemically cleavable linkage or labile chemical linkage. Such linkages may typically be cleaved by methods that are well known to those of skill in the art, such as by acid, base, oxidation, reduction, displacement or elimination. In a particular embodiment, the chemistry cleavable linkage comprises a modified base, a modified sugar, a disulfide bond, a chemically cleavable group incorporated into the cross-linker or spacer. Some examples of these linkages are described in PCT WO 96/37630 and U.S. Pat. No. 7,132,519, incorporated herein by reference. Release groups encompassed by the invention also include groups or linkages cleavable by an enzyme. Enzymatically-cleavable release groups include phosphodiester or amide linkages as well as restriction endonuclease recognition sites. In one embodiment, the invention provides compositions comprising one or more payloads in which a cleavable linker of valine-citrulline is between the payload and the XTEN, permitting cleavage by cathepsin when the composition is intermalized intracellularly; e.g., inside a tumour cell. In another embodiment, release groups are cleavable by nucleases. These nucleases may typically be an exonuclease or a restriction endonuclease. Typical exonucleases include exonucleases specific for both double-stranded and single-stranded polynucleic acids. Additionally, restriction endonucleases encompassed by certain embodiments include Type IIS and Type II restriction endonucleases. In other embodiments the release group may be a sequence that is cleavable by a protease, wherein the sequence is selected from the sequences set fort in Table 9. Typical proteases acting on

sequences suitable for inclusion in the inventive compositions include endoproteinases, including the proteinases of Table 9.

7. Libraries of XTEN-Payload Configurations

[00396] In another aspect, the invention provides libraries of XTEN-payload precursors, methods to make the libraries, and methods to combine the library precursors in a combinatorial approach, as illustrated in FIGS. 34-35, to achieve optimal combinations of, as well as the optimal ratio of payloads. In one embodiment, the invention provides a library of individual XTEN each linked to 1, or 2, or 3, or 4, or 5, or 6, or 7, or 8, or 9, or 10 or more or more molecules of a given payload, including those described herein, to create the library of XTEN-payload precursors. In the method, a series of XTEN-payload precursors to be linked are further conjugated to a linker, and then is subsequently mixed and reacted with the other XTEN-payload precursors capable of reacting with the linker under conditions to effect the conjugation, resulting in a library of the various permutations and ratios of payloads linked to XTEN. Such a library is then screened in an in vitro or in vivo assay suitable to assess a parameter in a given clinical indication (e.g., cancer, metabolic disorder, diabetes) in order to determine those compositions providing the optimal response. In one exemplary embodiment, one category of payload precursor includes varyious targeting modules, such as peptides (e.g., the targeting moieties of Table 17) with binding affinity to a tumor-associated antigen of Table 20, and the second category of precursor is one or more drugs, such as a cytotoxic drug or a drug chosen from Table 9. Each category of precursor to be linked is further conjugated to a linker, and, as illustrated in FIG. 36, is subsequently mixed and reacted with the other XTEN-payload precursors capable of reacting with the linker under conditions to effect the conjugation, resulting in a library of the various targeting moieties and drug permutations in varying ratios to each other. The XTEN-payload conjugates are designed to permit fixed ratios of one payload to another; e.g., is 1:1, or 1:1.5, or 1:2, or 1:3, or 2:3, or 1:4, or 1:5 or 1:9 in the case of two different payloads. Similar ranges of ratios would be applied for library conjugates comprising 3, 4, 5 or more payloads.

[00397] In other embodiments, the libraries are constructed using three or more payloads known to have a beneficial effect in the treatment of a common disease. In one embodiment, a library comprises payloads linked to XTEN, wherein each payload is a drug or biologically effective for ameliorating a common disease. In another embodiment, a library comprises payloads linked to XTEN, wherein each drug or biologic is effective for treating different symptoms of a common disease. In another embodiment, a library comprises payloads linked to XTEN, wherein each drug or biologic mediates their therapeutic effect via a common biological pathway. In the foregoing embodiments of the libraries, the common disease is selected from cancer, cancer supportive care, cardiovascular, central nervous system, endocrine disease, gastrointestinal, genitourinary, hematological, HIV infection, hormonal system, inflammation, autoimmune

disease, infectious diseases, metabolic disease, musculoskeletal disease, nephrology disorders, ophthalmologic diseases, pain, and respiratory. With greater particularity, the disease for which the libraries are constructed with payloads known to have a beneficial effect is selected from Table 16. Payloads suitable for use in the treatment or prevention of such diseases include those described herein (e.g., the payloads of Tables 11, 12, 18, and 21), or can be found in commonly accessible databases or would otherwise be known to those of ordinary skill in the art.

Table 16: Diseases for which Payloads are Indicated

Disease		
Achondroplasia	Diabetic nephropathy	Mucositis
Acromegaly	Diabetic neuropathy	Multiple sclerosis
AIDS	Diagnostic	Muscular dystrophy
Alzheimer's disease	Eating disorder	Musculoskeletal
Anemia	Erythropoietic protoporphyria	Myocardial infarction/ischemia
Arthritis	Gastrointestinal disorder	Neutropenia
Asthma	Gout	Obesity
Atherosclerosis	Growth hormone deficiency	Osteoarthritis
Autism	Hemophilia	Osteoporosis
Autoimmune disease	Hepatitis B	Pain
Batten disease	Hepatitis C	Parkinsons disease
Bone & cartilage repair	Hereditary emphysema	Paroxysmal nocturnal hemoglobinuria
Cachexia	HIV	Phenylketonuria
Cancer (all types)	Hyperlipidemia/Dyslipidemia	Psoriasis
Cardiovascular diseases	Hyperparathyroidism	Pulmonary arterial hypertension
Chemotherapy-induced diseases	Hypertension	Pulmonary hypertension
Chronic kidney disease-induced complication	Hypoglycemia	Radiotherapy-induced diseases
Coagulation disorder	Hypoparathyroidism	Sepsis
Colitis	Hypothyroidism	Sexual dysfunction
Congenital hyperinsulinism	Infectious diseases	Short bowel syndrome
Congestive heart failure	Infertility	Stroke
COPD	Inflammatory diseases	Thrombocytopenia
Crohn's disease	Lipodystrophy	Thyroid disease
Cystic fibrosis	Lymphopenia	Transplantation
Diabetes Diabetes-induced complication	Macular degeneration Metabolic conditions	Viral infection

[00398] In one embodiment, as illustrated in FIG. 37, the bispecific conjugate has a drug module linked to the XTEN by a cleavable or labile linker, wherein the linker can be cleaved or disassociates after administration to a subject, including upon intracellular internalization in a cell targeted by the targeting modules. In another embodiment the drug is linked to XTEN by an

non-cleavable linker but the conjugate remains susceptible to degradation. Upon internalization the XTEN is cleaved by proteases and the drug connected to its linker is liberated resulting in cytotoxicity.

[00399] In one exemplary embodiment, the targeting module is luteinizing hormone-releasing hormone (aka LHRH, GnRH, and gonadotropin-releasing hormone), the drug is doxorubicin, wherein the ratio of LHRH to doxorubicin is 1:1, or 1:1.5, or 1:2, or 1:3, or 1:9, or 2:3, or 3:1, or 3:2, or 2:1, or 1.5:1. The conjugate can be generated starting from XTEN precursors. One XTEN precursor can carry 1, 2, or more drug molecules and a reactive cross-linker or click chemistry reactant or a reactive amino acid. A second XEN precursor carries 1, 2, or more LHRH domains for targeting and a reactive cross-linker or click chemistry reactant or a reactive amino acid. Both precursor segments are then joined by reaction between reactive groups of the respective XTEN. In one exemplary embodiment the reactive group is an azide that is conjugated to the N-terminus of first XTEN segment via a cross-linker; and reactive group of the second XTEN is an alkyne that is conjugated to the N-terminus of the second XTEN segment via a cross-linker. In another embodiment of the LHRH-XTEN-drug conjugate, the drug is maytansin. In another embodiment of the LHRH-XTEN-drug conjugate the drug is auristatin.

8. Conjugates of XTEN-Payload Linked to Targeting Moieties

[00400] In another aspect, the present invention provides conjugate compositions comprising one or more XTEN-payload compositions linked to targeting moieties. The subject targeted compositions find use in the treatment of a variety of conditions where selective delivery of a therapeutic or toxic payload to a cell, tissue or organ is desired. The invention contemplates a diversity of targeting moieties for use in the subject compositions, including antibodies, antibody fragments, and antibody mimetics including, but not limited to those set forth in Table 17, as well as peptides and small molecules capable of binding ligands or receptors associated with disease or metabolic or physiologic abnormalities. In one embodiment, the invention provides a conjugate comprising at least one targeting moiety from Tables 17, 18 or 21 linked to at least one XTEN. In another embodiment, the invention provides a conjugate comprising at least one targeting moiety from Tables 17, 18 or 21 linked to each of at least two, or three, or four XTEN. In another embodiment, the invention provides a conjugate comprising at least one targeting moiety from Tables 17, 18 or 21 linked to at least one XTEN and at least one drug or biologic payload selected from the group consisting of the payloads set forth in Table 11, Table 12, Table 18, or Table 21 linked to the at least one XTEN. In one embodiment, the invention provides targeting moiety-XTEN-drug conjugate compositions wherein the composition is selectively delivered to a ligand or receptor on a targeted cell, which can then be internalized into the cell, as illustrated in FIG. 37, resulting in a pharmacologic effect know in the art for the drug component..

[00401] As illustrated in FIGS. 21-24, and 28-32, such conjugate compositions can have different valencies, with one, two, three, or four or more XTEN-payload molecules linked to one or more targeting antibody or targeting moiety. In the case of antibody targeting moieties, in one embodiment the XTEN-payload is linked by a cross-linker to a cysteine in a hinge region of the antibody. In another embodiment, the XTEN-payload is linked by a disulfide bridge to a cysteine in a hinge region of the antibody. Accordingly, an antibody-XTEN-payload conjugate can comprise 1, 2, 3, or 4 or more XTEN-payload segments linked to the antibody, antibody fragment or mimetic. In another embodiment XTEN is conjugated outside of the hinge region, which includes inserting cysteine in the antibody to control conjugation sites or by conjugation to existing lysine side chains. The linking of XTEN-payload to create the antibody conjugates has many benefits: a) the XTEN payload serves as a cleavable linker, b) it provides solubility, c) it allows setting the ratio of drugload per IgG, and d) it can be pre-conjugated with drug to simplify manufacturing.

Table 17: Targeting Moieties: Antibody fragments, scaffolds and mimetics

Targeting Moieties
ABDURINS
AdNectins/Fibronectin type III domain
Adnexins/Fibronectin
Affibodies/Protein Z
Affilins
AFFINILUTE
AFFINIMIP
AFIM
Anticalins/Lipocalins
Aptabody
Aptamers
Armadillo repeat proteins
Avimers
Azymetric
Bispecific diabodies
BiTEs
Bivalent diabodies
Centyrins
DARPins/Ankyrin repeat proteins
Diabodies
Domain antibodies/dAbs/human Vh
Engineered affinity proteins
Evibodies
Fabs
Fv
Fynomers
Glubody
Im7/ColE7 immunity protein
iMabs
Knottin/Cysteine-knot miniproteins
Kunitz domains

Targeting Moieties
Maxibodies
Microbodies
Minibodies
Molecular imprinted polymers (MIPs)
Monobodies
Monoclonal T cell receptors (mTCR)
MonoLex
Nanobodies
Nanofitins
Phylomers
Shark Vhh
SMIPs
SOMAmers
Stable scFV
Spiegelmers
Synbodies
TandAbs®
Telobodies
Tetrabodies
Tetranectins
Tetravalent bispecific antibodies
Trans-body
Triabodies

[00402] In some embodiments, the invention provides conjugates comprising a targeting component as one payload and a toxin as a second payload, with one or more copies of each payload type linked to the XTEN of the composition. In a variation of the foregoing, the conjugate can optionally have the toxin linked to the XTEN with a labile or a cleavable linker such that the toxin is liberated when delivered to or is internalized within the target. In another variation of the foregoing, the targeting component is an antibody or antibody fragment, with one, two, three, or four XTEN-payload compositions conjugated with linkers to the antibody (e.g., conjugated to cysteines in the hinge region as illustrated in FIGS. 28-29), providing conjugates for use in targeted therapy of clinical indications such as, but not limited to, various treatment of tumors and other cancers wherein the antibody provides the targeting component and the XTEN-payload effects the intended activity (e.g, cytotoxicity in a tumor cell). Hence, the inventive conjugates are a type of immunoconjugate. The targeted conjugates can be designed with targeting components that are derived from antibodies, or antibody mimetics, or are peptides or small molecules that bind ligands associated with diseases cells or organs. Non-limiting examples of categories of antibody fragments, scaffolds and mimetics are provided in Table 17. Non-limited examples of specific targeting components, the targets to which they are directed, and toxins that may be utilized as payloads in the inventive conjugates are provided in Table 18. It is specifically contemplated that the targeted conjugate compositions of the present disclosure include compositions of any given targeting component that can be used in

combination with one or more of any of the toxins of Table 18 or the payloads provided in Table 11 or Table 12. It is further contemplated that an XTEN-payload conjugate can comprise two or more targeting components, which may be identical or may be different. It is contemplated that such conjugates can be used in treatment of conditions such as, but not limited to those set forth in Table 15.

Table 18: Exemplary targeting moieties, toxin payloads, and targets to which conjugate compositions can be directed

Class	Target	Targeting Moiety	Toxin
Peptide	LHRHR	LHRH & analogues (e.g. D-Lys-(6)-LHRH)	doxorubicin paclitaxel auristatin (e.g. monomethyl auristatin E; monomethyl auristatin F) maytansine (e.g. maytansinoid DM1; maytansinoid DM4) dolastatin calicheamicin vinca alkaloid (e.g. desacetylvinblastine monohydrazide) camptothecin mitomycin C epothilone hTNF IL-12 Bortezomib Ranpirnase pseudomonas exotoxin SN-38 Rachelmycin m-TOR inhibitor rapamycin tubulysin (tubulysin B; tubulysin M) duocarmycin
	CD13, Aminopeptidase	NGR class (e.g. CNGRC, CNGRCG, GNGRG, KNGRE, (GNGRG)2KGK, CVLNGRMEC, NGRAHA, CNGRCVSGCAGRC)	
	Folate receptor	Folate & analogue (e.g. γ-folate, α-folate; pteroate-gly)	
	Integrin	Cilengitide; RGD-4C; iRGD	
	LRP receptor	Angiopep-2	
	Somatostatin receptor	Somatostatin & analogues (e.g. octreotide; pasireotide; lanreotide; vapreotide, JF-07-69)	
	Nucleolin	F3 peptide	
	PDGFR-beta	RGR	
	LyP-1 receptor	LyP-1; CGNKRTRGC	
	Chondroitin sulfate proteoglygan NG2	TAASGVRSMH; LTLRWVGLMS	
	VPAC1 and VPAC2	Vasoactive intestinal peptide	
	CCK1 and CCK2	Cholecystokinin	
	Gastrin receptor, CCK1 & CCK2	Gastrin	
	GRP receptor subtype	Gastrin-releasing peptide	
	Neurotensin receptor	Neurotensin	
	Alpha-MSH receptor	Alpha-melanocyte stimulating hormone	
	Oxytocin receptor	Oxytocin	
	Lymphatic vessels	LyP-2; CNRRTKAGC	
	Lymphatic vessels	LSD; CLSDGKRKC	
	Lymphatic vessels	REA; CREAGRKAC	
	Lymphatic vessels	AGR, CAGRRSAYC	
	Pericytes & endothelia cells	RSR; CRSRKG	
	Pericytes & endothelia cells	KAA; CKAAKNK	
	Blood vessels	CSRPRRSEC	
	Angiogenic blood vessels & tumor cells	KRK; CGKRK	
	Angiogenic blood vessels	CDTRL	
	Angiogenic blood vessels & tumor cells	CGTKRKC	
Protein	DR4, DR5	TRAIL	

Class	Target	Targeting Moiety	Toxin
Antibody-like scaffold	Various	DARPINS	
	Various	Centyrins	
Antibody	Lewis-Y-related antigen	Br96; anti-Lewis-Y-related antigen antibody	
	HER2	Trastuzumab; Pertuzumab; anti-HER2 antibody	
	EGFR	Cetuximab; anti-EGFR antibody	
	Nectin -4	anti-nectin-4 antibody	
	CanAg (mucin-type glycoprotein)	huC242, anti-CanAg antibody	
	CD138	anti-CD138 antibody	
	CD19	MDX-1342; MOR-208; HuB4; anti-CD19 antibody	
	CD22	Epratuzumab; Bectumomab; Inotuzumab; Moxetumomab, RFB4; anti-CD22 antibody	
	CD23	Lumiliximab, anti-CD23 antibody	
	CD25 (IL-2 receptor)	Daclizumab, anti-CD25 antibody	
	CD30	Xmab2513; cAC10; MDX-060; anti-CD30 antibody	
	CD33	Gemtuzumab; HuM195; huMy9-6; anti-CD33 antibody	
	CD38	Daratumumab, anti-CD38 antibody	
	CD40	SGN-40; HCD122; anti-CD40 antibody	
	CD56	huN901; anti-CD56 antibody	
	CD70	MDX-1411; anti-CD70 antibody	
	CD74	Milatuzumab; anti-CD74 antibody	
	CD79b	anti-CD79b antibody	
	CD80	Galiximab; anti-CD80 antibody	
	Carcinoembryonic antigen (CEA)	Lapetuzumab, hCOL-1anti-CEA antibody	
	Cripto	anti-Cripto antibody	
	cMET	CE-355621, DN30, MetMAb; antagonist anti-cMET antibody	
	EpCAM	Adecatumumab; Edrecolomab; Catumaxomab; anti-EpCAM antibody	
	EphA2	1C1, anti-EphA2 antibody	
	GPNMB (human gylcoprotein NMB (osteoactivin))	glembatumumab, anti-GPNMB antibody	
	Integrins	anti-integrin antibody	
	MUC-1 (epitope CA6)	anti-MUC-1 antibody	
	PSMA	MDX-070, MLN591, anti-PSMA antibody	
	TGFa	anti-TGFa antibody	
	TIM1	anti-TIM1 antibody	

Class	Target	Targeting Moiety	Toxin
	Folate receptor 1	M9346A, Farletuzumab, anti-folate receptor antibody	
	IL-13 receptor	anti-IL-13 receptor antibody	

[00403] In particular embodiments, the invention provides XTEN-payload conjugates comprising one or more LHRH targeting components selected from Table 19 and one or more drug components selected from Table 11. In the foregoing embodiment, the LHRH can be linked to one XTEN segment that, in turn, is linked to one or more XTEN segments to which the drug components are conjugated. Alternatively, the LHRH and drug components can be conjugated to a monomeric XTEN. Further, the drug components can optionally be linked to XTEN using labile or cleavable linkers that permit the drug to be liberated from the conjugate after administration to a subject.

Table 19: Exemplary LHRH

Composition
pGlu-HWSYGLRPG-NH2
pGlu-HWSY[D-Lys]LRPG-NH2
pGlu-HWSY[D-Trp]LRPG-NH2
pGlu-HWSY[D-Leu]LRP-NHEt
pGlu-HWSY[D-Ser(tBu)]LRP-NHEt
pGlu-HWSY[D-2-Nal]LRPG-NH2
pGlu-HWSY[D-His(Bzl)]LRP-NHEt
pGlu-HWSY[D-Ser(tBu)]LRP-Azagly-NH2
pGlu-HWSY[D-Trp]LRP-NHEt
pGlu-HWSHDWLPG-NH2

[00404] Additional targets contemplated for which the XTEN-payload conjugates can be directed include tumor-associated antigens listed in Table 20. In one embodiment, the invention provides XTEN-payload conjugates comprisiing one or more targeting components capable of binding one or more targets of Table 20.

Table 20: Tumor-associated antigen targets

TAA targets (synonyms)	Accession Number and References
Her2 (ErbB2)	GenBank accession no. M11730; U.S. Pat. No. 5,869,445; WO2004048938; WO2004027049; WO2004009622; WO2003081210; WO2003089904; WO2003016475; US2003118592; WO2003008537; WO2003055439; WO2003025228; WO200222636; WO200212341; WO200213847; WO200214503; WO200153463; WO200141787; WO200044899; WO200020579; WO9630514; EP1439393; WO2004043361; WO2004022709; WO200100244
BMPR1B (bone morphogenetic protein receptor-type IB)	GenBank accession no. NM_001203; WO2004063362; WO2003042661; US 2003134790; WO2002102235;

TAA targets (synonyms)	Accession Number and References
	WO2003055443; WO200299122; WO2003029421; WO2003024392; WO200298358' WO200254940; WO200259377; WO200230268
E16 (LAT1, SLC7A5)	GenBank accession no. NM _003486); WO2004048938; WO2004032842; WO2003042661; WO2003016475; WO200278524; WO200299074; WO200286443; WO2003003906; WO200264798; WO200014228; US2003224454; WO2003025138
STEAP1 (six transmembrane epithelial antigen of prostate)	GenBank accession no. NM _012449; WO2004065577; WO2004027049; EP1394274; WO2004016225; WO2003042661; US2003157089; US2003185830; US2003064397; WO200289747618; WO2003022995
STEAP2 (six transmembrane epithelial antigen of prostate 2)	GenBank accession no. AF455138; WO2003087306; US2003064397; WO200272596; WO200172962; WO2003104270; WO2003104270; US2004005598; WO2003042661; US2003060612; WO200226822; WO200216429
CA125/0772P (MUC16)	GenBank accession no. AF361486; WO2004045553; WO200292836; WO200283866; US2003124140
megakaryocyte potentiating factor (MPF, mesothelin)	GenBank accession no. NM _005823; WO2003101283; WO2002102235; WO2002101075; WO200271928; WO9410312
Na/Pi cotransporter type IIb (NaPi3b)	GenBank accession no. NM _006424; WO2004022778; EP1394274; WO2002102235; EP875569; WO200157188; WO2004032842; WO200175177
Semaphorin 5b (SEMA5B, SEMAG)	GenBank accession no. AB040878; WO2004000997; WO2003003984; WO200206339; WO200188133; WO2003054152; WO2003101400
Prostate cancer stem cell antigen (PSCA hlg)	GenBank accession no. AY358628; US2003129192; US2004044180; US2004044179; US2003096961; US2003232056; WO2003105758; US2003206918; EP1347046; WO2003025148
ETBR (Endothelin type B receptor)	GenBank accession no. AY275463; WO2004045516; WO2004048938; WO2004040000; WO2003087768; WO2003016475; WO2003016475; WO200261087; WO2003016494; WO2003025138; WO200198351; EP522868; WO200177172; US2003109676; U.S. Pat. No. 6,518,404; U.S. Pat. No. 5,773,223; WO2004001004
TRPV4 (Transient receptor potential cation channel, subfamily V)	US Pat App No. 20090208514
CDC45L	GenBank Accession NO. AJ223728; US Pat App No. 20090208514
CRIPTO (CR, CR1, CRGF)	GenBank accession no. NP _003203 or NM _003212; US2003224411; WO2003083041; WO2003034984; WO200288170; WO2003024392; WO200216413; WO200222808; U.S. 5,854,399; U.S. Pat. No. 5,792,616
CD21 (CR2 (Complement receptor 2) or C3DR (C3d/Epstein Barr virus receptor)	GenBank accession no. M26004; WO2004045520; US2004005538; WO2003062401; WO2004045520; WO9102536; WO2004020595
CD79b (CD79B, CD79β, IGb (immunoglobulin-associated beta), B29)	GenBank accession no. NM _000626 or 11038674; WO2004016225; WO2003087768; US2004101874; WO2003062401; WO200278524; US2002150573; U.S. Pat. No. 5,644,033; WO2003048202; WO 99/558658,

TAA targets (synonyms)	Accession Number and References
	U.S. Pat. No. 6,534,482; WO200055351
FcRH2 (IFGP4, IRTA4, SPAP1A (SH2 domain containing phosphatase anchor protein 1a), SPAP1B, SPAP1C)	GenBank accession no. NM _ 030764, AY358130; WO2004016225; WO2003077836; WO200138490; WO2003097803; WO2003089624
NCA (CEACAM6)	GenBank accession no. M18728; WO2004063709; EP1439393; WO2004044178; WO2004031238; WO2003042661; WO200278524; WO200286443; WO200260317
MDP (DPEP1)	GenBank accession no. BC017023; WO2003016475; WO200264798
IL20Rα (IL20Ra, ZCYTOR7)	GenBank accession no. AF184971; EP1394274; US2004005320; WO2003029262; WO2003002717; WO200222153; US2002042366; WO200146261; WO200146232; WO9837193
BECAN (Brevican core protein)	GenBank accession no. AF229053; US2003186372; US2003186373; US2003119131; US2003119122; US2003119126; US2003119121; US2003119129; US2003119130; US2003119128; US2003119125; WO2003016475; WO200202634
EphB2R (DRT, ERK, Hek5, EPHT3, Tyro5)	GenBank accession no. NM _ 004442; WO2003042661; WO200053216; WO2004065576 (Claim 1); WO2004020583; WO2003004529; WO200053216
B7h (ASLG659)	GenBank accession no. AX092328; US20040101899; WO2003104399; WO2004000221; US2003165504; US2003124140; US2003065143; WO2002102235; US2003091580; WO200210187; WO200194641; WO200202624; US2002034749; WO200206317; WO200271928; WO200202587; WO200140269; WO200036107; WO2004053079; WO2003004989; WO200271928
PSCA (Prostate stem cell antigen precursor	GenBank accession no. AJ297436; WO2004022709; EP1394274; US2004018553; WO2003008537 (Claim 1); WO200281646; WO2003003906; WO200140309; US2001055751; WO200032752; WO9851805; WO9851824; WO9840403
BAFF-R (B cell-activating factor receptor, BLyS receptor 3, BR3)	GenBank accession No. AF116456; WO2004058309; WO2004011611; WO2003045422; WO2003014294; WO2003035846; WO200294852; WO200238766; WO200224909
CD22 (B-cell receptor CD22-β-form, BL-CAM, Lyb-8, Lyb8, SIGLEC-2, FLJ22814)	GenBank accession No. AK026467; WO2003072036
CD79a (immunoglobulin-associated alpha)	GenBank accession No. NP _ 001774.10; WO2003088808, US20030228319; WO2003062401; US2002150573; WO9958658; WO9207574; U.S. Pat. No. 5,644,033
CXCR5 (Burkitt's lymphoma receptor 1)	GenBank accession No. NP _ 001707.1; WO2004040000; WO2004015426; US2003105292; U.S. Pat. No. 6,555,339; WO200261087; WO200157188; WO200172830; WO200022129; WO9928468; U.S. Pat. No. 5,440,021; WO9428931; WO9217497
HLA-DOB	GenBank accession No. NP _ 002111.1; WO9958658;

TAA targets (synonyms)	Accession Number and References
	U.S. Pat. No. 6,153,408; U.S. Pat. No. 5,976,551; U.S. Pat. No. 6,011,146
P2X5	GenBank accession No. NP _002552.2; WO2004047749; WO2003072035; WO200222660; WO2003093444; WO2003087768; WO2003029277
CD72 (B-cell differentiation antigen CD72, Lyb-2)	GenBank accession No. NP _001773.1; WO2004042346; WO2003026493; WO200075655
CD180 (LY64)	GenBank accession No. NP _005573.1; US2002193567; WO9707198; WO2003083047; WO9744452
FcRH1 (Fc receptor-like protein 1)	GenBank accession No. NP _443170.1) WO2003077836; WO200138490; WO2003089624; EP1347046; WO2003089624
IRTA2 (Immunoglobulin superfamily receptor translocation associated 2)	GenBank accession No. Human:AF343662, AF343663, AF343664, AF343665, AF369794, AF397453; WO2003024392; WO2003077836; WO200138490
TENB2 (TMEFF2, tomoregulin, TPEF, HPP1)	GenBank accession No. AF179274; AY358907, CAF85723, CQ782436; WO2004074320; WO2003042661; WO2003009814; EP1295944; WO200230268; WO200190304; US2004249130; US2004022727; WO2004063355; US2004197325; US2003232350; US2004005563; US2003124579
CS1 (CRACC, 19A, APEX-1, FOAP12)	GenBank Accession No. NM 021181; US 20100168397
DLL4	GenBank Accession No. NM 019074; US 20100303812
Lewis Y	ADB235860; US 7879983
CD40 (Bp50, CDW40, MGC9013, TNFRSF5, p50)	AL035662.65; US 6946129
OBA1 (5T4)	GenBank Accession No. NP_001159864.1; US 20100021483
p97	Woodbury et al., 1980, Proc. Natl. Acad. Sci. USA 77: 2183-2186; Brown et al., 1981, J. Immunol. 127: 539-546
carcinoembryonic antigen (CEA)	GenBank Accession No. NP_004354.2; US 6,676,924
TAG-72	US 7256004
DNA	
Neuropilin -1 (NRP1)	GenBank Accession No. NP_001019799.1; US 20080213268
A33	GenBank Accession No. NP_005805.1; US 7579187
Mucin-1 (MUC1)	GenBank Accession No. NP_001018016.1; NP_001018017.1; US 7183388
ED-B fibronectin	US 7785591
Thomsen-Friedenreich antigen (TF)	US 7374755; US 20100297159
Bombesin receptor	US5750370
CanAg	
Carcinoembryonic antigen (CEA)	US4818709
CD13	
CD138	
CD30	
CD47	
CD56	
CD70	
Chondroitin sulfate proteoglygan	

TAA targets (synonyms)	Accession Number and References
NG2	
EphA2	
Folate receptor 1	US5547668
gastrin receptor	
GPNMB (human gylcoprotein)	
NMB (osteoactivin)	
GRP receptor subtype	
integrin avb3	US20110166072
LHRHR	US20110104074
LRP receptor	
LyP-1 receptor	
Nectin-4	
Neurotensin receptor	US8058230
Nucleolin	
Somatostatin receptor	
TIM1	
VPAC1	
VPAC2	
Alpha-MSH receptor	
CD25	
Interleukin-1 receptor	

[00405] In particular embodiments, the invention provides XTEN-payload conjugates comprising one, two or more targeting components and one, two or more drug components conjugated to XTEN. Non-limiting embodiments of specific conjugate compositions are provided in Table 21, in which the named composition of column 2 has specified components of: i) XTEN sequences of Table 3 designated in the XTEN column of the Table; ii) targeting moiety payloads specified in the Targeting Moiety column of the Table that provide targeting capability of the composition (with the number of moieties specified; e.g., 1x or 3x); and iii) drug pharmacophore specified in the Drug Moiety column of the Table (with the number of drug molecules conjugated to the XTEN; e.g., 3x or 9x). As would be appreciated by one of skill in the art, the invention contemplates other combinations of the disclosed components, as well as different numbers or ratios of the respective specified components, as well as different XTEN sequences to which the payloads are conjugated. For example, the invention contemplates that the number of drug moieties attached to a given XTEN can be 1, or 2, or 3, or 4, or 5, or 6, or 7, or 8, or 9, or 10 or more and that the XTEN would have, for example, the corresponding number of cysteine or lysine residues to which the drug moieties would be conjugated. Further, the invention contemplates that the number of targeting moieties attached to the conjugate can be 1, or 2, or 3 or more, which would similarly be linked to XTEN with an N-terminal amino group or a corresponding number of lysine or cysteine residues.

Table 21: Exemplary conjugates

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
1	1xLHRH-XTEN-3xDox	Seg 174		1xLHRH	3xDoxorubicin
2	1xLHRH-XTEN-9xDox	Seg 175		1xLHRH	9xDoxorubicin
3	3xLHRH-XTEN-3xDox	Seg 176	Seg 176	3xLHRH	3xDoxorubicin
4	3xLHRH-XTEN-9xDox	Seg 176	Seg 177	3xLHRH	9xDoxorubicin
5	XTEN-3xDox	Seg 174			3xDoxorubicin
6	XTEN-9xDox	Seg 175			9xDoxorubicin
7	1xLHRH-XTEN-3xMMAE	Seg 174		1xLHRH	3xMMAE ***
8	1xLHRH-XTEN-9xMMAE	Seg 175		1xLHRH	9xMMAE
9	3xLHRH-XTEN-3xMMAE	Seg 176	Seg 176	3xLHRH	3xMMAE
10	3xLHRH-XTEN-9xMMAE	Seg 176	Seg 177	3xLHRH	9xMMAE
11	XTEN-3xMMAE	Seg 174			3xMMAE
12	XTEN-9xMMAE	Seg 175			9xMMAE
13	1xLHRH-XTEN-3xMMAF	Seg 174		1xLHRH	3xMMAF ****
14	1xLHRH-XTEN-9xMMAF	Seg 175		1xLHRH	9xMMAF
15	3xLHRH-XTEN-3xMMAF	Seg 176	Seg 176	3xLHRH	3xMMAF
16	3xLHRH-XTEN-9xMMAF	Seg 176	Seg 177	3xLHRH	9xMMAF
17	XTEN-3xMMAF	Seg 174			3xMMAF
18	XTEN-9xMMAF	Seg 175			9xMMAF
19	1xLHRH-XTEN-3xMertansine	Seg 174		1xLHRH	3xMertansine
20	1xLHRH-XTEN-9xMertansine	Seg 175		1xLHRH	9xMertansine
21	3xLHRH-XTEN-3xMertansine	Seg 176	Seg 176	3xLHRH	3xMertansine
22	3xLHRH-XTEN-9xMertansine	Seg 176	Seg 177	3xLHRH	9xMertansine
23	XTEN-3xMertansine	Seg 174			3xMertansine
24	XTEN-9xMertansine	Seg 175			9xMertansine
25	1xLHRH-XTEN-3xMaytansinoid DM4	Seg 174		1xLHRH	3xMaytansinoid DM4
26	1xLHRH-XTEN-9xMaytansinoid DM4	Seg 175		1xLHRH	9xMaytansinoid DM4
27	3xLHRH-XTEN-3xMaytansinoid DM4	Seg 176	Seg 176	3xLHRH	3xMaytansinoid DM4

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
28	3xLHRH-XTEN-9xMaytansinoid DM4	Seg 176	Seg 177	3xLHRH	9xMaytansinoid DM4
29	XTEN-3xMaytansinoid DM4	Seg 174			3xMaytansinoid DM4
30	XTEN-9xMaytansinoid DM4	Seg 175			9xMaytansinoid DM4
31	1xLHRH-XTEN-3xPaclitaxel	Seg 174		1xLHRH	3xPaclitaxel
32	1xLHRH-XTEN-9xPaclitaxel	Seg 175		1xLHRH	9xPaclitaxel
33	3xLHRH-XTEN-3xPaclitaxel	Seg 176	Seg 176	3xLHRH	3xPaclitaxel
34	3xLHRH-XTEN-9xPaclitaxel	Seg 176	Seg 177	3xLHRH	9xPaclitaxel
35	XTEN-3xPaclitaxel	Seg 174			3xPaclitaxel
36	XTEN-9xPaclitaxel	Seg 175			9xPaclitaxel
37	1xLHRH-XTEN-3xSN-38	Seg 174		1xLHRH	3xSN-38
38	1xLHRH-XTEN-9xSN-38	Seg 175		1xLHRH	9xSN-38
39	3xLHRH-XTEN-3xSN-38	Seg 176	Seg 176	3xLHRH	3xSN-38
40	3xLHRH-XTEN-9xSN-38	Seg 176	Seg 177	3xLHRH	9xSN-38
41	XTEN-3xSN-38	Seg 174			3xSN-38
42	XTEN-9xSN-38	Seg 175			9xSN-38
43	1xLHRH-XTEN-3xGemcitabine	Seg 174		1xLHRH	3xGemcitabine
44	1xLHRH-XTEN-9xGemcitabine	Seg 175		1xLHRH	9xGemcitabine
45	3xLHRH-XTEN-3xGemcitabine	Seg 176	Seg 176	3xLHRH	3xGemcitabine
46	3xLHRH-XTEN-9xGemcitabine	Seg 176	Seg 177	3xLHRH	9xGemcitabine
47	XTEN-3xGemcitabine	Seg 174			3xGemcitabine
48	XTEN-9xGemcitabine	Seg 175			9xGemcitabine
49	1xLHRH-XTEN-3xCarboplatin	Seg 174		1xLHRH	3xCarboplatin
50	1xLHRH-XTEN-9xCarboplatin	Seg 175		1xLHRH	9xCarboplatin
51	3xLHRH-XTEN-3xCarboplatin	Seg 176	Seg 176	3xLHRH	3xCarboplatin
52	3xLHRH-XTEN-9xCarboplatin	Seg 176	Seg 177	3xLHRH	9xCarboplatin
53	XTEN-3xCarboplatin	Seg 174			3xCarboplatin

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
54	XTEN-9xCarboplatin	Seg 175			9xCarboplatin
55	1xLHRH-XTEN-Human RNase			1xLHRH	Human RNase
56	3xLHRH-XTEN-Human RNase			3xLHRH	Human RNase
57	1xLHRH-XTEN-Bovine RNase			1xLHRH	Bovine RNase
58	3xLHRH-XTEN-Bovine RNase			3xLHRH	Bovine RNase
59	1xLHRH-XTEN-Ranpirnase			1xLHRH	Ranpirnase
60	3xLHRH-XTEN-Ranpirnase			3xLHRH	Ranpirnase
61	1xLHRH-XTEN-Pokeweed antiviral protein			1xLHRH	Pokeweed antiviral protein
62	3xLHRH-XTEN-Pokeweed antiviral protein			3xLHRH	Pokeweed antiviral protein
63	1xfolate-XTEN-3xDox	Seg 174		1xfolate	3xDoxorubicin
64	1xfolate-XTEN-9xDox	Seg 175		1xfolate	9xDoxorubicin
65	3xfolate-XTEN-3xDox	Seg 176	Seg 176	3xfolate	3xDoxorubicin
66	3xfolate-XTEN-9xDox	Seg 176	Seg 177	3xfolate	9xDoxorubicin
67	XTEN-3xDox	Seg 174			3xDoxorubicin
68	XTEN-9xDox	Seg 175			9xDoxorubicin
69	1xfolate-XTEN-3xMMAE	Seg 174		1xfolate	3xMMAE
70	1xfolate-XTEN-9xMMAE	Seg 175		1xfolate	9xMMAE
71	3xfolate-XTEN-3xMMAE	Seg 176	Seg 176	3xfolate	3xMMAE
72	3xfolate-XTEN-9xMMAE	Seg 176	Seg 177	3xfolate	9xMMAE
73	XTEN-3xMMAE	Seg 174			3xMMAE
74	XTEN-9xMMAE	Seg 175			9xMMAE
75	1xfolate-XTEN-3xMMAF	Seg 174		1xfolate	3xMMAF
76	1xfolate-XTEN-9xMMAF	Seg 175		1xfolate	9xMMAF
77	3xfolate-XTEN-3xMMAF	Seg 176	Seg 176	3xfolate	3xMMAF
78	3xfolate-XTEN-9xMMAF	Seg 176	Seg 177	3xfolate	9xMMAF
79	XTEN-3xMMAF	Seg 174			3xMMAF
80	XTEN-9xMMAF	Seg 175			9xMMAF
81	1xfolate-XTEN-3xMertansine	Seg 174		1xfolate	3xMertansine
82	1xfolate-XTEN-9xMertansine	Seg 175		1xfolate	9xMertansine
83	3xfolate-XTEN-3xMertansine	Seg 176	Seg 176	3xfolate	3xMertans

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
					ine
84	3xfolate-XTEN-9xMertansine	Seg 176	Seg 177	3xfolate	9xMertansine
85	XTEN-3xMertansine	Seg 174			3xMertansine
86	XTEN-9xMertansine	Seg 175			9xMertansine
87	1xfolate-XTEN-3xMaytansinoid DM4	Seg 174		1xfolate	3xMaytansinoid DM4
88	1xfolate-XTEN-9xMaytansinoid DM4	Seg 175		1xfolate	9xMaytansinoid DM4
89	3xfolate-XTEN-3xMaytansinoid DM4	Seg 176	Seg 176	3xfolate	3xMaytansinoid DM4
90	3xfolate-XTEN-9xMaytansinoid DM4	Seg 176	Seg 177	3xfolate	9xMaytansinoid DM4
91	XTEN-3xMaytansinoid DM4	Seg 174			3xMaytansinoid DM4
92	XTEN-9xMaytansinoid DM4	Seg 175			9xMaytansinoid DM4
93	1xfolate-XTEN-3xPaclitaxel	Seg 174		1xfolate	3xPaclitaxel
94	1xfolate-XTEN-9xPaclitaxel	Seg 175		1xfolate	9xPaclitaxel
95	3xfolate-XTEN-3xPaclitaxel	Seg 176	Seg 176	3xfolate	3xPaclitaxel
96	3xfolate-XTEN-9xPaclitaxel	Seg 176	Seg 177	3xfolate	9xPaclitaxel
97	XTEN-3xPaclitaxel	Seg 174			3xPaclitaxel
98	XTEN-9xPaclitaxel	Seg 175			9xPaclitaxel
99	1xfolate-XTEN-3xSN-38	Seg 174		1xfolate	3xSN-38
100	1xfolate-XTEN-9xSN-38	Seg 175		1xfolate	9xSN-38
101	3xfolate-XTEN-3xSN-38	Seg 176	Seg 176	3xfolate	3xSN-38
102	3xfolate-XTEN-9xSN-38	Seg 176	Seg 177	3xfolate	9xSN-38
103	XTEN-3xSN-38	Seg 174			3xSN-38
104	XTEN-9xSN-38	Seg 175			9xSN-38
105	1xfolate-XTEN-3xGemcitabine	Seg 174		1xfolate	3xGemcitabine
106	1xfolate-XTEN-9xGemcitabine	Seg 175		1xfolate	9xGemcitabine
107	3xfolate-XTEN-3xGemcitabine	Seg 176	Seg 176	3xfolate	3xGemcitabine

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
108	3xfolate-XTEN-9xGemcitabine	Seg 176	Seg 177	3xfolate	9xGemcitabine
109	XTEN-3xGemcitabine	Seg 174			3xGemcitabine
110	XTEN-9xGemcitabine	Seg 175			9xGemcitabine
111	1xfolate-XTEN-3xCarboplatin	Seg 174		1xfolate	3xCarboplatin
112	1xfolate-XTEN-9xCarboplatin	Seg 175		1xfolate	9xCarboplatin
113	3xfolate-XTEN-3xCarboplatin	Seg 176	Seg 176	3xfolate	3xCarboplatin
114	3xfolate-XTEN-9xCarboplatin	Seg 176	Seg 177	3xfolate	9xCarboplatin
115	XTEN-3xCarboplatin	Seg 174			3xCarboplatin
116	XTEN-9xCarboplatin	Seg 175			9xCarboplatin
117	1xoctreotide-XTEN-3xDox	Seg 174		1xoctreotide	3xDoxorubicin
118	1xoctreotide-XTEN-9xDox	Seg 175		1xoctreotide	9xDoxorubicin
119	3xoctreotide-XTEN-3xDox	Seg 176	Seg 176	3xoctreotide	3xDoxorubicin
120	3xoctreotide-XTEN-9xDox	Seg 176	Seg 177	3xoctreotide	9xDoxorubicin
121	XTEN-3xDox	Seg 174			3xDoxorubicin
122	XTEN-9xDox	Seg 175			9xDoxorubicin
123	1xoctreotide-XTEN-3xMMAE	Seg 174		1xoctreotide	3xMMAE
124	1xoctreotide-XTEN-9xMMAE	Seg 175		1xoctreotide	9xMMAE
125	3xoctreotide-XTEN-3xMMAE	Seg 176	Seg 176	3xoctreotide	3xMMAE
126	3xoctreotide-XTEN-9xMMAE	Seg 176	Seg 177	3xoctreotide	9xMMAE
127	XTEN-3xMMAE	Seg 174			3xMMAE
128	XTEN-9xMMAE	Seg 175			9xMMAE
129	1xoctreotide-XTEN-3xMMAF	Seg 174		1xoctreotide	3xMMAF
130	1xoctreotide-XTEN-9xMMAF	Seg 175		1xoctreotide	9xMMAF
131	3xoctreotide-XTEN-3xMMAF	Seg 176	Seg 176	3xoctreotide	3xMMAF
132	3xoctreotide-XTEN-9xMMAF	Seg 176	Seg 177	3xoctreotide	9xMMAF
133	XTEN-3xMMAF	Seg 174			3xMMAF
134	XTEN-9xMMAF	Seg 175			9xMMAF
135	1xoctreotide-XTEN-3xMertansine	Seg 174		1xoctreotide	3xMertansine
136	1xoctreotide-XTEN-9xMertansine	Seg 175		1xoctreotide	9xMertansine
137	3xoctreotide-XTEN-3xMertansine	Seg 176	Seg 176	3xoctreotide	3xMertansine

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
138	3xoctreotide-XTEN-9xMertansine	Seg 176	Seg 177	3xoctreotide	9xMertansine
139	XTEN-3xMertansine	Seg 174			3xMertansine
140	XTEN-9xMertansine	Seg 175			9xMertansine
141	1xoctreotide-XTEN-3xMaytansinoid DM4	Seg 174		1xoctreotide	3xMaytansinoid DM4
142	1xoctreotide-XTEN-9xMaytansinoid DM4	Seg 175		1xoctreotide	9xMaytansinoid DM4
143	3xoctreotide-XTEN-3xMaytansinoid DM4	Seg 176	Seg 176	3xoctreotide	3xMaytansinoid DM4
144	3xoctreotide-XTEN-9xMaytansinoid DM4	Seg 176	Seg 177	3xoctreotide	9xMaytansinoid DM4
145	XTEN-3xMaytansinoid DM4	Seg 174			3xMaytansinoid DM4
146	XTEN-9xMaytansinoid DM4	Seg 175			9xMaytansinoid DM4
147	1xoctreotide-XTEN-3xPaclitaxel	Seg 174		1xoctreotide	3xPaclitaxel
148	1xoctreotide-XTEN-9xPaclitaxel	Seg 175		1xoctreotide	9xPaclitaxel
149	3xoctreotide-XTEN-3xPaclitaxel	Seg 176	Seg 176	3xoctreotide	3xPaclitaxel
150	3xoctreotide-XTEN-9xPaclitaxel	Seg 176	Seg 177	3xoctreotide	9xPaclitaxel
151	XTEN-3xPaclitaxel	Seg 174			3xPaclitaxel
152	XTEN-9xPaclitaxel	Seg 175			9xPaclitaxel
153	1xoctreotide-XTEN-3xSN-38	Seg 174		1xoctreotide	3xSN-38
154	1xoctreotide-XTEN-9xSN-38	Seg 175		1xoctreotide	9xSN-38
155	3xoctreotide-XTEN-3xSN-38	Seg 176	Seg 176	3xoctreotide	3xSN-38
156	3xoctreotide-XTEN-9xSN-38	Seg 176	Seg 177	3xoctreotide	9xSN-38
157	XTEN-3xSN-38	Seg 174			3xSN-38
158	XTEN-9xSN-38	Seg 175			9xSN-38
159	1xoctreotide-XTEN-3xGemcitabine	Seg 174		1xoctreotide	3xGemcitabine
160	1xoctreotide-XTEN-9xGemcitabine	Seg 175		1xoctreotide	9xGemcitabine
161	3xoctreotide-XTEN-3xGemcitabine	Seg 176	Seg 176	3xoctreotide	3xGemcitabine
162	3xoctreotide-XTEN-	Seg 176	Seg 177	3xoctreotide	9xGemcit

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
	9xGemcitabine				abine
163	XTEN-3xGemcitabine	Seg 174			3xGemcit abine
164	XTEN-9xGemcitabine	Seg 175			9xGemcit abine
165	1xoctreotide-XTEN-3xCarboplatin	Seg 174		1xoctreotide	3xCarbopl atin
166	1xoctreotide-XTEN-9xCarboplatin	Seg 175		1xoctreotide	9xCarbopl atin
167	3xoctreotide-XTEN-3xCarboplatin	Seg 176	Seg 176	3xoctreotide	3xCarbopl atin
168	3xoctreotide-XTEN-9xCarboplatin	Seg 176	Seg 177	3xoctreotide	9xCarbopl atin
169	XTEN-3xCarboplatin	Seg 174			3xCarbopl atin
170	XTEN-9xCarboplatin	Seg 175			9xCarbopl atin
171	1xoctreotide-XTEN-3xEverolimus	Seg 174		1xoctreotide	3xEveroli mus
172	1xoctreotide-XTEN-9xEverolimus	Seg 175		1xoctreotide	9xEveroli mus
173	3xoctreotide-XTEN-3xEverolimus	Seg 176	Seg 176	3xoctreotide	3xEveroli mus
174	3xoctreotide-XTEN-9xEverolimus	Seg 176	Seg 177	3xoctreotide	9xEveroli mus
175	XTEN-3xEverolimus	Seg 174			3xEveroli mus
176	XTEN-9xEverolimus	Seg 175			9xEveroli mus
177	1xpasireotide-XTEN-3xDox	Seg 174		1xpasireotide	3xDoxoru bicin
178	1xpasireotide-XTEN-9xDox	Seg 175		1xpasireotide	9xDoxoru bicin
179	3xpasireotide-XTEN-3xDox	Seg 176	Seg 176	3xpasireotide	3xDoxoru bicin
180	3xpasireotide-XTEN-9xDox	Seg 176	Seg 177	3xpasireotide	9xDoxoru bicin
181	XTEN-3xDox	Seg 174			3xDoxoru bicin
182	XTEN-9xDox	Seg 175			9xDoxoru bicin
183	1xpasireotide-XTEN-3xMMAE	Seg 174		1xpasireotide	3xMMAE
184	1xpasireotide-XTEN-9xMMAE	Seg 175		1xpasireotide	9xMMAE
185	3xpasireotide-XTEN-3xMMAE	Seg 176	Seg 176	3xpasireotide	3xMMAE
186	3xpasireotide-XTEN-9xMMAE	Seg 176	Seg 177	3xpasireotide	9xMMAE

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
187	XTEN-3xMMAE	Seg 174			3xMMAE
188	XTEN-9xMMAE	Seg 175			9xMMAE
189	1xpasireotide-XTEN-3xMMAF	Seg 174		1xpasireotide	3xMMAF
190	1xpasireotide-XTEN-9xMMAF	Seg 175		1xpasireotide	9xMMAF
191	3xpasireotide-XTEN-3xMMAF	Seg 176	Seg 176	3xpasireotide	3xMMAF
192	3xpasireotide-XTEN-9xMMAF	Seg 176	Seg 177	3xpasireotide	9xMMAF
193	XTEN-3xMMAF	Seg 174			3xMMAF
194	XTEN-9xMMAF	Seg 175			9xMMAF
195	1xpasireotide-XTEN-3xMertansine	Seg 174		1xpasireotide	3xMertansine
196	1xpasireotide-XTEN-9xMertansine	Seg 175		1xpasireotide	9xMertansine
197	3xpasireotide-XTEN-3xMertansine	Seg 176	Seg 176	3xpasireotide	3xMertansine
198	3xpasireotide-XTEN-9xMertansine	Seg 176	Seg 177	3xpasireotide	9xMertansine
199	XTEN-3xMertansine	Seg 174			3xMertansine
200	XTEN-9xMertansine	Seg 175			9xMertansine
201	1xpasireotide-XTEN-3xMaytansinoid DM4	Seg 174		1xpasireotide	3xMaytansinoid DM4
202	1xpasireotide-XTEN-9xMaytansinoid DM4	Seg 175		1xpasireotide	9xMaytansinoid DM4
203	3xpasireotide-XTEN-3xMaytansinoid DM4	Seg 176	Seg 176	3xpasireotide	3xMaytansinoid DM4
204	3xpasireotide-XTEN-9xMaytansinoid DM4	Seg 176	Seg 177	3xpasireotide	9xMaytansinoid DM4
205	-XTEN-3xMaytansinoid DM4	Seg 174			3xMaytansinoid DM4
206	-XTEN-9xMaytansinoid DM4	Seg 175			9xMaytansinoid DM4
207	1xpasireotide-XTEN-3xPaclitaxel	Seg 174		1xpasireotide	3xPaclitaxel
208	1xpasireotide-XTEN-9xPaclitaxel	Seg 175		1xpasireotide	9xPaclitaxel
209	3xpasireotide-XTEN-3xPaclitaxel	Seg 176	Seg 176	3xpasireotide	3xPaclitaxel
210	3xpasireotide-XTEN-	Seg 176	Seg 177	3xpasireotide	9xPaclitax

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
	9xPaclitaxel				el
211	XTEN-3xPaclitaxel	Seg 174			3xPaclitaxel
212	XTEN-9xPaclitaxel	Seg 175			9xPaclitaxel
213	1xpasireotide-XTEN-3xSN-38	Seg 174		1xpasireotide	3xSN-38
214	1xpasireotide-XTEN-9xSN-38	Seg 175		1xpasireotide	9xSN-38
215	3xpasireotide-XTEN-3xSN-38	Seg 176	Seg 176	3xpasireotide	3xSN-38
216	3xpasireotide-XTEN-9xSN-38	Seg 176	Seg 177	3xpasireotide	9xSN-38
217	XTEN-3xSN-38	Seg 174			3xSN-38
218	XTEN-9xSN-38	Seg 175			9xSN-38
219	1xpasireotide-XTEN-3xGemcitabine	Seg 174		1xpasireotide	3xGemcitabine
220	1xpasireotide-XTEN-9xGemcitabine	Seg 175		1xpasireotide	9xGemcitabine
221	3xpasireotide-XTEN-3xGemcitabine	Seg 176	Seg 176	3xpasireotide	3xGemcitabine
222	3xpasireotide-XTEN-9xGemcitabine	Seg 176	Seg 177	3xpasireotide	9xGemcitabine
223	-XTEN-3xGemcitabine	Seg 174			3xGemcitabine
224	-XTEN-9xGemcitabine	Seg 175			9xGemcitabine
225	1xpasireotide-XTEN-3xCarboplatin	Seg 174		1xpasireotide	3xCarboplatin
226	1xpasireotide-XTEN-9xCarboplatin	Seg 175		1xpasireotide	9xCarboplatin
227	3xpasireotide-XTEN-3xCarboplatin	Seg 176	Seg 176	3xpasireotide	3xCarboplatin
228	3xpasireotide-XTEN-9xCarboplatin	Seg 176	Seg 177	3xpasireotide	9xCarboplatin
229	-XTEN-3xCarboplatin	Seg 174			3xCarboplatin
230	-XTEN-9xCarboplatin	Seg 175			9xCarboplatin
231	1xpasireotide-XTEN-3xEverolimus	Seg 174		1xpasireotide	3xEverolimus
232	1xpasireotide-XTEN-9xEverolimus	Seg 175		1xpasireotide	9xEverolimus
233	3xpasireotide-XTEN-3xEverolimus	Seg 176	Seg 176	3xpasireotide	3xEverolimus
234	3xpasireotide-XTEN-9xEverolimus	Seg 176	Seg 177	3xpasireotide	9xEverolimus
235	XTEN-3xEverolimus	Seg 174			3xEverolimus
236	XTEN-9xEverolimus	Seg 175			9xEverolimus
237	1xbombesin-XTEN-3xDox	Seg 174		1xbombesin	3xDoxorubicin

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
238	1xbombesin-XTEN-9xDox	Seg 175		1xbombesin	9xDoxorubicin
239	3xbombesin-XTEN-3xDox	Seg 176	Seg 176	3xbombesin	3xDoxorubicin
240	3xbombesin-XTEN-9xDox	Seg 176	Seg 177	3xbombesin	9xDoxorubicin
241	XTEN-3xDox	Seg 174			3xDoxorubicin
242	XTEN-9xDox	Seg 175			9xDoxorubicin
243	1xbombesin-XTEN-3xMMAE	Seg 174		1xbombesin	3xMMAE
244	1xbombesin-XTEN-9xMMAE	Seg 175		1xbombesin	9xMMAE
245	3xbombesin-XTEN-3xMMAE	Seg 176	Seg 176	3xbombesin	3xMMAE
246	3xbombesin-XTEN-9xMMAE	Seg 176	Seg 177	3xbombesin	9xMMAE
247	XTEN-3xMMAE	Seg 174			3xMMAE
248	XTEN-9xMMAE	Seg 175			9xMMAE
249	1xbombesin-XTEN-3xMMAF	Seg 174		1xbombesin	3xMMAF
250	1xbombesin-XTEN-9xMMAF	Seg 175		1xbombesin	9xMMAF
251	3xbombesin-XTEN-3xMMAF	Seg 176	Seg 176	3xbombesin	3xMMAF
252	3xbombesin-XTEN-9xMMAF	Seg 176	Seg 177	3xbombesin	9xMMAF
253	XTEN-3xMMAF	Seg 174			3xMMAF
254	XTEN-9xMMAF	Seg 175			9xMMAF
255	1xbombesin-XTEN-3xMertansine	Seg 174		1xbombesin	3xMertansine
256	1xbombesin-XTEN-9xMertansine	Seg 175		1xbombesin	9xMertansine
257	3xbombesin-XTEN-3xMertansine	Seg 176	Seg 176	3xbombesin	3xMertansine
258	3xbombesin-XTEN-9xMertansine	Seg 176	Seg 177	3xbombesin	9xMertansine
259	XTEN-3xMertansine	Seg 174			3xMertansine
260	XTEN-9xMertansine	Seg 175			9xMertansine
261	1xbombesin-XTEN-3xMaytansinoid DM4	Seg 174		1xbombesin	3xMaytansinoid DM4
262	1xbombesin-XTEN-9xMaytansinoid DM4	Seg 175		1xbombesin	9xMaytansinoid DM4
263	3xbombesin-XTEN-3xMaytansinoid DM4	Seg 176	Seg 176	3xbombesin	3xMaytansinoid DM4
264	3xbombesin-XTEN-9xMaytansinoid DM4	Seg 176	Seg 177	3xbombesin	9xMaytansinoid DM4
265	XTEN-3xMaytansinoid DM4	Seg 174			3xMaytansinoid DM4

Conjugate	Conjugate Name*	XTEN linked to Targeting Moiety**	XTEN linked to Drug Moiety**	Targeting Moiety*	Drug Moiety*
266	XTEN-9xMaytansinoid DM4	Seg 175			9xMaytansinoid DM4
267	1xbombesin-XTEN-3xPaclitaxel	Seg 174		1xbombesin	3xPaclitaxel
268	1xbombesin-XTEN-9xPaclitaxel	Seg 175		1xbombesin	9xPaclitaxel
269	3xbombesin-XTEN-3xPaclitaxel	Seg 176	Seg 176	3xbombesin	3xPaclitaxel
270	3xbombesin-XTEN-9xPaclitaxel	Seg 176	Seg 177	3xbombesin	9xPaclitaxel
271	XTEN-3xPaclitaxel	Seg 174			3xPaclitaxel
272	XTEN-9xPaclitaxel	Seg 175			9xPaclitaxel
273	1xbombesin-XTEN-3xSN-38	Seg 174		1xbombesin	3xSN-38
274	1xbombesin-XTEN-9xSN-38	Seg 175		1xbombesin	9xSN-38
275	3xbombesin-XTEN-3xSN-38	Seg 176	Seg 176	3xbombesin	3xSN-38
276	3xbombesin-XTEN-9xSN-38	Seg 176	Seg 177	3xbombesin	9xSN-38
277	XTEN-3xSN-38	Seg 174			3xSN-38
278	XTEN-9xSN-38	Seg 175			9xSN-38
279	1xbombesin-XTEN-3xGemcitabine	Seg 174		1xbombesin	3xGemcitabine
280	1xbombesin-XTEN-9xGemcitabine	Seg 175		1xbombesin	9xGemcitabine
281	3xbombesin-XTEN-3xGemcitabine	Seg 176	Seg 176	3xbombesin	3xGemcitabine
282	3xbombesin-XTEN-9xGemcitabine	Seg 176	Seg 177	3xbombesin	9xGemcitabine
283	XTEN-3xGemcitabine	Seg 174			3xGemcitabine
284	XTEN-9xGemcitabine	Seg 175			9xGemcitabine
285	1xbombesin-XTEN-3xCarboplatin	Seg 174		1xbombesin	3xCarboplatin
286	1xbombesin-XTEN-9xCarboplatin	Seg 175		1xbombesin	9xCarboplatin
287	3xbombesin-XTEN-3xCarboplatin	Seg 176	Seg 176	3xbombesin	3xCarboplatin
288	3xbombesin-XTEN-9xCarboplatin	Seg 176	Seg 177	3xbombesin	9xCarboplatin
289	XTEN-3xCarboplatin	Seg 174			3xCarboplatin
290	XTEN-9xCarboplatin	Seg 175			9xCarboplatin

* 1x, 3x, 9x refers to the number of the indicated moiety conjugated to the XTEN
** refers to XTEN sequence from Table 3; e.g., Seg 174
***Monomethyl auristatin E ****Monomethyl auristatin F

V). PHARMACEUTICAL COMPOSITIONS

[00406] The present invention provides pharmaceutical compositions comprising XTEN-payload conjugates of the disclosure. In one embodiment, the pharmaceutical composition comprises a conjugate selected from the group consisting of the conjugates set forth in Table 21 and at least one pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition comprises a conjugate comprising at least a first XTEN sequence having at least about 80%, or at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or having 100% sequence identity to a sequence selected from the group of sequences set forth in Table 2 and Table 3 wherein the XTEN sequences of the composition are substantially homogeneous in length, and wherein the XTEN is conjugated to at least a first payload selected from the group of payloads set forth in Tables 11, 12, 18, 19, and 21, and wherein the composition further comprises at least one pharmaceutically acceptable carrier. In one embodiment, the invention provides a pharmaceutical composition comprising an XTEN-payload conjugate of any of the embodiments described herein and at least one pharmaceutically acceptable carrier.

[00407] The invention provides a method of preparing a pharmaceutical composition, comprising the step of combining a subject conjugate composition of the embodiments with at least one pharmaceutically acceptable carrier into a pharmaceutically acceptable formulation. The XTEN-payload conjugates of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the XTEN-payload is combined in admixture with a pharmaceutically acceptable carrier vehicle, such as aqueous solutions or buffers, pharmaceutically acceptable suspensions and emulsions. Examples of non-aqueous solvents include propyl ethylene glycol, polyethylene glycol and vegetable oils. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers, as described in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980), in the form of lyophilized formulations or aqueous solutions. The pharmaceutical compositions can be administered by any suitable means or route, including subcutaneously, subcutaneously by infusion pump, intramuscularly, and intravenously. It will be appreciated that the preferred route will vary with the disease and age of the recipient, and the severity of the condition being treated. Osmotic pumps may be used as slow release agents in the form of tablets, pills, capsules or implantable devices. Syringe pumps may also be used as slow release agents. Such devices are described in U.S. Pat. Nos. 4,976,696; 4,933,185; 5,017,378; 6,309,370; 6,254,573; 4,435,173; 4,398,908; 6,572,585; 5,298,022; 5,176,502; 5,492,534; 5,318,540; and 4,988,337, the contents of which are incorporated herein by reference. One

skilled in the art, considering both the disclosure of this invention and the disclosures of these other patents could produce a syringe pump for the extended release of the compositions of the present invention.

[00408] In another embodiment, the invention provides an XTEN-payload conjugate of any of the embodiments described herein for use in making a medicament useful for the treatment of a condition including, but not limited to the conditions set forth in Table 16.

VI). METHODS OF TREATMENT

[00409] The invention provides a method of treating a disease in a subject, comprising administering to the subject an effective amount of the XTEN-payload conjugate of any of the foregoing embodiments to a subject in need thereof. In one embodiment, the XTEN-payload comprises a single type of payload selected from Tables 11, 12, 18, 19, and 21. In another embodiment, the XTEN-payload comprises a two types of payloads selected from Tables 11, 12, 18, 19, and 21. In another embodiment, the XTEN-payload comprises a two types of payloads in which one payload is selected from Tables 11, 12, and 18 and the second payload is a targeting moiety with binding affinity to a target of Table 20 or is a targeting moiety of any one of Tables 18, 19, or 21. In another embodiment, the XTEN-payload comprises more than three or more types of payloads selected from Tables 11, 12, 18, 19, and 21. In the method, the payload of the conjugate is one that is known in the art to have a beneficial effect or has affinity to a disease target when administered to a subject with a particular disease or condition. In one embodiment, the payload(s) of the composition mediate their therapeutic effect via a common biological pathway. In the foregoing embodiments of the paragraph, the method is useful in treating or ameliorating or preventing a disease selected from cancer, cancer supportive care, cardiovascular, central nervous system, endocrine disease, gastrointestinal, genitourinary, hematological, HIV infection, hormonal system, inflammation, autoimmune disease, infectious diseases, metabolic disease, musculoskeletal disease, nephrology disorders, ophthalmologic diseases, pain, and respiratory. With greater particularity, the disease is selected from Table 16.

[00410] In some embodiments of the method of treatment, the conjugate composition can be administered subcutaneously, intramuscularly, or intravenously. In one embodiment, the composition is administered using a therapeutically effective amount. In one embodiment, administration of two or more consecutive doses of the therapeutically effective amount results in a gain in time spent within a therapeutic window for the composition compared to the payload not linked to XTEN and administered using comparable doses to a subject. The gain in time spent within the therapeutic window can be at least three-fold longer than unmodified payload, or alternatively, at least four-fold, or five-fold, or six-fold, or seven-fold, or eight-fold, or nine-fold, or at least 10-fold, or at least 20-fold, or at least about 30-fold, or at least about 50-fold, or at least about 100-fold longer than payload not linked to XTEN.

[00411] In one embodiment of the method of treatment, a smaller moles/kg amount of about two-fold less, or about three-fold less, or about four-fold less, or about five-fold less, or about six-fold less, or about eight-fold less, or about 10-fold less or greater of the conjugate or a pharmaceutical composition comprising the conjugate is administered to a subject in need thereof in comparison to the corresponding payload(s) not linked to the XTEN under a dose regimen needed to maintain a therapeutic effect and the conjugate achieves a comparable area under the curve as the corresponding moles/kg amount of the payload(s) not linked to the XTEN needed to maintain a therapeutic effect. In another embodiment, the conjugate or a pharmaceutical composition comprising the conjugate requires less frequent administration for routine treatment of a subject, wherein the dose of conjugate or pharmaceutical composition is administered about every four days, about every seven days, about every 10 days, about every 14 days, about every 21 days, or about monthly to the subject, and the conjugate achieves a comparable area under the curve as the corresponding payload(s) not linked to the XTEN and administered to the subject. In yet other embodiments, an accumulatively smaller amount of about 5%, or about 10%, or about 20%, or about 40%, or about 50%, or about 60%, or about 70%, or about 80%, or about 90% less of moles/kg of the conjugate is administered to a subject in comparison to the corresponding amount of the payload(s) not linked to the XTEN under a dose regimen needed to maintain an effective blood concentration, yet the conjugate achieves at least a comparable area under the curve as the corresponding payload(s) not linked to the XTEN. The accumulatively smaller amount is measure for a period of at least about one week, or about 14 days, or about 21 days, or about one month. In some embodiments of the method, the therapeutic effect is a measured parameter, clinical symptom or endpoint known in the art to be associated with the underlying condition of the subject to be treated or prevented.

[00412] In one embodiment, the invention provides a method of treating a cancer cell in vitro, comprising administering to a culture of a cancer cell a composition comprising an effective amount of an XTEN-payload composition, wherein a first payload is a targeting moiety and the second payload is a toxin of Table 21. In another embodiment, the invention provides a method of treating a cancer in a subject, comprising administering to the subject a pharmaceutical composition comprising an effective amount of an XTEN-payload composition wherein a first payload is a targeting moiety and the second payload is a toxin of Table 21. In one embodiment of the method, the pharmaceutical composition comprises the composition having the structure set forth in FIG. 117. In another embodiment of the method, the cancer is selected from the group consisting of non-small cell lung cancer or mesothelioma. platinum-resistant ovarian cancer, endometrial cancer, adenocarcinoma of the lung, and refractory advanced tumors. In another embodiment of the method, the administration results in at least a 10%, or 20%, or 30%, or 40%, or 50%, or 60%, or 70%, or 80%, or 90% greater improvement of at least one, two, or

three parameters associated with a cancer compared to an untreated subject wherein the parameters are selected from the group consisting of response rate as defined by the Response Evaluation Criteria in Solid Tumors (RECIST), time-to-progression of the cancer (relapse), discovery of local recurrence, discovery of regional metastasis, discovery of distant metastasis, onset of symptoms, hospitalization, increase in pain medication requirement, requirement of salvage chemotherapy, requirement of salvage surgery, requirement of salvage radiotherapy, time-to-treatment failure, and increased time of survival.

[00413] In another aspect, the invention provides a regimen for treating a subject with a disease, said regimen comprising a composition comprising a conjugate of any of the embodiments described herein. In one embodiment of the regimen, the regimen further comprises the step of determining the amount of pharmaceutical composition comprising the CFXTEN needed to achieve a therapeutic effect in the patient.

[00414] The invention provides conjugates comprising a treatment regimen for a diseased subject comprising administering a pharmaceutical composition comprising a conjugate of any of the embodiments described herein in two or more successive doses adminitered at an effective amount, wherein the adminstration results in the improvement of at least one parameter associated with the disease.

VII). CONJUGATION KITS

[00415] In another aspect, the invention provides a kit to facilitate the use of the XTEN-crosslinker conjugate compositions. In one embodiment, the kit comprises an XTEN-crosslinker in a formulation, a container and a label on or associated with the container. In the foregoing embodiment, the XTEN-crosslinker can be any one of the embodiments described herein. The container holds the XTEN-crosslinker at a defined concentration in a buffer suitable for use in a conjugation reaction to link to a payload.

VIII). PHARMACEUTICAL KITS

[00416] In another aspect, the invention provides a kit to facilitate the use of the conjugate compositions. The kit comprises a pharmaceutical composition provided herein, a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, etc., formed from a variety of materials such as glass or plastic. The container holds a pharmaceutical composition as a formulation that is effective for treating a subject and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The package insert can list the approved indications for the drug, instructions for the reconstitution and/or administration of the drug for the use for the approved indication, appropriate dosage and safety information, and information identifying the lot and expiration of the drug. In another embodiment of the foregoing, the kit can comprise a second container that can carry a suitable

diluent for the pharmaceutical composition, the use of which will provide the user with the appropriate concentration to be delivered to the subject. In another embodiment, the kit comprises, in at least a first container: a first container: an amount of a conjugate composition drug sufficient to administer in treatment of a subject with a disease; an amount of a pharmaceutically acceptable carrier; a second container that can carry a suitable diluent for the subject composition, which will provide the user with the appropriate concentration of the pharmaceutical composition to be delivered to the subject; together with a label identifying the drug and storage and handling conditions, and/or a sheet of the approved indications for the drug and instructions for the reconstitution and/or administration of the drug for the use for the treatment of a approved indication, appropriate dosage and safety information, and information identifying the lot and expiration of the drug.

IX). THE NUCLEIC ACIDS SEQUENCES OF THE INVENTION

[00417] The present invention provides isolated polynucleic acids encoding the polypeptide components of the conjugates and sequences complementary to polynucleic acid molecules encoding the polypeptide components of the conjugates. In some embodiments, the invention provides polynucleic acids encoding the XTEN of any of the conjugate embodiments described herein, or the complement of the polynucleic acid. In one embodiment, the polynucleic acids encodes an XTEN selected from the group consisting of the XTEN set forth in Tables 2 and 3, or the complement of the polynucleic acid.

[00418] In other embodiments, the invention provides polynucleic acids encoding the XTEN linked to cleavage sequences, affinity tags and helper sequences protein of any of the embodiments described herein, or the complement of the polynucleic acids. In one embodiment, the polynucleic acids encodes a protein payload selected from the group consisting of the protein payloads set forth in Tables 7, 18, 19, and 21, or the complement of the polynucleic acid.

[00419] In one embodiment, the invention encompasses methods to produce polynucleic acids encoding the XTEN and the XTEN linked to cleavage sequences, affinity tags and helper sequences protein embodiments, or sequences complementary to the polynucleic acids, including homologous variants thereof. In general, and as illustrated in FIGS. 38 and 39, the methods of producing a polynucleotide sequence coding for an XTEN and expressing the resulting gene product include assembling nucleotides encoding the XTEN, ligating the components in frame, incorporating the encoding gene into an expression vector appropriate for a host cell, transforming the appropriate host cell with the expression vector, and culturing the host cell under conditions causing or permitting the XTEN to be expressed in the transformed host cell, thereby producing the XTEN polypeptide, which is recovered by methods described herein or by standard protein purification methods known in the art. Standard recombinant techniques in

molecular biology are used to make the polynucleotides and expression vectors of the present invention.

[00420] In accordance with the invention, nucleic acid sequences that encode XTEN or XTEN linked to cleavage sequences, affinity tags and helper sequences protein (or its complement) are used to generate recombinant DNA molecules that direct the expression in appropriate host cells. Several cloning strategies are suitable for performing the present invention, many of which are used to generate a construct that comprises a gene coding for an XTEN or a payload composition of the present invention, or its complement. In one embodiment, the cloning strategy is used to create a gene that encodes an XTEN that comprises nucleotides encoding the XTEN that is used to transform a host cell for expression of the XTEN composition. In the foregoing embodiments hereinabove described in this paragraph, the genes can further comprise nucleotides encoding cleavage sequeces, affinity tags, and helper sequences. In another embodiment, the cloning strategy is used to create a gene that encodes a protein payload that comprises nucleotides encoding the payload that is used to transform a host cell for expression of the payload composition.

[00421] In designing a desired XTEN sequences, it was discovered that the non-repetitive nature of the XTEN of the inventive compositions is achieved despite use of a "building block" molecular approach in the creation of the XTEN-encoding sequences. This was achieved by the use of a library of polynucleotides encoding peptide sequence motifs, described above, that are then ligated and/or multimerized to create the genes encoding the XTEN sequences (see FIGS. 38 and 39 and Examples). Thus, while the XTEN(s) of the expressed polypeptide may consist of multiple units of as few as four different sequence motifs, because the motifs themselves consist of non-repetitive amino acid sequences, the overall XTEN sequence is rendered non-repetitive. Accordingly, in one embodiment, the XTEN-encoding polynucleotides comprise multiple polynucleotides that encode non-repetitive sequences, or motifs, operably linked in frame and in which the resulting expressed XTEN amino acid sequences are non-repetitive.

[00422] In one approach, a construct is first prepared containing the DNA sequence corresponding to XTEN. Exemplary methods for the preparation of such constructs are described in the Examples. The construct is then used to create an expression vector suitable for transforming a host cell, such as a prokaryotic host cell (e.g., E. coli) for the expression and recovery of the XTEN. Exemplary methods for the creation of expression vectors, the tranformation of host cells and the expression and recovery of XTEN are described in the Examples.

[00423] The gene encoding for the XTEN can be made in one or more steps, either fully synthetically or by synthesis combined with enzymatic processes, such as restriction enzyme-mediated cloning, PCR and overlap extension, including methods more fully described in the

Examples. The methods disclosed herein can be used, for example, to ligate short sequences of polynucleotides encoding XTEN into longer XTEN genes of a desired length and sequence. In one embodiment, the method ligates two, three, four or more codon-optimized oligonucleotides encoding XTEN motif or segment sequences of about 9 to 14 amino acids, or about 12 to 20 amino acids, or about 18 to 36 amino acids, or about 48 to about 144 amino acids, or about 144 to about 288 or longer, or any combination of the foregoing ranges of motif or segment lengths. Alternatively, the disclosed method is used to multimerize XTEN-encoding sequences into longer sequences of a desired length; e.g., a gene encoding 36 amino acids of XTEN can be dimerized into a gene encoding 72 amino acids, then 144, then 288, etc. Even with multimerization, XTEN polypeptides can be constructed such that the XTEN-encoding gene has low or virtually no repetitiveness through design of the codons selected for the motifs of the shortest unit being used, which can reduce recombination and increase stability of the encoding gene in the transformed host. Genes encoding XTEN with non-repetitive sequences are assembled from oligonucleotides using standard techniques of gene synthesis. The gene design can be performed using algorithms that optimize codon usage and amino acid composition. In one method of the invention, a library of relatively short XTEN-encoding polynucleotide constructs is created and then assembled, as described above. The resulting genes are then assembled with genes encoding payload peptide or polypeptide, and the resulting genes used to transform a host cell and produce and recover the XTEN-payload for evaluation of its properties, as described herein.

[00424] The resulting polynucleotides encoding the XTEN and the peptide sequences to which it is linked can then be individually cloned into an expression vector. The nucleic acid sequence is inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan. Such techniques are well known in the art and well described in the scientific and patent literature. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage that may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e., a vector, which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s)

into which it has been integrated. Representative plasmids are illustrated in FIG. 17, with encoding regions for different configurations of FVIII and XTEN components portrayed.

[00425] The invention provides for the use of plasmid expression vectors containing replication and control sequences that are compatible with and recognized by the host cell, and are operably linked to the gene encoding the polypeptide for controlled expression of the polypeptide. The vector ordinarily carries a replication site, as well as sequences that encode proteins that are capable of providing phenotypic selection in transformed cells. Such vector sequences are well known for a variety of bacteria, yeast, and viruses. Useful expression vectors that can be used include, for example, segments of chromosomal, non-chromosomal and synthetic DNA sequences. "Expression vector" refers to a DNA construct containing a DNA sequence that is operably linked to a suitable control sequence capable of effecting the expression of the DNA encoding the polypeptide in a suitable host. The requirements are that the vectors are replicable and viable in the host cell of choice. Low- or high-copy number vectors may be used as desired.

[00426] Suitable vectors include, but are not limited to, derivatives of SV40 and pcDNA and known bacterial plasmids such as col EI, pCRl, pBR322, pMal-C2, pET, pGEX as described by Smith, et al., Gene 57:31-40 (1988), pMB9 and derivatives thereof, plasmids such as RP4, phage DNAs such as the numerous derivatives of phage I such as NM98 9, as well as other phage DNA such as M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 micron plasmid or derivatives of the 2m plasmid, as well as centomeric and integrative yeast shuttle vectors; vectors useful in eukaryotic cells such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or the expression control sequences; and the like. Yeast expression systems that can also be used in the present invention include, but are not limited to, the non-fusion pYES2 vector (Invitrogen), the fusion pYESHisA, B, C (Invitrogen), pRS vectors and the like. The control sequences of the vector include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome binding sites, and sequences that control termination of transcription and translation. The promoter may be any DNA sequence, which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell. Promoters suitable for use in expression vectors with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)], all is operably linked to the DNA encoding CFXTEN polypeptides. Promoters for use in bacterial systems can also contain a Shine-Dalgarno (S.D.) sequence, operably linked to the DNA encoding CFXTEN polypeptides..

EXAMPLES

[00427] Example 1: Construction of XTEN_AD36 motif segments

[00428] The following example describes the construction of a collection of codon-optimized genes encoding motif sequences of 36 amino acids. As a first step, a stuffer vector pCW0359 was constructed based on a pET vector and that includes a T7 promoter. pCW0359 encodes a cellulose binding domain (CBD) and a TEV protease recognition site followed by a stuffer sequence that is flanked by BsaI, BbsI, and KpnI sites. The BsaI and BbsI sites were inserted such that they generate compatible overhangs after digestion. The stuffer sequence is followed by a truncated version of the GFP gene and a His tag. The stuffer sequence contains stop codons and thus E. coli cells carrying the stuffer plasmid pCW0359 form non-fluorescent colonies. The stuffer vector pCW0359 was digested with BsaI and KpnI to remove the stuffer segment and the resulting vector fragment was isolated by agarose gel purification. The sequences were designated XTEN_AD36, reflecting the AD family of motifs. Its segments have the amino acid sequence $[X]_3$ where X is a 12mer peptide with the sequences: GESPGGSSGSES, GSEGSSGPGESS, GSSESGSSEGGP, or GSGGEPSESGSS. The insert was obtained by annealing the following pairs of phosphorylated synthetic oligonucleotide pairs:

AD1for: AGGTGAATCTCCDGGTGGYTCYAGCGGTTCYGARTC
AD1rev: ACCTGAYTCRGAACCGCTRGARCCACCHGGAGATTC
AD2for: AGGTAGCGAAGGTTCTTCYGGTCCDGGYGARTCYTC
AD2rev: ACCTGARGAYTCRCCHGGACCRGAAGAACCTTCGCT
AD3for: AGGTTCYTCYGAAAGCGGTTCTTCYGARGGYGGTCC
AD3rev: ACCTGGACCRCCYTCRGAAGAACCGCTTTCRGARGA
AD4for: AGGTTCYGGTGGYGAACCDTCYGARTCTGGTAGCTC

[00429] We also annealed the phosphorylated oligonucleotide 3KpnIstopperFor: AGGTTCGTCTTCACTCGAGGGTAC and the non-phosphorylated oligonucleotide pr_3KpnIstopperRev: CCTCGAGTGAAGACGA. The annealed oligonucleotide pairs were ligated, which resulted in a mixture of products with varying length that represents the varying number of 12mer repeats ligated to one BbsI/KpnI segment. The products corresponding to the length of 36 amino acids were isolated from the mixture by preparative agarose gel electrophoresis and ligated into the BsaI/KpnI digested stuffer vector pCW0359. Most of the clones in the resulting library designated LCW0401 showed green fluorescence after induction, which shows that the sequence of XTEN_AD36 had been ligated in frame with the GFP gene and that most sequences of XTEN_AD36 had good expression levels.

[00430] We screened 96 isolates from library LCW0401 for high level of fluorescence by stamping them onto agar plate containing IPTG. The same isolates were evaluated by PCR and 48 isolates were identified that contained segments with 36 amino acids as well as strong

fluorescence. These isolates were sequenced and 39 clones were identified that contained correct XTEN_AD36 segments. The file names of the nucleotide and amino acid constructs for these segments are listed in Table 22.

Table 22: DNA and Amino Acid Sequences for 36-mer motifs

File name	Amino acid sequence	Nucleotide sequence
LCW0401_001_ GFP-N_A01.ab1	GSGGEPSESGSSGESPGG SSGSESGESPGGSSGSES	GGTTCTGGTGGCGAACCGTCCGAGTCTGGTAGC TCAGGTGAATCTCCGGGTGGCTCTAGCGGTTCC GAGTCAGGTGAATCTCCTGGTGGTTCCAGCGGT TCCGAGTCA
LCW0401_002_ GFP-N_B01.ab1	GSEGSSGPGESSGESPGG SSGSESGSSESGSSEGGP	GGTAGCGAAGGTTCTTCTGGTCCTGGCGAGTCT TCAGGTGAATCTCCTGGTGGTTCCAGCGGTTCT GAATCAGGTTCCTCCGAAAGCGGTTCTTCCGAG GGCGGTCCA
LCW0401_003_ GFP-N_C01.ab1	GSSESGSSEGGPGSSESG SSEGGPGESPGGSSGSES	GGTTCCTCTGAAAGCGGTTCTTCCGAAGGTGGT CCAGGTTCCTCTGAAAGCGGTTCTTCTGAGGGT GGTCCAGGTGAATCTCCGGGTGGCTCCAGCGGT TCCGAGTCA
LCW0401_004_ GFP-N_D01.ab1	GSGGEPSESGSSGSSESG SSEGGPGSGGEPSESGSS	GGTTCCGGTGGCGAACCGTCTGAATCTGGTAGC TCAGGTTCTTCTGAAAGCGGTTCTTCCGAGGGT GGTCCAGGTTCTGGTGGTGAACCTTCCGAGTCT GGTAGCTCA
LCW0401_007_ GFP-N_F01.ab1	GSSESGSSEGGPGSEGSS GPGESSGSEGSSGPGESS	GGTTCTTCCGAAAGCGGTTCTTCTGAGGGTGGT CCAGGTAGCGAAGGTTCTTCCGGTCCAGGTGAG TCTTCAGGTAGCGAAGGTTCTTCTGGTCCTGGT GAATCTTCA
LCW0401_008_ GFP-N_G01.ab1	GSSESGSSEGGPGESPGG SSGSESGSEGSSGPGESS	GGTTCCTCTGAAAGCGGTTCTTCCGAGGGTGGT CCAGGTGAATCTCCAGGTGGTTCCAGCGGTTCT GAGTCAGGTAGCGAAGGTTCTTCTGGTCCAGGT GAATCCTCA
LCW0401_012_ GFP-N_H01.ab1	GSGGEPSESGSSGSGGEP SESGSSGSEGSSGPGESS	GGTTCTGGTGGTGAACCGTCTGAGTCTGGTAGC TCAGGTTCCGGTGGCGAACCATCCGAATCTGGT AGCTCAGGTAGCGAAGGTTCTTCCGGTCCAGGT GAGTCTTCA
LCW0401_015_ GFP-N_A02.ab1	GSSESGSSEGGPGSEGSS GPGESSGESPGGSSGSES	GGTTCTTCCGAAAGCGGTTCTTCCGAAGGCGGT CCAGGTAGCGAAGGTTCTTCTGGTCCAGGCGAA TCTTCAGGTGAATCTCCTGGTGGCTCCAGCGGT TCTGAGTCA
LCW0401_016_ GFP-N_B02.ab1	GSSESGSSEGGPGSSESG SSEGGPGSSESGSSEGGP	GGTTCCTCCGAAAGCGGTTCTTCTGAGGGCGGT CCAGGTTCCTCCGAAAGCGGTTCTTCCGAGGGC GGTCCAGGTTCTTCTGAAAGCGGTTCTTCCGAG GGCGGTCCA
LCW0401_020_ GFP-N_E02.ab1	GSGGEPSESGSSGSEGSS GPGESSGSSESGSSEGGP	GGTTCCGGTGGCGAACCGTCCGAATCTGGTAGC TCAGGTAGCGAAGGTTCTTCTGGTCCAGGCGAA TCTTCAGGTTCCTCTGAAAGCGGTTCTTCTGAG GGCGGTCCA
LCW0401_022_ GFP-N_F02.ab1	GSGGEPSESGSSGSSESG SSEGGPGSGGEPSESGSS	GGTTCTGGTGGTGAACCGTCCGAATCTGGTAGC TCAGGTTCTTCCGAAAGCGGTTCTTCTGAAGGT GGTCCAGGTTCCGGTGGCGAACCTTCTGAATCT GGTAGCTCA
LCW0401_024_ GFP-N_G02.ab1	GSGGEPSESGSSGSSESG SSEGGPGESPGGSSGSES	GGTTCTGGTGGCGAACCGTCCGAATCTGGTAGC TCAGGTTCCTCCGAAAGCGGTTCTTCTGAAGGT GGTCCAGGTGAATCTCCAGGTGGTTCTAGCGGT TCTGAATCA
LCW0401_026_ GFP-N_H02.ab1	GSGGEPSESGSSGESPGG SSGSESGSEGSSGPGESS	GGTTCTGGTGGCGAACCGTCTGAGTCTGGTAGC TCAGGTGAATCTCCTGGTGGCTCCAGCGGTTCT GAATCAGGTAGCGAAGGTTCTTCTGGTCCTGGT GAATCTTCA

File name	Amino acid sequence	Nucleotide sequence
LCW0401_027_ GFP-N_A03.ab1	GSGGEPSESGSSGESPGG SSGSESGSGGEPSESGSS	GGTTCCGGTGGCGAACCTTCCGAATCTGGTAGC TCAGGTGAATCTCCGGGTGGTTCTAGCGGTTCT GAGTCAGGTTCTGGTGGTGAACCTTCCGAGTCT GGTAGCTCA
LCW0401_028_ GFP-N_B03.ab1	GSSESGSSEGGPGSSESG SSEGGPGSSESGSSEGGP	GGTTCCTCTGAAAGCGGTTCTTCTGAGGGCGGT CCAGGTTCTTCCGAAAGCGGTTCTTCCGAGGGC GGTCCAGGTTCTTCCGAAAGCGGTTCTTCTGAA GGCGGTCCA
LCW0401_030_ GFP-N_C03.ab1	GESPGGSSGSESGSEGSS GPGESSGSEGSSGPGESS	GGTGAATCTCCGGGTGGCTCCAGCGGTTCTGAG TCAGGTAGCGAAGGTTCTTCCGGTCCGGGTGAG TCCTCAGGTAGCGAAGGTTCTTCCGGTCCTGGT GAGTCTTCA
LCW0401_031_ GFP-N_D03.ab1	GSGGEPSESGSSGSGGEP SESGSSGSSESGSSEGGP	GGTTCTGGTGGCGAACCTTCCGAATCTGGTAGC TCAGGTTCCGGTGGTGAACCTTCTGAATCTGGT AGCTCAGGTTCTTCTGAAAGCGGTTCTTCCGAG GGCGGTCCA
LCW0401_033_ GFP-N_E03.ab1	GSGGEPSESGSSGSGGEP SESGSSGSGGEPSESGSS	GGTTCCGGTGGTGAACCTTCTGAATCTGGTAGC TCAGGTTCCGGTGGCGAACCATCCGAGTCTGGT AGCTCAGGTTCCGGTGGTGAACCATCCGAGTCT GGTAGCTCA
LCW0401_037_ GFP-N_F03.ab1	GSGGEPSESGSSGSSESG SSEGGPGSEGSSGPGESS	GGTTCCGGTGGCGAACCTTCTGAATCTGGTAGC TCAGGTTCCTCCGAAAGCGGTTCTTCTGAGGGC GGTCCAGGTAGCGAAGGTTCTTCTGGTCCGGGC GAGTCTTCA
LCW0401_038_ GFP-N_G03.ab1	GSGGEPSESGSSGSEGSS GPGESSGSGGEPSESGSS	GGTTCCGGTGGTGAACCGTCCGAGTCTGGTAGC TCAGGTAGCGAAGGTTCTTCTGGTCCGGGTGAG TCTTCAGGTTCTGGTGGCGAACCGTCCGAATCT GGTAGCTCA
LCW0401_039_ GFP-N_H03.ab1	GSGGEPSESGSSGESPGG SSGSESGSGGEPSESGSS	GGTTCTGGTGGCGAACCGTCCGAATCTGGTAGC TCAGGTGAATCTCCTGGTGGTTCCAGCGGTTCC GAGTCAGGTTCTGGTGGCGAACCTTCCGAATCT GGTAGCTCA
LCW0401_040_ GFP-N_A04.ab1	GSSESGSSEGGPGSGGEP SESGSSGSSESGSSEGGP	GGTTCTTCCGAAAGCGGTTCTTCCGAGGGCGGT CCAGGTTCCGGTGGTGAACCATCTGAATCTGGT AGCTCAGGTTCTTCTGAAAGCGGTTCTTCTGAA GGTGGTCCA
LCW0401_042_ GFP-N_C04.ab1	GSEGSSGPGESSGESPGG SSGSESGSEGSSGPGESS	GGTAGCGAAGGTTCTTCCGGTCCTGGTGAGTCT TCAGGTGAATCTCCAGGTGGCTCTAGCGGTTCC GAGTCAGGTAGCGAAGGTTCTTCTGGTCCTGGC GAGTCCTCA
LCW0401_046_ GFP-N_D04.ab1	GSSESGSSEGGPGSSESG SSEGGPGSSESGSSEGGP	GGTTCCTCTGAAAGCGGTTCTTCCGAAGGCGGT CCAGGTTCTTCCGAAAGCGGTTCTTCTGAGGGC GGTCCAGGTTCCTCCGAAAGCGGTTCTTCTGAG GGTGGTCCA
LCW0401_047_ GFP-N_E04.ab1	GSGGEPSESGSSGESPGG SSGSESGESPGGSSGSES	GGTTCTGGTGGCGAACCTTCCGAGTCTGGTAGC TCAGGTGAATCTCCGGGTGGTTCTAGCGGTTCC GAGTCAGGTGAATCTCCGGGTGGTTCCAGCGGT TCTGAGTCA
LCW0401_051_ GFP-N_F04.ab1	GSGGEPSESGSSGSEGSS GPGESSGESPGGSSGSES	GGTTCTGGTGGCGAACCATCTGAGTCTGGTAGC TCAGGTAGCGAAGGTTCTTCCGGTCCAGGCGAG TCTTCAGGTGAATCTCCTGGTGGCTCCAGCGGT TCTGAGTCA
LCW0401_053_ GFP-N_H04.ab1	GESPGGSSGSESGESPGG SSGSESGESPGGSSGSES	GGTGAATCTCCTGGTGGTTCCAGCGGTTCCGAG TCAGGTGAATCTCCAGGTGGCTCTAGCGGTTCC GAGTCAGGTGAATCTCCTGGTGGTTCTAGCGGT TCTGAATCA
LCW0401_054_ GFP-N_A05.ab1	GSEGSSGPGESSGSEGSS GPGESSGSGGEPSESGSS	GGTAGCGAAGGTTCTTCCGGTCCAGGTGAATCT TCAGGTAGCGAAGGTTCTTCTGGTCCTGGTGAA

File name	Amino acid sequence	Nucleotide sequence
		TCCTCAGGTTCCGGTGGCGAACCATCTGAATCT GGTAGCTCA
LCW0401_059_ GFP-N_D05.ab1	GSGGEPSESGSSGSEGSS GPGESSGESPGGSSGSES	GGTTCTGGTGGCGAACCATCCGAATCTGGTAGC TCAGGTAGCGAAGGTTCTTCTGGTCCTGGCGAA TCTTCAGGTGAATCTCCAGGTGGCTCTAGCGGT TCCGAATCA
LCW0401_060_ GFP-N_E05.ab1	GSGGEPSESGSSGSSESG SSEGGPGSGGEPSESGSS	GGTTCCGGTGGTGAACCGTCCGAATCTGGTAGC TCAGGTTCCTCTGAAAGCGGTTCTTCCGAGGGT GGTCCAGGTTCCGGTGGTGAACCTTCTGAGTCT GGTAGCTCA
LCW0401_061_ GFP-N_F05.ab1	GSSESGSSEGGPGSGGEP SESGSSGSEGSSGPGESS	GGTTCCTCTGAAAGCGGTTCTTCTGAGGGCGGT CCAGGTTCTGGTGGCGAACCATCTGAATCTGGT AGCTCAGGTAGCGAAGGTTCTTCCGGTCCGGGT GAATCTTCA
LCW0401_063_ GFP-N_H05.ab1	GSGGEPSESGSSGSEGSS GPGESSGSEGSSGPGESS	GGTTCTGGTGGTGAACCGTCCGAATCTGGTAGC TCAGGTAGCGAAGGTTCTTCTGGTCCTGGCGAG TCTTCAGGTAGCGAAGGTTCTTCTGGTCCTGGT GAATCTTCA
LCW0401_066_ GFP-N_B06.ab1	GSGGEPSESGSSGSSESG SSEGGPGSGGEPSESGSS	GGTTCTGGTGGCGAACCATCCGAGTCTGGTAGC TCAGGTTCTTCCGAAAGCGGTTCTTCCGAAGGC GGTCCAGGTTCTGGTGGTGAACCGTCCGAATCT GGTAGCTCA
LCW0401_067_ GFP-N_C06.ab1	GSGGEPSESGSSGESPGG SSGSESGESPGGSSGSES	GGTTCCGGTGGCGAACCTTCCGAATCTGGTAGC TCAGGTGAATCTCCGGGTGGTTCTAGCGGTTCC GAATCAGGTGAATCTCCAGGTGGTTCTAGCGGT TCCGAATCA
LCW0401_069_ GFP-N_D06.ab1	GSGGEPSESGSSGSGGEP SESGSSGESPGGSSGSES	GGTTCCGGTGGTGAACCATCTGAGTCTGGTAGC TCAGGTTCCGGTGGCGAACCGTCCGAGTCTGGT AGCTCAGGTGAATCTCCGGGTGGTTCCAGCGGT TCCGAATCA
LCW0401_070_ GFP-N_E06.ab1	GSEGSSGPGESSGSSESG SSEGGPGSEGSSGPGESS	GGTAGCGAAGGTTCTTCTGGTCCGGGCGAATCC TCAGGTTCCTCCGAAAGCGGTTCTTCCGAAGGT GGTCCAGGTAGCGAAGGTTCTTCCGGTCCTGGT GAATCTTCA
LCW0401_078_ GFP-N_F06.ab1	GSSESGSSEGGPGESPGG SSGSESGESPGGSSGSES	GGTTCCTCTGAAAGCGGTTCTTCTGAAGGCGGT CCAGGTGAATCTCCGGGTGGCTCCAGCGGTTCT GAATCAGGTGAATCTCCTGGTGGCTCCAGCGGT TCCGAGTCA
LCW0401_079_ GFP-N_G06.ab1	GSEGSSGPGESSGSEGSS GPGESSGSGGEPSESGSS	GGTAGCGAAGGTTCTTCTGGTCCAGGCGAGTCT TCAGGTAGCGAAGGTTCTTCCGGTCCTGGCGAG TCTTCAGGTTCCGGTGGCGAACCGTCCGAATCT GGTAGCTCA

[00431] Example 2: Construction of XTEN_AE36 segments

[00432] A codon library encoding XTEN sequences of 36 amino acid length was constructed. The XTEN sequence was designated XTEN_AE36. Its segments have the amino acid sequence $[X]_3$ where X is a 12mer peptide with the sequence: GSPAGSPTSTEE, GSEPATSGSE TP, GTSESA TPESGP, or GTSTEPSEGSAP. The insert was obtained by annealing the following pairs of phosphorylated synthetic oligonucleotide pairs:

AE1for: AGGTAGCCCDGCWGGYTCTCCDACYTCYACYGARGA
AE1rev: ACCTTCYTCRGTRGARGTHGGAGARCCWGCHGGGCT
AE2for: AGGTAGCGAACCKGCWACYTCYGGYTCTGARACYCC
AE2rev: ACCTGGRGTYTCAGARCCRGARGTWGCMGGTTCGCT

AE3for: AGGTACYTCTGAAAGCGCWACYCCKGARTCYGGYCC
AE3rev: ACCTGGRCCRGAYTCMGGRGTWGCGCTTTCAGARGT
AE4for: AGGTACYTCTACYGAACCKTCYGARGGYAGCGCWCC
AE4rev: ACCTGGWGCGCTRCCYTCRGAMGGTTCRGTAGARGT

[00433] We also annealed the phosphorylated oligonucleotide 3KpnIstopperFor: AGGTTCGTCTTCACTCGAGGGTAC and the non-phosphorylated oligonucleotide pr_3KpnIstopperRev: CCTCGAGTGAAGACGA. The annealed oligonucleotide pairs were ligated, which resulted in a mixture of products with varying length that represents the varying number of 12mer repeats ligated to one BbsI/KpnI segment. The products corresponding to the length of 36 amino acids were isolated from the mixture by preparative agarose gel electrophoresis and ligated into the BsaI/KpnI digested stuffer vector pCW0359. Most of the clones in the resulting library designated LCW0402 showed green fluorescence after induction which shows that the sequence of XTEN_AE36 had been ligated in frame with the GFP gene and most sequences of XTEN_AE36 show good expression.

[00434] We screened 96 isolates from library LCW0402 for high level of fluorescence by stamping them onto agar plate containing IPTG. The same isolates were evaluated by PCR and 48 isolates were identified that contained segments with 36 amino acids as well as strong fluorescence. These isolates were sequenced and 37 clones were identified that contained correct XTEN_AE36 segments. The file names of the nucleotide and amino acid constructs for these segments are listed in Table 23.

Table 23: DNA and Amino Acid Sequences for 36-mer motifs

File name	Amino acid sequence	Nucleotide sequence
LCW0402_002_ GFP-N_A07.ab1	GSPAGSPTSTEEGTSE SATPESGPGTSTEPSE GSAP	GGTAGCCCGGCAGGCTCTCCGACCTCTACTGAGGAA GGTACTTCTGAAAGCGCAACCCCGGAGTCCGGCCCA GGTACCTCTACCGAACCGTCTGAGGGCAGCGCACCA
LCW0402_003_ GFP-N_B07.ab1	GTSTEPSEGSAPGTST EPSEGSAPGTSTEPSE GSAP	GGTACTTCTACCGAACCGTCCGAAGGCAGCGCTCCA GGTACCTCTACTGAACCTTCCGAGGGCAGCGCTCCA GGTACCTCTACCGAACCTTCTGAAGGTAGCGCACCA
LCW0402_004_ GFP-N_C07.ab1	GTSTEPSEGSAPGTSE SATPESGPGTSESATP ESGP	GGTACCTCTACCGAACCGTCTGAAGGTAGCGCACCA GGTACCTCTGAAAGCGCAACTCCTGAGTCCGGTCCA GGTACTTCTGAAAGCGCAACCCCGGAGTCTGGCCCA
LCW0402_005_ GFP-N_D07.ab1	GTSTEPSEGSAPGTSE SATPESGPGTSESATP ESGP	GGTACTTCTACTGAACCGTCTGAAGGTAGCGCACCA GGTACTTCTGAAAGCGCAACCCCGGAATCCGGCCCA GGTACCTCTGAAAGCGCAACCCCGGAGTCCGGCCCA
LCW0402_006_ GFP-N_E07.ab1	GSEPATSGSETPGTSE SATPESGPGSPAGSPT STEE	GGTAGCGAACCGGCAACCTCCGGCTCTGAAACCCCA GGTACCTCTGAAAGCGCTACTCCTGAATCCGGCCCA GGTAGCCCGGCAGGTTCTCCGACTTCCACTGAGGAA
LCW0402_008_ GFP-N_F07.ab1	GTSESATPESGPGSEP ATSGSETPGTSTEPSE GSAP	GGTACTTCTGAAAGCGCAACCCCTGAATCCGGTCCA GGTAGCGAACCGGCTACTTCTGGCTCTGAGACTCCA GGTACTTCTACCGAACCGTCCGAAGGTAGCGCACCA
LCW0402_009_ GFP-N_G07.ab1	GSPAGSPTSTEEGSPA GSPTSTEEGSEPATSG SETP	GGTAGCCCGGCTGGCTCTCCAACCTCCACTGAGGAA GGTAGCCCGGCTGGCTCTCCAACCTCCACTGAAGAA GGTAGCGAACCGGCTACCTCCGGCTCTGAAACTCCA
LCW0402_011_ GFP-N_A08.ab1	GSPAGSPTSTEEGTSE SATPESGPGTSTEPSE GSAP	GGTAGCCCGGCTGGCTCTCCTACCTCTACTGAGGAA GGTACTTCTGAAAGCGCTACTCCTGAGTCTGGTCCA GGTACCTCTACTGAACCGTCCGAAGGTAGCGCTCCA

File name	Amino acid sequence	Nucleotide sequence
LCW0402_012_ GFP-N_B08.ab1	GSPAGSPTSTEEGSPA GSPTSTEEGTSTEPSE GSAP	GGTAGCCCTGCTGGCTCTCCGACTTCTACTGAGGAA GGTAGCCCGGCTGGTTCTCCGACTTCTACTGAGGAA GGTACTTCTACCGAACCTTCCGAAGGTAGCGCTCCA
LCW0402_013_ GFP-N_C08.ab1	GTSESATPESGPGTST EPSEGSAPGTSTEPSE GSAP	GGTACTTCTGAAAGCGCTACTCCGGAGTCCGGTCCA GGTACCTCTACCGAACCGTCCGAAGGCAGCGCTCCA GGTACTTCTACTGAACCTTCTGAGGGTAGCGCTCCA
LCW0402_014_ GFP-N_D08.ab1	GTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSE GSAP	GGTACCTCTACCGAACCTTCCGAAGGTAGCGCTCCA GGTAGCCCGGCAGGTTCTCCTACTTCCACTGAGGAA GGTACTTCTACCGAACCTTCTGAGGGTAGCGCACCA
LCW0402_015_ GFP-N_E08.ab1	GSEPATSGSETPGSPA GSPTSTEEGTSESATP ESGP	GGTAGCGAACCGGCTACTTCCGGCTCTGAGACTCCA GGTAGCCCTGCTGGCTCTCCGACCTCTACCGAAGAA GGTACCTCTGAAAGCGCTACCCCTGAGTCTGGCCCA
LCW0402_016_ GFP-N_F08.ab1	GTSTEPSEGSAPGTSE SATPESGPGTSESATP ESGP	GGTACTTCTACCGAACCTTCCGAGGGCAGCGCACCA GGTACTTCTGAAAGCGCTACCCCTGAGTCCGGCCCA GGTACTTCTGAAAGCGCTACTCCTGAATCCGGTCCA
LCW0402_020_ GFP-N_G08.ab1	GTSTEPSEGSAPGSEP ATSGSETPGSPAGSPT STEE	GGTACTTCTACTGAACCGTCTGAAGGCAGCGCACCA GGTAGCGAACCGGCTACTTCCGGTTCTGAAACCCCA GGTAGCCCAGCAGGTTCTCCAACTTCTACTGAAGAA
LCW0402_023_ GFP-N_A09.ab1	GSPAGSPTSTEEGTSE SATPESGPGSEPATSG SETP	GGTAGCCCTGCTGGCTCTCCAACCTCCACCGAAGAA GGTACCTCTGAAAGCGCAACCCCTGAATCCGGCCCA GGTAGCGAACCGGCAACCTCCGGTTCTGAAACCCCA
LCW0402_024_ GFP-N_B09.ab1	GTSESATPESGPGSPA GSPTSTEEGSPAGSPT STEE	GGTACTTCTGAAAGCGCTACTCCTGAGTCCGGCCCA GGTAGCCCGGCTGGCTCTCCGACTTCCACCGAGGAA GGTAGCCCGGCTGGCTCTCCAACTTCTACTGAAGAA
LCW0402_025_ GFP-N_C09.ab1	GTSTEPSEGSAPGTSE SATPESGPGTSTEPSE GSAP	GGTACCTCTACTGAACCTTCTGAGGGCAGCGCTCCA GGTACTTCTGAAAGCGCTACCCCGGAGTCCGGTCCA GGTACTTCTACTGAACCGTCCGAAGGTAGCGCACCA
LCW0402_026_ GFP-N_D09.ab1	GSPAGSPTSTEEGTST EPSEGSAPGSEPATSG SETP	GGTAGCCCGGCAGGCTCTCCGACTTCCACCGAGGAA GGTACCTCTACTGAACCTTCTGAGGGTAGCGCTCCA GGTAGCGAACCGGCAACCTCTGGCTCTGAAACCCCA
LCW0402_027_ GFP-N_E09.ab1	GSPAGSPTSTEEGTST EPSEGSAPGTSTEPSE GSAP	GGTAGCCCAGCAGGCTCTCCGACTTCCACTGAGGAA GGTACTTCTACTGAACCTTCCGAAGGCAGCGCACCA GGTACCTCTACTGAACCTTCTGAGGGCAGCGCTCCA
LCW0402_032_ GFP-N_H09.ab1	GSEPATSGSETPGTSE SATPESGPGSPAGSPT STEE	GGTAGCGAACCTGCTACCTCCGGTTCTGAAACCCCA GGTACCTCTGAAAGCGCAACTCCGGAGTCTGGTCCA GGTAGCCCTGCAGGTTCTCCTACCTCCACTGAGGAA
LCW0402_034_ GFP-N_A10.ab1	GTSESATPESGPGTST EPSEGSAPGTSTEPSE GSAP	GGTACCTCTGAAAGCGCTACTCCGGAGTCTGGCCCA GGTACCTCTACTGAACCGTCTGAGGGTAGCGCTCCA GGTACTTCTACTGAACCGTCCGAAGGTAGCGCACCA
LCW0402_036_ GFP-N_C10.ab1	GSPAGSPTSTEEGTST EPSEGSAPGTSTEPSE GSAP	GGTAGCCCGGCTGGTTCTCCGACTTCCACCGAGGAA GGTACCTCTACTGAACCTTCTGAGGGTAGCGCTCCA GGTACCTCTACTGAACCTTCCGAAGGCAGCGCTCCA
LCW0402_039_ GFP-N_E10.ab1	GTSTEPSEGSAPGTST EPSEGSAPGTSTEPSE GSAP	GGTACTTCTACCGAACCGTCCGAGGGCAGCGCTCCA GGTACTTCTACTGAACCTTCTGAAGGCAGCGCTCCA GGTACTTCTACTGAACCTTCCGAAGGTAGCGCACCA
LCW0402_040_ GFP-N_F10.ab1	GSEPATSGSETPGTSE SATPESGPGTSTEPSE GSAP	GGTAGCGAACCTGCAACCTCTGGCTCTGAAACCCCA GGTACCTCTGAAAGCGCTACTCCTGAATCTGGCCCA GGTACTTCTACTGAACCGTCCGAGGGCAGCGCACCA
LCW0402_041_ GFP-N_G10.ab1	GTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSE GSAP	GGTACTTCTACCGAACCGTCCGAGGGTAGCGCACCA GGTAGCCCAGCAGGTTCTCCTACCTCCACCGAGGAA GGTACTTCTACCGAACCGTCCGAGGGTAGCGCACCA
LCW0402_050_ GFP-N_A11.ab1	GSEPATSGSETPGTSE SATPESGPGSEPATSG SETP	GGTAGCGAACCGGCAACCTCCGGCTCTGAAACTCCA GGTACTTCTGAAAGCGCTACTCCGGAATCCGGCCCA GGTAGCGAACCGGCTACTTCCGGCTCTGAAACCCCA
LCW0402_051_ GFP-N_B11.ab1	GSEPATSGSETPGTSE SATPESGPGSEPATSG SETP	GGTAGCGAACCGGCAACTTCCGGCTCTGAAACCCCA GGTACTTCTGAAAGCGCTACTCCTGAGTCTGGCCCA GGTAGCGAACCTGCTACCTCTGGCTCTGAAACCCCA
LCW0402_059_	GSEPATSGSETPGSEP	GGTAGCGAACCGGCAACCTCTGGCTCTGAAACTCCA

File name	Amino acid sequence	Nucleotide sequence
GFP-N_E11.ab1	ATSGSETPGTSTEPSE GSAP	GGTAGCGAACCTGCAACCTCCGGCTCTGAAACCCCA GGTACTTCTACTGAACCTTCTGAGGGCAGCGCACCA
LCW0402_060_ GFP-N_F11.ab1	GTSESATPESGPGSEP ATSGSETPGSEPATSG SETP	GGTACTTCTGAAAGCGCTACCCCGGAATCTGGCCCA GGTAGCGAACCGGCTACTTCTGGTTCTGAAACCCCA GGTAGCGAACCGGCTACCTCCGGTTCTGAAACTCCA
LCW0402_061_ GFP-N_G11.ab1	GTSTEPSEGSAPGTST EPSEGSAPGTSESATP ESGP	GGTACCTCTACTGAACCTTCCGAAGGCAGCGCTCCA GGTACCTCTACCGAACCGTCCGAGGGCAGCGCACCA GGTACTTCTGAAAGCGCAACCCCTGAATCCGGTCCA
LCW0402_065_ GFP-N_A12.ab1	GSEPATSGSETPGTSE SATPESGPGTSESATP ESGP	GGTAGCGAACCGGCAACCTCTGGCTCTGAAACCCCA GGTACCTCTGAAAGCGCTACTCCGGAATCTGGTCCA GGTACTTCTGAAAGCGCTACTCCGGAATCCGGTCCA
LCW0402_066_ GFP-N_B12.ab1	GSEPATSGSETPGSEP ATSGSETPGTSTEPSE GSAP	GGTAGCGAACCTGCTACCTCCGGCTCTGAAACTCCA GGTAGCGAACCGGCTACTTCCGGTTCTGAAACTCCA GGTACCTCTACCGAACCTTCCGAAGGCAGCGCACCA
LCW0402_067_ GFP-N_C12.ab1	GSEPATSGSETPGTST EPSEGSAPGSEPATSG SETP	GGTAGCGAACCTGCTACTTCTGGTTCTGAAACTCCA GGTACTTCTACCGAACCGTCCGAGGGTAGCGCTCCA GGTAGCGAACCTGCTACTTCTGGTTCTGAAACTCCA
LCW0402_069_ GFP-N_D12.ab1	GTSTEPSEGSAPGTST EPSEGSAPGSEPATSG SETP	GGTACCTCTACCGAACCGTCCGAGGGTAGCGCACCA GGTACCTCTACTGAACCGTCTGAGGGTAGCGCTCCA GGTAGCGAACCGGCAACCTCCGGTTCTGAAACTCCA
LCW0402_073_ GFP-N_F12.ab1	GTSTEPSEGSAPGSEP ATSGSETPGSPAGSPT STEE	GGTACTTCTACTGAACCTTCCGAAGGTAGCGCTCCA GGTAGCGAACCTGCTACTTCTGGTTCTGAAACCCCA GGTAGCCCGGCTGGCTCTCCGACCTCCACCGAGGAA
LCW0402_074_ GFP-N_G12.ab1	GSEPATSGSETPGSPA GSPTSTEEGTSESATP ESGP	GGTAGCGAACCGGCTACTTCCGGCTCTGAGACTCCA GGTAGCCCAGCTGGTTCTCCAACCTCTACTGAGGAA GGTACTTCTGAAAGCGCTACCCCTGAATCTGGTCCA
LCW0402_075_ GFP-N_H12.ab1	GTSESATPESGPGSEP ATSGSETPGTSESATP ESGP	GGTACCTCTGAAAGCGCAACTCCTGAGTCTGGCCCA GGTAGCGAACCTGCTACCTCCGGCTCTGAGACTCCA GGTACCTCTGAAAGCGCAACCCCCGGAATCTGGTCCA

[00435] Example 3: Construction of XTEN_AF36 segments

[00436] A codon library encoding sequences of 36 amino acid length was constructed. The sequences were designated XTEN_AF36. Its segments have the amino acid sequence [X]3 where X is a 12mer peptide with the sequence: GSTSESPSGTAP, GTSTPESGSASP, GTSPSGESSTAP, or GSTSSTAESPGP. The insert was obtained by annealing the following pairs of phosphorylated synthetic oligonucleotide pairs:

AF1for: AGGTTCTACYAGCGAATCYCCKTCTGGYACYGCWCC
AF1rev: ACCTGGWGCRGTRCCAGAMGGRGATTCGCTRGTAGA
AF2for: AGGTACYTCTACYCCKGAAAGCGGYTCYGCWTCTCC
AF2rev: ACCTGGAGAWGCRGARCCGCTTTCMGGRGTAGARGT
AF3for: AGGTACYTCYCCKAGCGGYGAATCTTCTACYGCWCC
AF3rev: ACCTGGWGCRGTAGAAGATTCRCCGCTMGGRGARGT
AF4for: AGGTTCYACYAGCTCTACYGCWGAATCTCCKGGYCC
AF4rev: ACCTGGRCCMGGAGATTCWGCRGTAGAGCTRGTRGA

[00437] We also annealed the phosphorylated oligonucleotide 3KpnIstopperFor: AGGTTCGTCTTCACTCGAGGGTAC and the non-phosphorylated oligonucleotide pr_3KpnIstopperRev: CCTCGAGTGAAGACGA. The annealed oligonucleotide pairs were ligated, which resulted in a mixture of products with varying length that represents the varying

number of 12mer repeats ligated to one BbsI/KpnI segment The products corresponding to the length of 36 amino acids were isolated from the mixture by preparative agarose gel electrophoresis and ligated into the BsaI/KpnI digested stuffer vector pCW0359. Most of the clones in the resulting library designated LCW0403 showed green fluorescence after induction which shows that the sequence of XTEN_AF36 had been ligated in frame with the GFP gene and most sequences of XTEN_AF36 show good expression.

[00438] We screened 96 isolates from library LCW0403 for high level of fluorescence by stamping them onto agar plate containing IPTG. The same isolates were evaluated by PCR and 48 isolates were identified that contained segments with 36 amino acids as well as strong fluorescence. These isolates were sequenced and 44 clones were identified that contained correct XTEN_AF36 segments. The file names of the nucleotide and amino acid constructs for these segments are listed in Table 24.

Table 24: DNA and Amino Acid Sequences for 36-mer motifs

File name	Amino acid sequence	Nucleotide sequence
LCW0403_004_ GFP-N_A01.ab1	GTSTPESGSASPGTSP SGESSTAPGTSPSGES STAP	GGTACTTCTACTCCGGAAAGCGGTTCCGCATCTCCA GGTACTTCTCCTAGCGGTGAATCTTCTACTGCTCCAG GTACCTCTCCTAGCGGCGAATCTTCTACTGCTCCA
LCW0403_005_ GFP-N_B01.ab1	GTSPSGESSTAPGSTS STAESPGPGTSPSGES STAP	GGTACTTCTCCGAGCGGTGAATCTTCTACCGCACCA GGTTCTACTAGCTCTACCGCTGAATCTCCGGGCCCAG GTACTTCTCCGAGCGGTGAATCTTCTACTGCTCCA
LCW0403_006_ GFP-N_C01.ab1	GSTSSTAESPGPGTSP SGESSTAPGTSTPESG SASP	GGTTCCACCAGCTCTACTGCTGAATCTCCTGGTCCAG GTACCTCTCCTAGCGGTGAATCTTCTACTGCTCCAGG TACTTCTACTCCTGAAAGCGGCTCTGCTTCTCCA
LCW0403_007_ GFP-N_D01.ab1	GSTSSTAESPGPGSTS STAESPGPGTSPSGES STAP	GGTTCTACCAGCTCTACTGCAGAATCTCCTGGCCCAG GTTCCACCAGCTCTACCGCAGAATCTCCGGGTCCAG GTACTTCCCCTAGCGGTGAATCTTCTACCGCACCA
LCW0403_008_ GFP-N_E01.ab1	GSTSSTAESPGPGTSP SGESSTAPGTSTPESG SASP	GGTTCTACTAGCTCTACTGCTGAATCTCCTGGCCCAG GTACTTCTCCTAGCGGTGAATCTTCTACCGCTCCAGG TACCTCTACTCCGGAAAGCGGTTCTGCATCTCCA
LCW0403_010_ GFP-N_F01.ab1	GSTSSTAESPGPGTST PESGSASPGSTSESPS GTAP	GGTTCTACCAGCTCTACCGCAGAATCTCCTGGTCCAG GTACCTCTACTCCGGAAAGCGGCTCTGCATCTCCAG GTTCTACTAGCGAATCTCCTTCTGGCACTGCACCA
LCW0403_011_ GFP-N_G01.ab1	GSTSSTAESPGPGTST PESGSASPGTSTPESG SASP	GGTTCTACTAGCTCTACTGCAGAATCTCCTGGCCCAG GTACCTCTACTCCGGAAAGCGGCTCTGCATCTCCAG GTACTTCTACCCCTGAAAGCGGTTCTGCATCTCCA
LCW0403_012_ GFP-N_H01.ab1	GSTSESPSGTAPGTSP SGESSTAPGSTSESPS GTAP	GGTTCTACCAGCGAATCTCCTTCTGGCACCGCTCCAG GTACCTCTCCTAGCGGCGAATCTTCTACCGCTCCAGG TTCTACTAGCGAATCTCCTTCTGGCACTGCACCA
LCW0403_013_ GFP-N_A02.ab1	GSTSSTAESPGPGSTS STAESPGPGTSPSGES STAP	GGTTCCACCAGCTCTACTGCAGAATCTCCGGGCCCA GGTTCTACTAGCTCTACTGCAGAATCTCCGGGTCCAG GTACTTCTCCTAGCGGCGAATCTTCTACCGCTCCA
LCW0403_014_ GFP-N_B02.ab1	GSTSSTAESPGPGTST PESGSASPGSTSESPS GTAP	GGTTCCACTAGCTCTACTGCAGAATCTCCTGGCCCAG GTACCTCTACCCCTGAAAGCGGCTCTGCATCTCCAG GTTCTACCAGCGAATCCCCGTCTGGCACCGCACCA
LCW0403_015_ GFP-N_C02.ab1	GSTSSTAESPGPGSTS STAESPGPGTSPSGES STAP	GGTTCTACTAGCTCTACTGCTGAATCTCCGGGTCCAG GTTCTACCAGCTCTACTGCTGAATCTCCTGGTCCAGG TACCTCCCCGAGCGGTGAATCTTCTACTGCACCA
LCW0403_017_ GFP-N_D02.ab1	GSTSSTAESPGPGSTS ESPSGTAPGSTSSTAE SPGP	GGTTCTACCAGCTCTACCGCTGAATCTCCTGGCCCAG GTTCTACCAGCGAATCCCCGTCTGGCACCGCACCAG GTTCTACTAGCTCTACCGCTGAATCTCCGGGTCCA

File name	Amino acid sequence	Nucleotide sequence
LCW0403_018_ GFP-N_E02.ab1	GSTSSTAESPGPGSTS STAESPGPGSTSSTAE SPGP	GGTTCTACCAGCTCTACCGCAGAATCTCCTGGCCCA GGTTCCACTAGCTCTACCGCTGAATCTCCTGGTCCAG GTTCTACTAGCTCTACCGCTGAATCTCCTGGTCCA
LCW0403_019_ GFP-N_F02.ab1	GSTSESPSGTAPGSTS STAESPGPGSTSSTAE SPGP	GGTTCTACTAGCGAATCCCCTTCTGGTACTGCTCCAG GTTCCACTAGCTCTACCGCTGAATCTCCTGGCCCAGG TTCCACTAGCTCTACTGCAGAATCTCCTGGTCCA
LCW0403_023_ GFP-N_H02.ab1	GSTSESPSGTAPGSTS ESPSGTAPGSTSESPS GTAP	GGTTCTACTAGCGAATCTCCTTCTGGTACCGCTCCAG GTTCTACCAGCGAATCCCCGTCTGGTACTGCTCCAGG TTCTACCAGCGAATCTCCTTCTGGTACTGCACCA
LCW0403_024_ GFP-N_A03.ab1	GSTSSTAESPGPGSTS STAESPGPGSTSSTAE SPGP	GGTTCCACCAGCTCTACTGCTGAATCTCCTGGCCCAG GTTCTACCAGCTCTACTGCTGAATCTCCGGGCCCAGG TTCCACCAGCTCTACCGCTGAATCTCCGGGTCCA
LCW0403_025_ GFP-N_B03.ab1	GSTSSTAESPGPGSTS STAESPGPGTSPSGES STAP	GGTTCCACTAGCTCTACCGCAGAATCTCCTGGTCCAG GTTCTACTAGCTCTACTGCTGAATCTCCGGGTCCAGG TACCTCCCCTAGCGGCGAATCTTCTACCGCTCCA
LCW0403_028_ GFP-N_D03.ab1	GSSPSASTGTGPGSST PSGATGSPGSSTPSGA TGSP	GGTTCTAGCCCTTCTGCTTCCACCGGTACCGGCCCAG GTAGCTCTACTCCGTCTGGTGCAACTGGCTCTCCAGG TAGCTCTACTCCGTCTGGTGCAACCGGCTCCCCA
LCW0403_029_ GFP-N_E03.ab1	GTSPSGESSTAPGTST PESGSASPGSTSSTAE SPGP	GGTACTTCCCCTAGCGGTGAATCTTCTACTGCTCCAG GTACCTCTACTCCGGAAAGCGGCTCCGCATCTCCAG GTTCTACTAGCTCTACTGCTGAATCTCCTGGTCCA
LCW0403_030_ GFP-N_F03.ab1	GSTSSTAESPGPGSTS STAESPGPGTSTPESG SASP	GGTTCTACTAGCTCTACCGCTGAATCTCCGGGTCCAG GTTCTACCAGCTCTACTGCAGAATCTCCTGGCCCAGG TACTTCTACTCCGGAAAGCGGTTCCGCTTCTCCA
LCW0403_031_ GFP-N_G03.ab1	GTSPSGESSTAPGSTS STAESPGPGTSTPESG SASP	GGTACTTCTCCTAGCGGTGAATCTTCTACCGCTCCAG GTTCTACCAGCTCTACTGCTGAATCTCCTGGCCCAGG TACTTCTACCCCGGAAAGCGGCTCCGCTTCTCCA
LCW0403_033_ GFP-N_H03.ab1	GSTSESPSGTAPGSTS STAESPGPGSTSSTAE SPGP	GGTTCTACTAGCGAATCCCCTTCTGGTACTGCACCAG GTTCTACCAGCTCTACTGCTGAATCTCCGGGCCCAGG TTCCACCAGCTCTACCGCAGAATCTCCTGGTCCA
LCW0403_035_ GFP-N_A04.ab1	GSTSSTAESPGPGSTS ESPSGTAPGSTSSTAE SPGP	GGTTCCACCAGCTCTACCGCTGAATCTCCGGGCCCA GGTTCTACCAGCGAATCCCCTTCTGGCACTGCACCA GGTTCTACTAGCTCTACCGCAGAATCTCCGGGCCCA
LCW0403_036_ GFP-N_B04.ab1	GSTSSTAESPGPGTSP SGESSTAPGTSTPESG SASP	GGTTCTACCAGCTCTACTGCTGAATCTCCGGGTCCAG GTACTTCCCCGAGCGGTGAATCTTCTACTGCACCAG GTACTTCTACTCCGGAAAGCGGTTCCGCTTCTCCA
LCW0403_039_ GFP-N_C04.ab1	GSTSESPSGTAPGSTS ESPSGTAPGTSPSGES STAP	GGTTCTACCAGCGAATCTCCTTCTGGCACCGCTCCAG GTTCTACTAGCGAATCCCCGTCTGGTACCGCACCAG GTACTTCTCCTAGCGGCGAATCTTCTACCGCACCA
LCW0403_041_ GFP-N_D04.ab1	GSTSESPSGTAPGSTS ESPSGTAPGTSTPESG SASP	GGTTCTACCAGCGAATCCCCTTCTGGTACTGCTCCAG GTTCTACCAGCGAATCCCCTTCTGGCACCGCACCAG GTACTTCTACCCCTGAAAGCGGCTCCGCTTCTCCA
LCW0403_044_ GFP-N_E04.ab1	GTSTPESGSASPGSTS STAESPGPGSTSSTAE SPGP	GGTACCTCTACTCCTGAAAGCGGTTCTGCATCTCCAG GTTCCACTAGCTCTACCGCAGAATCTCCGGGCCCAG GTTCTACTAGCTCTACTGCTGAATCTCCTGGCCCA
LCW0403_046_ GFP-N_F04.ab1	GSTSESPSGTAPGSTS ESPSGTAPGTSPSGES STAP	GGTTCTACCAGCGAATCCCCTTCTGGCACTGCACCA GGTTCTACTAGCGAATCCCCTTCTGGTACCGCACCAG GTACTTCTCCGAGCGGCGAATCTTCTACTGCTCCA
LCW0403_047_ GFP-N_G04.ab1	GSTSSTAESPGPGSTS STAESPGPGSTSESPS GTAP	GGTTCTACTAGCTCTACCGCTGAATCTCCTGGCCCAG GTTCCACTAGCTCTACCGCAGAATCTCCGGGCCCAG GTTCTACTAGCGAATCCCCTTCTGGTACCGCTCCA
LCW0403_049_ GFP-N_H04.ab1	GSTSSTAESPGPGSTS STAESPGPGTSTPESG SASP	GGTTCCACCAGCTCTACTGCAGAATCTCCTGGCCCA GGTTCTACTAGCTCTACCGCAGAATCTCCTGGTCCAG GTACCTCTACTCCTGAAAGCGGTTCCGCATCTCCA
LCW0403_051_ GFP-N_A05.ab1	GSTSSTAESPGPGSTS STAESPGPGSTSESPS GTAP	GGTTCTACTAGCTCTACTGCTGAATCTCCGGGCCCAG GTTCTACTAGCTCTACCGCTGAATCTCCGGGTCCAGG TTCTACTAGCGAATCTCCTTCTGGTACCGCTCCA
LCW0403_053_	GTSPSGESSTAPGSTS	GGTACCTCCCCGAGCGGTGAATCTTCTACTGCACCA

File name	Amino acid sequence	Nucleotide sequence
GFP-N_B05.ab1	ESPSGTAPGSTSSTAE SPGP	GGTTCTACTAGCGAATCCCCTTCTGGTACTGCTCCAG GTTCCACCAGCTCTACTGCAGAATCTCCGGGTCCA
LCW0403_054_ GFP-N_C05.ab1	GSTSESPSGTAPGTSP SGESSTAPGSTSSTAE SPGP	GGTTCTACTAGCGAATCCCCGTCTGGTACTGCTCCAG GTACTTCCCCTAGCGGTGAATCTTCTACTGCTCCAGG TTCTACCAGCTCTACCGCAGAATCTCCGGGTCCA
LCW0403_057_ GFP-N_D05.ab1	GSTSSTAESPGPGSTS ESPSGTAPGTSPSGES STAP	GGTTCTACCAGCTCTACCGCTGAATCTCCTGGCCCAG GTTCTACTAGCGAATCTCCGTCTGGCACCGCACCAG GTACTTCCCCTAGCGGTGAATCTTCTACTGCACCA
LCW0403_058_ GFP-N_E05.ab1	GSTSESPSGTAPGSTS ESPSGTAPGTSTPESG SASP	GGTTCTACTAGCGAATCTCCTTCTGGCACTGCACCAG GTTCTACCAGCGAATCTCCGTCTGGCACTGCACCAG GTACCTCTACCCCTGAAAGCGGTTCCGCTTCTCCA
LCW0403_060_ GFP-N_F05.ab1	GTSTPESGSASPGSTS ESPSGTAPGSTSSTAE SPGP	GGTACCTCTACTCCGGAAAGCGGTTCCGCATCTCCA GGTTCTACCAGCGAATCCCCGTCTGGCACCGCACCA GGTTCTACTAGCTCTACTGCTGAATCTCCGGGCCCA
LCW0403_063_ GFP-N_G05.ab1	GSTSSTAESPGPGTSP SGESSTAPGTSPSGES STAP	GGTTCTACTAGCTCTACTGCAGAATCTCCGGGCCCA GGTACCTCTCCTAGCGGTGAATCTTCTACCGCTCCAG GTACTTCTCCGAGCGGTGAATCTTCTACCGCTCCA
LCW0403_064_ GFP-N_H05.ab1	GTSPSGESSTAPGTSP SGESSTAPGTSPSGES STAP	GGTACCTCCCCTAGCGGCGAATCTTCTACTGCTCCAG GTACCTCTCCTAGCGGCGAATCTTCTACCGCTCCAGG TACCTCCCCTAGCGGTGAATCTTCTACCGCACCA
LCW0403_065_ GFP-N_A06.ab1	GSTSSTAESPGPGTST PESGSASPGSTSESPS GTAP	GGTTCCACTAGCTCTACTGCTGAATCTCCTGGCCCAG GTACTTCTACTCCGGAAAGCGGTTCCGCTTCTCCAGG TTCTACTAGCGAATCTCCGTCTGGCACCGCACCA
LCW0403_066_ GFP-N_B06.ab1	GSTSESPSGTAPGTSP SGESSTAPGTSPSGES STAP	GGTTCTACTAGCGAATCTCCGTCTGGCACTGCTCCAG GTACTTCTCCTAGCGGTGAATCTTCTACCGCTCCAGG TACTTCCCCTAGCGGCGAATCTTCTACCGCTCCA
LCW0403_067_ GFP-N_C06.ab1	GSTSESPSGTAPGTST PESGSASPGSTSSTAE SPGP	GGTTCTACTAGCGAATCTCCTTCTGGTACCGCTCCAG GTACTTCTACCCCTGAAAGCGGCTCCGCTTCTCCAGG TTCCACTAGCTCTACCGCTGAATCTCCGGGTCCA
LCW0403_068_ GFP-N_D06.ab1	GSTSSTAESPGPGSTS STAESPGPGSTSESPS GTAP	GGTTCCACTAGCTCTACTGCTGAATCTCCTGGCCCAG GTTCTACCAGCTCTACCGCTGAATCTCCTGGCCCAGG TTCTACCAGCGAATCTCCGTCTGGCACCGCACCA
LCW0403_069_ GFP-N_E06.ab1	GSTSESPSGTAPGTST PESGSASPGTSTPESG SASP	GGTTCTACTAGCGAATCCCCGTCTGGTACCGCACCA GGTACTTCTACCCCGGAAAGCGGCTCTGCTTCTCCAG GTACTTCTACCCCGGAAAGCGGCTCCGCATCTCCA
LCW0403_070_ GFP-N_F06.ab1	GSTSESPSGTAPGTST PESGSASPGTSTPESG SASP	GGTTCTACTAGCGAATCCCCGTCTGGTACTGCTCCAG GTACTTCTACTCCTGAAAGCGGTTCCGCTTCTCCAGG TACCTCTACTCCGGAAAGCGGTTCTGCATCTCCA

[00439] Example 4: Construction of XTEN_AG36 segments

[00440] A codon library encoding sequences of 36 amino acid length was constructed. The sequences were designated XTEN_AG36. Its segments have the amino acid sequence $[X]_3$ where X is a 12mer peptide with the sequence: GTPGSGTASSSP, GSSTPSGATGSP, GSSPSASTGTGP, or GASPGTSSTGSP. The insert was obtained by annealing the following pairs of phosphorylated synthetic oligonucleotide pairs:

AG1for: AGGTACYCCKGGYAGCGGTACYGCWTCTTCYTCTCC
AG1rev: ACCTGGAGARGAAGAWGCRGTACCGCTRCCMGGRGT
AG2for: AGGTAGCTCTACYCCKTCTGGTGCWACYGGYTCYCC
AG2rev: ACCTGGRGARCCRGTWGCACCAGAMGGRGTAGAGCT
AG3for: AGGTTCTAGCCCKTCTGCWTCYACYGGTACYGGYCC
AG3rev: ACCTGGRCCRGTACCRGTRGAWGCAGAMGGGCTAGA
AG4for: AGGTGCWTCYCCKGGYACYAGCTCTACYGGTTCTCC

AG4rev: ACCTGGAGAACCRGTAGAGCTRGTRCCMGGRGAWGC

[00441] We also annealed the phosphorylated oligonucleotide 3KpnIstopperFor: AGGTTCGTCTTCACTCGAGGGTAC and the non-phosphorylated oligonucleotide pr_3KpnIstopperRev: CCTCGAGTGAAGACGA. The annealed oligonucleotide pairs were ligated, which resulted in a mixture of products with varying length that represents the varying number of 12mer repeats ligated to one BbsI/KpnI segment. The products corresponding to the length of 36 amino acids were isolated from the mixture by preparative agarose gel electrophoresis and ligated into the BsaI/KpnI digested stuffer vector pCW0359. Most of the clones in the resulting library designated LCW0404 showed green fluorescence after induction which shows that the sequence of XTEN_AG36 had been ligated in frame with the GFP gene and most sequences of XTEN_AG36 show good expression.

[00442] We screened 96 isolates from library LCW0404 for high level of fluorescence by stamping them onto agar plate containing IPTG. The same isolates were evaluated by PCR and 48 isolates were identified that contained segments with 36 amino acids as well as strong fluorescence. These isolates were sequenced and 44 clones were identified that contained correct XTEN_AG36 segments. The file names of the nucleotide and amino acid constructs and the sequences for these segments are listed in Table 25.

Table 25: DNA and Amino Acid Sequences for 36-mer motifs

File name	Amino acid sequence	Nucleotide sequence
LCW0404_001_ GFP-N_A07.ab1	GASPGTSSTGSPGTPG SGTASSSPGSSTPSGA TGSP	GGTGCATCCCCGGGCACTAGCTCTACCGGTTCTCCA GGTACTCCTGGTAGCGGTACTGCTTCTTCTTCTCCAG GTAGCTCTACTCCTTCTGGTGCTACTGGTTCTCCA
LCW0404_003_ GFP-N_B07.ab1	GSSTPSGATGSPGSSP SASTGTGPGSSTPSGA TGSP	GGTAGCTCTACCCCTTCTGGTGCTACCGGCTCTCCAG GTTCTAGCCCGTCTGCTTCTACCGGTACCGGTCCAGG TAGCTCTACCCCTTCTGGTGCTACTGGTTCTCCA
LCW0404_006_ GFP-N_C07.ab1	GASPGTSSTGSPGSSP SASTGTGPGSSTPSGA TGSP	GGTGCATCTCCGGGTACTAGCTCTACCGGTTCTCCAG GTTCTAGCCCTTCTGCTTCCACTGGTACCGGCCCAGG TAGCTCTACCCCGTCTGGTGCTACTGGTTCCCCA
LCW0404_007_ GFP-N_D07.ab1	GTPGSGTASSSPGSST PSGATGSPGASPGTSS TGSP	GGTACTCCGGGCAGCGGTACTGCTTCTTCCTCTCCAG GTAGCTCTACCCCTTCTGGTGCAACTGGTTCCCCAGG TGCATCCCCTGGTACTAGCTCTACCGGTTCTCCA
LCW0404_009_ GFP-N_E07.ab1	GTPGSGTASSSPGASP GTSSTGSPGSRPSAST GTGP	GGTACCCCTGGCAGCGGTACTGCTTCTTCTTCTCCAG GTGCTTCCCCTGGTACCAGCTCTACCGGTTCTCCAGG TTCTAGACCTTCTGCATCCACCGGTACTGGTCCA
LCW0404_011_ GFP-N_F07.ab1	GASPGTSSTGSPGSST PSGATGSPGASPGTSS TGSP	GGTGCATCTCCTGGTACCAGCTCTACCGGTTCTCCAG GTAGCTCTACTCCTTCTGGTGCTACTGGCTCTCCAGG TGCTTCCCCGGGTACCAGCTCTACCGGTTCTCCA
LCW0404_012_ GFP-N_G07.ab1	GTPGSGTASSSPGSST PSGATGSPGSSTPSGA TGSP	GGTACCCCGGGCAGCGGTACCGCATCTTCCTCTCCA GGTAGCTCTACCCCGTCTGGTGCTACCGGTTCCCCAG GTAGCTCTACCCCGTCTGGTGCAACCGGCTCCCCA
LCW0404_014_ GFP-N_H07.ab1	GASPGTSSTGSPGASP GTSSTGSPGASPGTSS TGSP	GGTGCATCTCCGGGCACTAGCTCTACTGGTTCTCCAG GTGCATCCCCTGGCACTAGCTCTACTGGTTCTCCAGG TGCTTCTCCTGGTACCAGCTCTACTGGTTCTCCA
LCW0404_015_ GFP-N_A08.ab1	GSSTPSGATGSPGSSP SASTGTGPGASPGTSS TGSP	GGTAGCTCTACTCCGTCTGGTGCAACCGGCTCCCCA GGTTCTAGCCCGTCTGCTTCCACTGGTACTGGCCCAG GTGCTTCCCCGGGCACCAGCTCTACTGGTTCTCCA
LCW0404_016_ GFP-N_B08.ab1	GSSTPSGATGSPGSST PSGATGSPGTPGSGT	GGTAGCTCTACTCCTTCTGGTGCTACCGGTTCCCCAG GTAGCTCTACTCCTTCTGGTGCTACTGGTTCCCCAGG

File name	Amino acid sequence	Nucleotide sequence
	ASSSP	TACTCCGGGCAGCGGTACTGCTTCTTCCTCTCCA
LCW0404_017_ GFP-N_C08.ab1	GSSTPSGATGSPGSST PSGATGSPGASPGTSS TGSP	GGTAGCTCTACTCCGTCTGGTGCAACCGGTTCCCCAG GTAGCTCTACTCCTTCTGGTGCTACTGGCTCCCCAGG TGCATCCCCTGGCACCAGCTCTACCGGTTCTCCA
LCW0404_018_ GFP-N_D08.ab1	GTPGSGTASSSPGSSP SASTGTGPGSSTPSGA TGSP	GGTACTCCTGGTAGCGGTACCGCATCTTCCTCTCCAG GTTCTAGCCCTTCTGCATCTACCGGTACCGGTCCAGG TAGCTCTACTCCTTCTGGTGCTACTGGCTCTCCA
LCW0404_023_ GFP-N_F08.ab1	GASPGTSSTGSPGSSP SASTGTGPGTPGSGT ASSSP	GGTGCTTCCCCGGGCACTAGCTCTACCGGTTCTCCAG GTTCTAGCCCTTCTGCATCTACTGGTACTGGCCCAGG TACTCCGGGCAGCGGTACTGCTTCTTCCTCTCCA
LCW0404_025_ GFP-N_G08.ab1	GSSTPSGATGSPGSST PSGATGSPGASPGTSS TGSP	GGTAGCTCTACTCCGTCTGGTGCTACCGGCTCTCCAG GTAGCTCTACCCCTTCTGGTGCAACCGGCTCCCCAGG TGCTTCTCCGGGTACCAGCTCTACTGGTTCTCCA
LCW0404_029_ GFP-N_A09.ab1	GTPGSGTASSSPGSST PSGATGSPGSSPSAST GTGP	GGTACCCCTGGCAGCGGTACCGCTTCTTCCTCTCCAG GTAGCTCTACCCCGTCTGGTGCTACTGGCTCTCCAGG TTCTAGCCCGTCTGCATCTACCGGTACCGGCCCA
LCW0404_030_ GFP-N_B09.ab1	GSSTPSGATGSPGTPG SGTASSSPGTPGSGTA SSSP	GGTAGCTCTACTCCTTCTGGTGCAACCGGCTCCCCAG GTACCCCGGGCAGCGGTACCGCATCTTCCTCTCCAG GTACTCCGGGTAGCGGTACTGCTTCTTCTTCTCCA
LCW0404_031_ GFP-N_C09.ab1	GTPGSGTASSSPGSST PSGATGSPGASPGTSS TGSP	GGTACCCCGGGTAGCGGTACTGCTTCTTCCTCTCCAG GTAGCTCTACCCCTTCTGGTGCAACCGGCTCTCCAGG TGCTTCTCCGGGCACCAGCTCTACCGGTTCTCCA
LCW0404_034_ GFP-N_D09.ab1	GSSTPSGATGSPGSST PSGATGSPGASPGTSS TGSP	GGTAGCTCTACCCCGTCTGGTGCTACCGGCTCTCCAG GTAGCTCTACCCCGTCTGGTGCAACCGGCTCCCCAG GTGCATCCCCGGGTACTAGCTCTACCGGTTCTCCA
LCW0404_035_ GFP-N_E09.ab1	GASPGTSSTGSPGTPG SGTASSSPGSSTPSGA TGSP	GGTGCTTCTCCGGGCACCAGCTCTACTGGTTCTCCAG GTACCCCGGGCAGCGGTACCGCATCTTCTTCTCCAG GTAGCTCTACTCCTTCTGGTGCAACTGGTTCTCCA
LCW0404_036_ GFP-N_F09.ab1	GSSPSASTGTGPGSST PSGATGSPGTPGSGT ASSSP	GGTTCTAGCCCGTCTGCTTCCACCGGTACTGGCCCAG GTAGCTCTACCCCGTCTGGTGCAACTGGTTCCCCAGG TACCCCTGGTAGCGGTACCGCTTCTTCTTCTCCA
LCW0404_037_ GFP-N_G09.ab1	GASPGTSSTGSPGSSP SASTGTGPGSSTPSGA TGSP	GGTGCTTCTCCGGGCACCAGCTCTACTGGTTCTCCAG GTTCTAGCCCTTCTGCATCCACCGGTACCGGTCCAGG TAGCTCTACCCCTTCTGGTGCAACCGGCTCTCCA
LCW0404_040_ GFP-N_H09.ab1	GASPGTSSTGSPGSST PSGATGSPGSSTPSGA TGSP	GGTGCATCCCCGGGCACCAGCTCTACCGGTTCTCCA GGTAGCTCTACCCCGTCTGGTGCTACCGGCTCTCCAG GTAGCTCTACCCCGTCTGGTGCTACTGGCTCTCCA
LCW0404_041_ GFP-N_A10.ab1	GTPGSGTASSSPGSST PSGATGSPGTPGSGT ASSSP	GGTACCCCTGGTAGCGGTACTGCTTCTTCCTCTCCAG GTAGCTCTACTCCGTCTGGTGCTACCGGTTCTCCAGG TACCCCGGGTAGCGGTACCGCATCTTCTTCTCCA
LCW0404_043_ GFP-N_C10.ab1	GSSPSASTGTGPGSST PSGATGSPGSSTPSGA TGSP	GGTTCTAGCCCTTCTGCTTCCACCGGTACTGGCCCAG GTAGCTCTACCCCTTCTGGTGCTACCGGCTCCCCAGG TAGCTCTACTCCTTCTGGTGCAACTGGCTCTCCA
LCW0404_045_ GFP-N_D10.ab1	GASPGTSSTGSPGSSP SASTGTGPGSSPSAST GTGP	GGTGCTTCTCCTGGCACCAGCTCTACTGGTTCTCCAG GTTCTAGCCCTTCTGCTTCTACCGGTACTGGTCCAGG TTCTAGCCCTTCTGCATCCACTGGTACTGGTCCA
LCW0404_047_ GFP-N_F10.ab1	GTPGSGTASSSPGASP GTSSTGSPGASPGTSS TGSP	GGTACTCCTGGCAGCGGTACCGCTTCTTCTTCTCCAG GTGCTTCTCCTGGTACTAGCTCTACTGGTTCTCCAGG TGCTTCTCCGGGCACTAGCTCTACTGGTTCTCCA
LCW0404_048_ GFP-N_G10.ab1	GSSTPSGATGSPGASP GTSSTGSPGSSTPSGA TGSP	GGTAGCTCTACCCCGTCTGGTGCTACCGGTTCCCCAG GTGCTTCTCCTGGTACTAGCTCTACCGGTTCTCCAGG TAGCTCTACCCCGTCTGGTGCTACTGGCTCTCCA
LCW0404_049_ GFP-N_H10.ab1	GSSTPSGATGSPGTPG SGTASSSPGSSTPSGA TGSP	GGTAGCTCTACCCCGTCTGGTGCTACTGGTTCTCCAG GTACTCCGGGCAGCGGTACTGCTTCTTCCTCTCCAGG TAGCTCTACCCCTTCTGGTGCTACTGGCTCTCCA
LCW0404_050_ GFP-N_A11.ab1	GASPGTSSTGSPGSSP SASTGTGPGSSTPSGA TGSP	GGTGCATCTCCTGGTACCAGCTCTACTGGTTCTCCAG GTTCTAGCCCTTCTGCTTCTACCGGTACCGGTCCAGG TAGCTCTACTCCTTCTGGTGCTACCGGTTCTCCA

File name	Amino acid sequence	Nucleotide sequence
LCW0404_051_ GFP-N_B11.ab1	GSSTPSGATGSPGSST PSGATGSPGSSTPSGA TGSP	GGTAGCTCTACCCCGTCTGGTGCTACTGGCTCTCCAG GTAGCTCTACTCCTTCTGGTGCTACTGGTTCCCCAGG TAGCTCTACCCCGTCTGGTGCAACTGGCTCTCCA
LCW0404_052_ GFP-N_C11.ab1	GASPGTSSTGSPGTPG SGTASSSPGASPGTSS TGSP	GGTGCATCCCCGGGTACCAGCTCTACCGGTTCTCCA GGTACTCCTGGCAGCGGTACTGCATCTTCCTCTCCAG GTGCTTCTCCGGGCACCAGCTCTACTGGTTCTCCA
LCW0404_053_ GFP-N_D11.ab1	GSSTPSGATGSPGSSP SASTGTGPGASPGTSS TGSP	GGTAGCTCTACTCCTTCTGGTGCAACTGGTTCTCCAG GTTCTAGCCCGTCTGCATCCACTGGTACCGGTCCAGG TGCTTCCCCTGGCACCAGCTCTACCGGTTCTCCA
LCW0404_057_ GFP-N_E11.ab1	GASPGTSSTGSPGSST PSGATGSPGSSPSAST GTGP	GGTGCATCTCCTGGTACTAGCTCTACTGGTTCTCCAG GTAGCTCTACTCCGTCTGGTGCAACCGGCTCTCCAGG TTCTAGCCCTTCTGCATCTACCGGTACTGGTCCA
LCW0404_060_ GFP-N_F11.ab1	GTPGSGTASSSPGSST PSGATGSPGASPGTSS TGSP	GGTACTCCTGGCAGCGGTACCGCATCTTCCTCTCCAG GTAGCTCTACTCCGTCTGGTGCAACTGGTTCCCCAGG TGCTTCTCCGGGTACCAGCTCTACCGGTTCTCCA
LCW0404_062_ GFP-N_G11.ab1	GSSTPSGATGSPGTPG SGTASSSPGSSTPSGA TGSP	GGTAGCTCTACCCCGTCTGGTGCAACCGGCTCCCCA GGTACTCCTGGTAGCGGTACCGCTTCTTCTTCTCCAG GTAGCTCTACTCCGTCTGGTGCTACCGGCTCCCCA
LCW0404_066_ GFP-N_H11.ab1	GSSPSASTGTGPGSSP SASTGTGPGASPGTSS TGSP	GGTTCTAGCCCTTCTGCATCCACCGGTACCGGCCCAG GTTCTAGCCCGTCTGCTTCTACCGGTACTGGTCCAGG TGCTTCTCCGGGTACTAGCTCTACTGGTTCTCCA
LCW0404_067_ GFP-N_A12.ab1	GTPGSGTASSSPGSST PSGATGSPGSNPSAST GTGP	GGTACCCCGGGTAGCGGTACCGCTTCTTCTTCTCCAG GTAGCTCTACTCCGTCTGGTGCTACCGGCTCTCCAGG TTCTAACCCTTCTGCATCCACCGGTACCGGCCCA
LCW0404_068_ GFP-N_B12.ab1	GSSPSASTGTGPGSST PSGATGSPGASPGTSS TGSP	GGTTCTAGCCCTTCTGCATCTACTGGTACTGGCCCAG GTAGCTCTACTCCTTCTGGTGCTACCGGCTCTCCAGG TGCTTCTCCGGGTACTAGCTCTACCGGTTCTCCA
LCW0404_069_ GFP-N_C12.ab1	GSSTPSGATGSPGASP GTSSTGSPGTPGSGTA SSSP	GGTAGCTCTACCCCTTCTGGTGCAACCGGCTCTCCAG GTGCATCCCCGGGTACCAGCTCTACCGGTTCTCCAG GTACTCCGGGTAGCGGTACCGCTTCTTCCTCTCCA
LCW0404_070_ GFP-N_D12.ab1	GSSTPSGATGSPGSST PSGATGSPGSSTPSGA TGSP	GGTAGCTCTACTCCGTCTGGTGCAACCGGTTCCCCAG GTAGCTCTACCCCTTCTGGTGCAACCGGCTCCCCAGG TAGCTCTACCCCTTCTGGTGCAACTGGCTCTCCA
LCW0404_073_ GFP-N_E12.ab1	GASPGTSSTGSPGTPG SGTASSSPGSSTPSGA TGSP	GGTGCTTCTCCTGGCACTAGCTCTACCGGTTCTCCAG GTACCCCTGGTAGCGGTACCGCATCTTCCTCTCCAGG TAGCTCTACTCCTTCTGGTGCTACTGGTTCCCCA
LCW0404_075_ GFP-N_F12.ab1	GSSTPSGATGSPGSSP SASTGTGPGSSPSAST GTGP	GGTAGCTCTACCCCGTCTGGTGCTACTGGCTCCCCAG GTTCTAGCCCTTCTGCATCCACCGGTACCGGTCCAGG TTCTAGCCCGTCTGCATCTACTGGTACTGGTCCA
LCW0404_080_ GFP-N_G12.ab1	GASPGTSSTGSPGSSP SASTGTGPGSSPSAST GTGP	GGTGCTTCCCCGGGCACCAGCTCTACTGGTTCTCCAG GTTCTAGCCCGTCTGCTTCTACTGGTACTGGTCCAGG TTCTAGCCCTTCTGCTTCCACTGGTACTGGTCCA
LCW0404_081_ GFP-N_H12.ab1	GASPGTSSTGSPGSSP SASTGTGPGTPGSGT ASSSP	GGTGCTTCCCCGGGTACCAGCTCTACCGGTTCTCCAG GTTCTAGCCCTTCTGCTTCTACCGGTACCGGTCCAGG TACCCCTGGCAGCGGTACCGCATCTTCCTCTCCA

[00443] Example 5: Construction of XTEN_AE864

[00444] XTEN_AE864 was constructed from serial dimerization of XTEN_AE36 to AE72, 144, 288, 576 and 864. A collection of XTEN_AE72 segments was constructed from 37 different segments of XTEN_AE36. Cultures of E. coli harboring all 37 different 36-amino acid segments were mixed and plasmid was isolated. This plasmid pool was digested with BsaI/NcoI to generate the small fragment as the insert. The same plasmid pool was digested with BbsI/NcoI to generate the large fragment as the vector. The insert and vector fragments were ligated resulting

in a doubling of the length and the ligation mixture was transformed into BL21Gold(DE3) cells to obtain colonies of XTEN_AE72.

[00445] This library of XTEN_AE72 segments was designated LCW0406. All clones from LCW0406 were combined and dimerized again using the same process as described above yielding library LCW0410 of XTEN_AE144. All clones from LCW0410 were combined and dimerized again using the same process as described above yielding library LCW0414 of XTEN_AE288. Two isolates LCW0414.001 and LCW0414.002 were randomly picked from the library and sequenced to verify the identities. All clones from LCW0414 were combined and dimerized again using the same process as described above yielding library LCW0418 of XTEN_AE576. We screened 96 isolates from library LCW0418 for high level of GFP fluorescence. 8 isolates with right sizes of inserts by PCR and strong fluorescence were sequenced and 2 isolates (LCW0418.018 and LCW0418.052) were chosen for future use based on sequencing and expression data.

[00446] The specific clone pCW0432 of XTEN_AE864 was constructed by combining LCW0418.018 of XTEN_AE576 and LCW0414.002 of XTEN_AE288 using the same dimerization process as described above.

[00447] Example 6: Construction of XTEN_AG864

[00448] Using the several consecutive rounds of dimerization, we assembled a collection of XTEN_AG864 sequences starting from segments of XTEN_AD36 listed in Example 1. These sequences were assembled as described in Example 3. Several isolates from XTEN_AG864 were evaluated and found to show good expression and excellent solubility under physiological conditions. A full length clone of XTEN_AG864 had excellent solubility and showed half-life exceeding 60h in cynomolgus monkeys.

[00449] Example 7: Construction of CBD-XTEN-Cys, a cysteine-engineered XTEN

[00450] A cysteine island (CysIsland) encoding the amino acid sequence GGSPAGSCTSP containing one cysteine was introduced by annealed oligos in the CBD-stuffer-GFP vector to obtain CBD-CysIsland-GFP, where CysIsland is flanked by the restriction sites BsaI and BbsI. The CBD-stuffer-GFP vector is a pET30 derivative from Novagen with TEV protease recognition site between CBD and the stuffer. Constructs were previously generated by replacing the stuffer in CBD-stuffer-GFP vector with genes encoding XTEN_AE288 and XTEN_AE576. The plasmid of CBD-XTEN_AE288-GFP was digested with BsaI/NcoI to generate the small fragment as the insert. The plasmid of CBD-CysIsland-GFP was digested with BbsI/NcoI to generate the large fragment as the vector. The insert and vector fragments were ligated and the ligation mixture was electroporated into BL21-Gold (DE3) cells to obtain transformants of CBD-CysIsland-XTEN_AE288-GFP. Similarly, the plasmid of CBD-CysIsland-XTEN_AE288-GFP was digested with BsaI/NcoI to generate the small fragment as the insert. The plasmid of CBD-

XTEN_AE576-GFP was digested with BbsI/NcoI to generate the large fragment as the vector. The insert and vector fragments were ligated and the ligation mixture was electroporated into BL21-Gold (DE3) cells to obtain transformants of CBD-XTEN_AE576-CysIsland-XTEN_AE288-GFP. Finally, the plasmid of CBD-XTEN_AE576-CysIsland-XTEN_AE288-GFP was digested with BbsI/HindIII to remove GFP and ligate with annealed oligos for the stop codon, and the ligation mixture was electroporated into BL21-Gold (DE3) cells to obtain transformants of CBD-XTEN_AE576-CysIsland-XTEN_AE288, which has the DNA and encoded amino acid sequences that follow in Table 26. Additional constructs can be created with cysteines inserted at different locations within the XTEN sequence by the selection of restriction sites appropriate for the given location, including multiple insertions. The method could also be utilized to create lysine-engineered XTEN by substitution of codons encoding lysine for those encoding cysteine in the oligonucleotides.

Table 26: DNA and amino acid sequence of Cys-engineered XTEN

Clone Name	DNA Sequence	Amino Acid Sequence
CBD-TEV-AE576-CysIsland-AE288	ATGGCAAATACACCGGTATCAGGCAATTTGAAGGTTGA	MANTPVSGNLK
	ATTCTACAACAGCAATCCTTCAGATACTACTAACTCAAT	VEFYNSNPSDTT
	CAATCCTCAGTTCAAGGTTACTAATACCGGAAGCAGTGC	NSINPQFKVTNT
	AATTGATTTGTCCAAACTCACATTGAGATATTATTATAC	GSSAIDLSKLTL
	AGTAGACGGACAGAAAGATCAGACCTTCTGGGCTGACC	RYYYTVDGQKD
	ATGCTGCAATAATCGGCAGTAACGGCAGCTACAACGGA	QTFWADHAAIIG
	ATTACTTCAAATGTAAAAGGAACATTTGTAAAAATGAGT	SNGSYNGITSNV
	TCCTCAACAAATAACGCAGACACCTACCTTGAAATCAGC	KGTFVKMSSST
	TTTACAGGCGGAACTCTTGAACCGGGTGCACATGTTCAG	NNADTYLEISFT
	ATACAAGGTAGATTTGCAAAGAATGACTGGAGTAACTA	GGTLEPGAHVQI
	TACACAGTCAAATGACTACTCATTCAAGTCTGCTTCACA	QGRFAKNDWSN
	GTTTGTTGAATGGGATCAGGTAACAGCATACTTGAACGG	YTQSNDYSFKSA
	TGTTCTTGTATGGGGTAAAGAACCCGGTGGCAGTGTAGT	SQFVEWDQVTA
	AGGTTCAGGTTCAGGATCCGAAAATCTGTATTTTCAGGG	YLNGVLVWGKE
	TGGGTCTCCAGGTAGCCCGGCTGGCTCTCCTACCTCTAC	PGGSVVGSGSGS
	TGAGGAAGGTACTTCTGAAAGCGCTACTCCTGAGTCTGG	ENLYFQGGSPGS
	TCCAGGTACCTCTACTGAACCGTCCGAAGGTAGCGCTCC	PAGSPTSTEEGT
	AGGTAGCCCAGCAGGCTCTCCGACTTCCACTGAGGAAG	SESATPESGPGT
	GTACTTCTACTGAACCTTCCGAAGGCAGCGCACCAGGTA	STEPSEGSAPGSP
	CCTCTACTGAACCTTCTGAGGGCAGCGCTCCAGGTACTT	AGSPTSTEEGTS
	CTGAAAGCGCTACCCCGGAATCTGGCCCAGGTAGCGAA	TEPSEGSAPGTS
	CCGGCTACTTCTGGTTCTGAAACCCCAGGTAGCGAACCG	TEPSEGSAPGTS
	GCTACCTCCGGTTCTGAAACTCCAGGTAGCCCGGCAGGC	ESATPESGPGSE
	TCTCCGACCTCTACTGAGGAAGGTACTTCTGAAAGCGCA	PATSGSETPGSE
	ACCCCGGAGTCCGGCCCAGGTACCTCTACCGAACCGTCT	PATSGSETPGSP
	GAGGGCAGCGCACCAGGTACTTCTACCGAACCGTCCGA	AGSPTSTEEGTS
	GGGTAGCGCACCAGGTAGCCCAGCAGGTTCTCCTACCTC	ESATPESGPGTS
	CACCGAGGAAGGTACTTCTACCGAACCGTCCGAGGGTA	TEPSEGSAPGTS
	GCGCACCAGGTACCTCTACTGAACCTTCTGAGGGCAGCG	TEPSEGSAPGSP
	CTCCAGGTACTTCTGAAAGCGCTACCCCGGAGTCCGGTC	AGSPTSTEEGTS
	CAGGTACTTCTACTGAACCGTCCGAAGGTAGCGCACCAG	TEPSEGSAPGTS
	GTACTTCTGAAAGCGCAACCCCTGAATCCGGTCCAGGTA	TEPSEGSAPGTS
	GCGAACCGGCTACTTCTGGCTCTGAGACTCCAGGTACTT	ESATPESGPGTS
	CTACCGAACCGTCCGAAGGTAGCGCACCAGGTACTTCTA	TEPSEGSAPGTS
	CTGAACCGTCTGAAGGTAGCGCACCAGGTACTTCTGAAA	ESATPESGPGSE
	GCGCAACCCCGGAATCCGGCCCAGGTACCTCTGAAAGC	PATSGSETPGTS

Clone Name	DNA Sequence	Amino Acid Sequence
	GCAACCCCGGAGTCCGGCCCAGGTAGCCCTGCTGGCTCT	TEPSEGSAPGTS
	CCAACCTCCACCGAAGAAGGTACCTCTGAAAGCGCAAC	TEPSEGSAPGTS
	CCCTGAATCCGGCCCAGGTAGCGAACCGGCAACCTCCG	ESATPESGPGTS
	GTTCTGAAACCCCAGGTACCTCTGAAAGCGCTACTCCGG	ESATPESGPGSP
	AGTCTGGCCCAGGTACCTCTACTGAACCGTCTGAGGGTA	AGSPTSTEEGTS
	GCGCTCCAGGTACTTCTACTGAACCGTCCGAAGGTAGCG	ESATPESGPGSE
	CACCAGGTACTTCTACCGAACCGTCCGAAGGCAGCGCTC	PATSGSETPGTS
	CAGGTACCTCTACTGAACCTTCCGAGGGCAGCGCTCCAG	ESATPESGPGTS
	GTACCTCTACCGAACCTTCTGAAGGTAGCGCACCAGGTA	TEPSEGSAPGTS
	CTTCTACCGAACCGTCCGAGGGTAGCGCACCAGGTAGCC	TEPSEGSAPGTS
	CAGCAGGTTCTCCTACCTCCACCGAGGAAGGTACTTCTA	TEPSEGSAPGTS
	CCGAACCGTCCGAGGGTAGCGCACCAGGTACCTCTGAA	TEPSEGSAPGTS
	AGCGCAACTCCTGAGTCTGGCCCAGGTAGCGAACCTGCT	TEPSEGSAPGTS
	ACCTCCGGCTCTGAGACTCCAGGTACCTCTGAAAGCGCA	TEPSEGSAPGSP
	ACCCCGGAATCTGGTCCAGGTAGCGAACCTGCAACCTCT	AGSPTSTEEGTS
	GGCTCTGAAACCCCAGGTACCTCTGAAAGCGCTACTCCT	TEPSEGSAPGTS
	GAATCTGGCCCAGGTACTTCTACTGAACCGTCCGAGGGC	ESATPESGPGSE
	AGCGCACCAGGTACTTCTGAAAGCGCTACTCCTGAGTCC	PATSGSETPGTS
	GGCCCAGGTAGCCCGGCTGGCTCTCCGACTTCCACCGAG	ESATPESGPGSE
	GAAGGTAGCCCGGCTGGCTCTCCAACTTCTACTGAAGAA	PATSGSETPGTS
	GGTAGCCCGGCAGGCTCTCCGACCTCTACTGAGGAAGGT	ESATPESGPGTS
	ACTTCTGAAAGCGCAACCCCGGAGTCCGGCCCAGGTACC	TEPSEGSAPGTS
	TCTACCGAACCGTCTGAGGGCAGCGCACCAGGTGGTAG	ESATPESGPGSP
	CCCGGCTGGCTCTTGTACCTCTCCAGGTACCTCTGAAAG	AGSPTSTEEGSP
	CGCAACTCCTGAGTCTGGCCCAGGTAGCGAACCTGCTAC	AGSPTSTEEGSP
	CTCCGGCTCTGAGACTCCAGGTACCTCTGAAAGCGCAAC	AGSPTSTEEGTS
	CCCGGAATCTGGTCCAGGTAGCGAACCTGCAACCTCTGG	ESATPESGPGTS
	CTCTGAAACCCCAGGTACCTCTGAAAGCGCTACTCCTGA	TEPSEGSAPGGS
	ATCTGGCCCAGGTACTTCTACTGAACCGTCCGAGGGCAG	PAGSCTSPGTSE
	CGCACCAGGTAGCCCTGCTGGCTCTCCAACCTCCACCGA	SATPESGPGSEP
	AGAAGGTACCTCTGAAAGCGCAACCCCTGAATCCGGCC	ATSGSETPGTSE
	CAGGTAGCGAACCGGCAACCTCCGGTTCTGAAACCCCA	SATPESGPGSEP
	GGTACTTCTGAAAGCGCTACTCCTGAGTCCGGCCCAGGT	ATSGSETPGTSE
	AGCCCGGCTGGCTCTCCGACTTCCACCGAGGAAGGTAGC	SATPESGPGTST
	CCGGCTGGCTCTCCAACTTCTACTGAAGAAGGTACTTCT	EPSEGSAPGSPA
	ACCGAACCTTCCGAGGGCAGCGCACCAGGTACTTCTGAA	GSPTSTEEGTSES
	AGCGCTACCCCTGAGTCCGGCCCAGGTACTTCTGAAAGC	ATPESGPGSEPA
	GCTACTCCTGAATCCGGTCCAGGTACTTCTGAAAGCGCT	TSGSETPGTSES
	ACCCCGGAATCTGGCCCAGGTAGCGAACCGGCTACTTCT	ATPESGPGSPAG
	GGTTCTGAAACCCCAGGTAGCGAACCGGCTACCTCCGGT	SPTSTEEGSPAG
	TCTGAAACTCCAGGTAGCCCAGCAGGCTCTCCGACTTCC	SPTSTEEGTSTEP
	ACTGAGGAAGGTACTTCTACTGAACCTTCCGAAGGCAGC	SEGSAPGTSESA
	GCACCAGGTACCTCTACTGAACCTTCTGAGGGCAGCGCT	TPESGPGTSESA
	CCAGGTAGCGAACCTGCAACCTCTGGCTCTGAAACCCCA	TPESGPGTSESA
	GGTACCTCTGAAAGCGCTACTCCTGAATCTGGCCCAGGT	TPESGPGSEPAT
	ACTTCTACTGAACCGTCCGAGGGCAGCGCACCAGGTTAA	SGSETPGSEPAT
		SGSETPGSPAGS
		PTSTEEGTSTEPS
		EGSAPGTSTEPS
		EGSAPGSEPATS
		GSETPGTSESAT
		PESGPGTSTEPSE
		GSAPG

[00451] Example 8: Construction of Cys3-XTEN

[00452] A pair of primers was designed to introduce the restriction site BamHI and cysteine island 1 of sequence GRATAEAAGCGTAEAA at the N-terminus of XTEN_AE432-1, and a partial cysteine island 2 of sequence TAEAAG and restriction site BbsI at C-terminus of XTEN_AE432-1. A second pair of primers was designed to introduce the restriction site BsaI and a partial cysteine island 2 of sequence GCGTAEAA at the N-terminus of XTEN_AE432-2, and cysteine island 4 of sequence TAEAAGCGTAEAAR with an 8xHis-tag (H8) and restriction site HindIII at the C-terminus of XTEN_AE432-2. The XTEN_AE432-1 contains the 1-432 amino acid sequence and XTEN_AE432-2 contains the 433-864 amino acid sequence encoded by the XTEN_AE864 gene. These two pairs of primers were used to amplify the XTEN_AE432-1 and XTEN_AE432-2 gene, respectively, by polymerase chain reaction (PCR). The PCR products of correct sizes were gel-purified and digested with the restriction enzymes BamHI/BbsI and BsaI/HindIII, respectively, as the inserts for ligation. A destination vector, a derivative of pET30 (Novagen) includes a CBD (cellulose binding domain)-stuffer with the flanking restriction sites BamHI and HindIII. The desitnation vector was digested with the restriction enzymes BamHI/HindIII to remove the stuffer and prepared as the vector. The vector was ligated with the BamHI/BbsI digested PCR product of XTEN_AE432-1 and BsaI/HindIII digested PCR of XTEN_AE432-2 above. The ligation mixture was transformed into *E. coli* TOP10 competent cells. Transformants were screened by DNA miniprep and the desired constructs were confirmed by DNA sequencing. Thus, the final plasmid yields the CBD-cysteine island 1-XTEN_AE432-cysteine island 2-XTEN_AE432-cysteine island 3-H8 gene under the control of a T7 promoter. The DNA sequences and protein sequences are provided in Table 27.

Table 27: Cys3-XTEN DNA and amino acid sequences

Clone Name	DNA Sequence	Amino Acid Sequence
CBD-Cys1-AE432-Cys2-AE432-Cys3-H8 (AC673)	ATGGCTAATACCCCAGTGAGCGGCAACCTGAAAGTG GAATTCTACAATAGCAACCCGAGCGACACCACCAAC AGCATTAATCCGCAGTTCAAAGTGACCAACACGGGT AGCTCCGCGATCGATCTGTCGAAGCTGACGCTGCGT TACTATTACACGGTTGACGGTCAGAAAGATCAGACG TTCTGGGCTGACCATGCGGCCATTATTGGCAGCAAC GGTTCCTACAACGGTATCACGAGCAATGTCAAAGGC ACTTTTGTTAAGATGAGCTCTTCGACCAACAATGCCG ATACCTATCTGGAGATTAGCTTCACCGGTGGTACTCT GGAGCCGGGTGCACACGTTCAAATCCAAGGTCGCTT CGCAAAGAATGACTGGAGCAACTATACCCAGTCCAA TGACTACAGCTTCAAAAGCGCTAGCCAATTTGTTGA ATGGGATCAGGTCACCGCATACCTGAACGGCGTGCT GGTCTGGGGCAAGGAACCGGGTGGTAGCGTTGTCGG TTCTGGCAGCGGATCCggtcgtGCGACGGCAGAAGCCG CTGGCtgcGGTACTGCTGAAGCGGCAGGTAGCCCAGC TGGTAGCCCAACCTCTACCGAAGAAGGTACCTCTGA ATCCGCTACTCCAGAATCCGGTCCTGGTACTAGCACT GAGCCAAGCGAAGGTTCTGCTCCAGGCTCCCCGGCA GGTAGCCCTACCTCTACCGAAGAGGGCACTAGCACC	MANTPVSGNLKVEFY NSNPSDTTNSINPQF KVTNTGSSAIDLSKL TLRYYYTVDGQKDQT FWADHAAIIGSNGSY NGITSNVKGTFVKMS SSTNNADTYLEISFT GGTLEPGAHVQIQGR FAKNDWSNYTQSNDY SFKSASQFVEWDQVT AYLNGVLVWGKEPGG SVVGSGSGSGRATAE AAGCGTAEAAGSPAG SPTSTEEGTSESATP ESGPGTSTEPSEGSA PGSPAGSPTSTEEGT STEPSEGSAPGTSTE PSEGSAPGTSESATP ESGPGSEPATSGSET PGSEPATSGSETPGS

Clone Name	DNA Sequence	Amino Acid Sequence
	GAACCATCTGAGGGTTCCGCTCCTGGCACCTCCACT	PAGSPTSTEEGTSES
	GAACCGTCCGAAGGCAGTGCTCCGGGTACTTCCGAA	ATPESGPGTSTEPSE
	AGCGCAACTCCGGAATCCGGCCCTGGTTCTGAGCCT	GSAPGTSTEPSEGSA
	GCTACTTCCGGCTCTGAAACTCCAGGTAGCGAGCCA	PGSPAGSPTSTEEGT
	GCGACTTCTGGTTCTGAAACTCCAGGTTCACCGGCG	STEPSEGSAPGTSTE
	GGTAGCCCGACGAGCACGGAGGAAGGTACCTCTGA	PSEGSAPGTSESATP
	GTCGGCCACTCCTGAGTCCGGTCCGGGCACGAGCAC	ESGPGTSTEPSEGSA
	CGAGCCGAGCGAGGGTTCAGCCCCGGGTACCAGCAC	PGTSESATPESGPGS
	GGAGCCGTCCGAGGGTAGCGCACCGGGTTCTCCGGC	EPATSGSETPGTSTE
	GGGCTCCCCTACGTCTACGGAAGAGGGTACGTCCAC	PSEGSAPGTSTEPSE
	TGAACCTAGCGAGGGCAGCGCGCCAGGCACCAGCA	GSAPGTSESATPESG
	CTGAACCGAGCGAAGGCAGCGCACCTGGCACTAGCG	PGTSESATPESGPGS
	AGTCTGCGACTCCGGAGAGCGGTCCGGGTACGAGCA	PAGSPTSTEEGTSES
	CGGAACCAAGCGAAGGCAGCGCCCCAGGTACCTCTG	ATPESGPGSEPATSG
	AATCTGCTACCCCAGAATCTGGCCCGGGTTCCGAGC	SETPGTSESATPESG
	CAGCTACCTCTGGTTCTGAAACCCCAGGTACTTCCAC	PGTSTEPSEGSAPGT
	TGAACCAAGCGAAGGTAGCGCTCCTGGCACTTCTAC	STEPSEGSAPGTSTE
	TGAACCATCCGAAGGTTCCGCTCCTGGTACGTCTGA	PSEGSAPGTSTEPSE
	AAGCGCTACCCCTGAAAGCGGCCCAGGCACCTCTGA	GSAPGTSTEPSEGSA
	AAGCGCTACTCCTGAGAGCGGTCCAGGCTCTCCAGC	PGTSTEPSEGSAPGS
	AGGTTCTCCAACCTCCACTGAAGAAGGCACCTCTGA	PAGSPTSTEEGTSTE
	GTCTGCTACCCCTGAATCTGGTCCTGGCTCCGAACCT	PSEGSAPTAEAAGCG
	GCTACCTCTGGTTCCGAAACTCCAGGTACCTCGGAA	TAEAAGTSESATPES
	TCTGCGACTCCGGAATCTGGCCCGGGCACGAGCACG	GPGSEPATSGSETPG
	GAGCCGTCTGAGGGTAGCGCACCAGGTACCAGCACT	TSESATPESGPGSEP
	GAGCCTTCTGAGGGCTCTGCACCGGGTACCTCCACG	ATSGSETPGTSESAT
	GAACCTTCGGAAGGTTCTGCGCCGGGTACCTCCACT	PESGPGTSTEPSEGS
	GAGCCATCCGAGGGTTCAGCACCAGGTACTAGCACG	APGTSESATPESGPG
	GAACCGTCCGAGGGCTCTGCACCAGGTACGAGCACC	SPAGSPTSTEEGSPA
	GAACCGTCGGAGGGTAGCGCTCCAGGTAGCCCAGCG	GSPTSTEEGSPAGSP
	GGCTCTCCGACAAGCACCGAAGAAGGCACCAGCACC	TSTEEGTSESATPES
	GAGCCGTCCGAAGGTTCCGCACCAACCGCTGAAGCC	GPGTSTEPSEGSAPG
	GCAGGTtgtGGCACTGCGGAAGCTGCAGGTACAAGCG	TSESATPESGPGSEP
	AGAGCGCGACTCCTGAATCTGGTCCGGGTAGCGAGC	ATSGSETPGTSESAT
	CTGCAACCAGCGGTTCTGAGACGCCGGGCACTTCCG	PESGPGSEPATSGSE
	AATCTGCGACCCCGGAGTCCGGTCCAGGTTCAGAGC	TPGTSESATPESGPG
	CGGCGACGAGCGGTTCGGAAACGCCGGGTACGTCTG	TSTEPSEGSAPGSPA
	AATCAGCCACGCCGGAGTCTGGTCCGGGTACCTCGA	GSPTSTEEGTSESAT
	CCGAACCAAGCGAAGGTTCGGCACCGGGTACTAGCG	PESGPGSEPATSGSE
	AGAGCGCAACCCCTGAAAGCGGTCCGGGCAGCCCG	TPGTSESATPESGPG
	GCAGGTTCTCCAACCAGCACCGAAGAAGGTTCCCCT	SPAGSPTSTEEGSPA
	GCTGGTAGCCCGACCTCTACGGAGGAAGGTAGCCCT	GSPTSTEEGTSTEPS
	GCAGGTTCCCCAACTTCTACTGAGGAAGGTACTTCT	EGSAPGTSESATPES
	GAGTCCGCTACCCCAGAAAGCGGTCCTGGTACCTCC	GPGTSESATPESGPG
	ACTGAACCGTCTGAAGGCTCTGCACCAGGCACTTCT	TSESATPESGPGSEP
	GAGTCTGCTACTCCAGAAAGCGGCCCAGGTTCTGAA	ATSGSETPGSEPATS
	CCAGCAACTTCTGGCTCTGAGACTCCAGGCACTTCTG	GSETPGSPAGSPTST
	AGTCCGCAACGCCTGAATCCGGTCCTGGTTCTGAAC	EEGTSTEPSEGSAPG
	CAGCTACTTCCGGCAGCGAAACCCCAGGTACCTCTG	TSTEPSEGSAPGSEP
	AGTCTGCGACTCCAGAGTCTGGTCCTGGTACTTCCAC	ATSGSETPGTSESAT
	TGAGCCTAGCGAGGGTTCCGCACCAGGTTCTCCGGC	PESGPGTSTEPSEGS
	TGGTAGCCCGACCAGCACGGAGGAGGGTACGTCTGA	APTAEAAGCGTAEAA
	ATCTGCAACGCCGGAATCGGGCCCAGGTTCGGAGCC	RHHHHHHHH
	TGCAACGTCTGGCAGCGAAACCCCGGGTACCTCCGA	
	ATCTGCTACACCGGAAAGCGGTCCTGGCAGCCCTGC	
	TGGTTCTCCAACCTCTACCGAGGAGGGTTCACCGGC	
	AGGTAGCCCGACTAGCACTGAAGAAGGTACTAGCAC	
	GGAGCCGAGCGAGGGTAGTGCTCCGGGTACGAGCG	

Clone Name	DNA Sequence	Amino Acid Sequence
	AGAGCGCAACGCCAGAGAGCGGTCCAGGCACCAGC GAATCGGCCACCCCTGAGAGCGGCCCAGGTACTTCT GAGAGCGCCACTCCTGAATCCGGCCCTGGTAGCGAG CCGGCAACCTCCGGCTCAGAAACTCCTGGTTCGGAA CCAGCGACCAGCGGTTCTGAAACTCCGGGTAGCCCG GCAGGCAGCCCAACGAGCACCGAAGAGGGTACCAG CACGGAACCGAGCGAGGGTTCTGCCCCGGGTACTTC CACCGAACCATCGGAGGGCTCTGCACCTGGTAGCGA ACCTGCGACGTCTGGTTCTGAAACGCCGGGTACCAG CGAAAGCGCTACCCCAGAATCCGGTCCGGGCACTAG CACCGAGCCATCGGAGGGCTCCGCACCAACTGCAGA AGCGGCTGGTtgtGGCACCGCCGAAGCAGCTcgtCATC ACCATCACCACCATCATCACTAA	

[00453] Example 9: Construction of Lys2-XTEN

[00454] A pair of primers was designed to introduce the restriction site BamHI and the amino acid sequence GRGSP at the N-terminus of XTEN_AE432-1, and the amino acid sequence TAEAAG and restriction site BbsI at the C-terminus of XTEN_AE432-1. A second pair of primers was designed to introduce the restriction site BsaI and an amino acid sequence with an incorporated lysine of GKPGTAEAA at the N-terminus of XTEN_AE432-2, and an amino acid sequence with an incorporated lysine of GKAT with an 8xHis-tag (H8) and restriction site HindIII at C-terminus of XTEN_AE432-2. XTEN_AE432-1 contains the 1-432 amino acid sequence and XTEN_AE432-2 contains the 433-864 amino acid sequence encoded by the XTEN_AE864 gene. These two pairs of primers were used to amplify the XTEN_AE432-1 and XTEN_AE432-2 gene, respectively, by polymerase chain reaction (PCR). The PCR products of right sizes were gel-purified and digested with the restriction enzymes BamHI/BbsI and BsaI/HindIII, respectively, as the inserts for ligation. A destination vector, derivative of pET30 (Novagen), of CBD (cellulose binding domain)-stuffer with the flanking restriction sites BamHI and HindIII was digested with the restriction enzymes BamHI/HindIII to remove the stuffer and prepared as the vector. Ligate the vector with the BamHI/BbsI digested PCR product of XTEN_AE432-1 and BsaI/HindIII digested PCR of XTEN_AE432-2 above. The ligation mixture was transformed into *E. coli* TOP10 competent cells. Transformants were screened by DNA miniprep and the desired constructs were confirmed by DNA sequencing. Thus, the final plasmid yields the CBD-GRGSP-XTEN_AE432-TAEAAGKPGTAEAA-XTEN_AE432-GKAT-H8 gene under the control of a T7 promoter. The DNA sequences and protein sequences are provided in Table 28.

Table 28: Lys2-XTEN DNA and amino acid sequences

Clone Name	DNA Sequence	Amino Acid Sequence
CBD-R-AE432-K-AE432-K-H8 (AC698)	ATGGCTAATACCCCAGTGAGCGGCAACCTGAAAGT GGAATTCTACAATAGCAACCCGAGCGACACCACC AACAGCATTAATCCGCAGTTCAAAGTGACCAACAC GGGTAGCTCCGCGATCGATCTGTCGAAGCTGACGC	MANTPVSGNLKVE FY NSNPSDTTNSINPQF KVTNTGSSAIDLSK

Clone Name	DNA Sequence	Amino Acid Sequence
	TGCGTTACTATTACACGGTTGACGGTCAGAAAGAT	L
	CAGACGTTCTGGGCTGACCATGCGGCCATTATTGG	TLRYYYTVDGQKD
	CAGCAACGGTTCCTACAACGGTATCACGAGCAATG	QT
	TCAAAGGCACTTTTGTTAAGATGAGCTCTTCGACC	FWADHAAIIGSNGS
	AACAATGCCGATACCTATCTGGAGATTAGCTTCAC	Y
	CGGTGGTACTCTGGAGCCGGGTGCACACGTTCAAA	NGITSNVKGTFVK
	TCCAAGGTCGCTTCGCAAAGAATGACTGGAGCAAC	MS
	TATACCCAGTCCAATGACTACAGCTTCAAAAGCGC	SSTNNADTYLEISFT
	TAGCCAATTTGTTGAATGGGATCAGGTCACCGCAT	GGTLEPGAHVQIQG
	ACCTGAACGGCGTGCTGGTCTGGGGCAAGGAACC	R
	GGGTGGTAGCGTTGTCGGTTCTGGCAGCGGATCCg	FAKNDWSNYTQSN
	gtcgtGGGTCTCCAGGTAGCCCAGCTGGTAGCCCAAC	DY
	CTCTACCGAAGAAGGTACCTCTGAATCCGCTACTC	SFKSASQFVEWDQ
	CAGAATCCGGTCCTGGTACTAGCACTGAGCCAAGC	VT
	GAAGGTTCTGCTCCAGGCTCCCCGGCAGGTAGCCC	AYLNGVLVWGKEP
	TACCTCTACCGAAGAGGGCACTAGCACCGAACCAT	GG
	CTGAGGGTTCCGCTCCTGGCACCTCCACTGAACCG	SVVGSGSGSGRGSP
	TCCGAAGGCAGTGCTCCGGGTACTTCCGAAAGCGC	G
	AACTCCGGAATCCGGCCCTGGTTCTGAGCCTGCTA	SPAGSPTSTEEGTSE
	CTTCCGGCTCTGAAACTCCAGGTAGCGAGCCAGCG	SATPESGPGTSTEPS
	ACTTCTGGTTCTGAAACTCCAGGTTCACCGGCGGG	EGSAPGSPAGSPTS
	TAGCCCGACGAGCACGGAGGAAGGTACCTCTGAG	T
	TCGGCCACTCCTGAGTCCGGTCCGGGCACGAGCAC	EEGTSTEPSEGSAP
	CGAGCCGAGCGAGGGTTCAGCCCCGGGTACCAGC	G
	ACGGAGCCGTCCGAGGGTAGCGCACCGGGTTCTCC	TSTEPSEGSAPGTSE
	GGCGGGCTCCCCTACGTCTACGGAAGAGGGTACGT	SATPESGPGSEPATS
	CCACTGAACCTAGCGAGGGCAGCGCGCCAGGCAC	GSETPGSEPATSGS
	CAGCACTGAACCGAGCGAAGGCAGCGCACCTGGC	E
	ACTAGCGAGTCTGCGACTCCGGAGAGCGGTCCGG	TPGSPAGSPTSTEE
	GTACGAGCACGGAACCAAGCGAAGGCAGCGCCCC	G
	AGGTACCTCTGAATCTGCTACCCCAGAATCTGGCC	TSESATPESGPGTST
	CGGGTTCCGAGCCAGCTACCTCTGGTTCTGAAACC	EPSEGSAPGTSTEPS
	CCAGGTACTTCCACTGAACCAAGCGAAGGTAGCGC	EGSAPGSPAGSPTS
	TCCTGGCACTTCTACTGAACCATCCGAAGGTTCCG	T
	CTCCTGGTACGTCTGAAAGCGCTACCCCTGAAAGC	EEGTSTEPSEGSAP
	GGCCCAGGCACCTCTGAAAGCGCTACTCCTGAGAG	G
	CGGTCCAGGCTCTCCAGCAGGTTCTCCAACCTCCA	TSTEPSEGSAPGTSE
	CTGAAGAAGGCACCTCTGAGTCTGCTACCCCTGAA	SATPESGPGTSTEPS
	TCTGGTCCTGGCTCCGAACCTGCTACCTCTGGTTCC	EGSAPGTSESATPE
	GAAACTCCAGGTACCTCGGAATCTGCGACTCCGGA	S
	ATCTGGCCCGGGCACGAGCACGGAGCCGTCTGAG	GPGSEPATSGSETP
	GGTAGCGCACCAGGTACCAGCACTGAGCCTTCTGA	G
	GGGCTCTGCACCGGGTACCTCCACGGAACCTTCGG	TSTEPSEGSAPGTST
	AAGGTTCTGCGCCGGGTACCTCCACTGAGCCATCC	EPSEGSAPGTSESA
	GAGGGTTCAGCACCAGGTACTAGCACGGAACCGT	T
	CCGAGGGCTCTGCACCAGGTACGAGCACCGAACC	PESGPGTSESATPES
	GTCGGAGGGTAGCGCTCCAGGTAGCCCAGCGGGC	GPGSPAGSPTSTEE
	TCTCCGACAAGCACCGAAGAAGGCACCAGCACCG	G
	AGCCGTCCGAAGGTTCCGCACCAACCGCTGAAGCC	TSESATPESGPGSEP
	GCAGGTaaaccgGGCACTGCGGAAGCTGCAGGTACA	ATSGSETPGTSESA
	AGCGAGAGCGCGACTCCTGAATCTGGTCCGGGTAG	T
	CGAGCCTGCAACCAGCGGTTCTGAGACGCCGGGC	PESGPGTSTEPSEGS
	ACTTCCGAATCTGCGACCCCGGAGTCCGGTCCAGG	APGTSTEPSEGSAP
	TTCAGAGCCGGCGACGAGCGGTTCGGAAACGCCG	G
	GGTACGTCTGAATCAGCCACGCCGGAGTCTGGTCC	TSTEPSEGSAPGTST
	GGGTACCTCGACCGAACCAAGCGAAGGTTCGGCA	EPSEGSAPGTSTEPS
	CCGGGTACTAGCGAGAGCGCAACCCCTGAAAGCG	EGSAPGTSTEPSEG
	GTCCGGGCAGCCCGGCAGGTTCTCCAACCAGCACC	S

Clone Name	DNA Sequence	Amino Acid Sequence
	GAAGAAGGTTCCCCTGCTGGTAGCCCGACCTCTAC GGAGGAAGGTAGCCCTGCAGGTTCCCCAACTTCTA CTGAGGAAGGTACTTCTGAGTCCGCTACCCCAGAA AGCGGTCCTGGTACCTCCACTGAACCGTCTGAAGG CTCTGCACCAGGCACTTCTGAGTCTGCTACTCCAG AAAGCGGCCCAGGTTCTGAACCAGCAACTTCTGGC TCTGAGACTCCAGGCACTTCTGAGTCCGCAACGCC TGAATCCGGTCCTGGTTCTGAACCAGCTACTTCCG GCAGCGAAACCCCAGGTACCTCTGAGTCTGCGACT CCAGAGTCTGGTCCTGGTACTTCCACTGAGCCTAG CGAGGGTTCCGCACCAGGTTCTCCGGCTGGTAGCC CGACCAGCACGGAGGAGGGTACGTCTGAATCTGC AACGCCGGAATCGGGCCCAGGTTCGGAGCCTGCA ACGTCTGGCAGCGAAACCCCGGGTACCTCCGAATC TGCTACACCGGAAAGCGGTCCTGGCAGCCCTGCTG GTTCTCCAACCTCTACCGAGGAGGGTTCACCGGCA GGTAGCCCGACTAGCACTGAAGAAGGTACTAGCA CGGAGCCGAGCGAGGGTAGTGCTCCGGGTACGAG CGAGAGCGCAACGCCAGAGAGCGGTCCAGGCACC AGCGAATCGGCCACCCCTGAGAGCGGCCCAGGTA CTTCTGAGAGCGCCACTCCTGAATCCGGCCCTGGT AGCGAGCCGGCAACCTCCGGCTCAGAAACTCCTGG TTCGGAACCAGCGACCAGCGGTTCTGAAACTCCGG GTAGCCCGGCAGGCAGCCCAACGAGCACCGAAGA GGGTACCAGCACGGAACCGAGCGAGGGTTCTGCC CCGGGTACTTCCACCGAACCATCGGAGGGCTCTGC ACCTGGTAGCGAACCTGCGACGTCTGGTTCTGAAA CGCCGGGTACCAGCGAAAGCGCTACCCCAGAATC CGGTCCGGGCACTAGCACCGAGCCATCGGAGGGC TCCGCACCAggtAAAgcgaccCATCACCATCACCACCA TCATCACTAA	APGSPAGSPTSTEE G TSTEPSEGSAPTAE A AGKPGTAEAAGTS ES ATPESGPGSEPATS G SETPGTSESATPESG PGSEPATSGSETPG T SESATPESGPGTSTE PSEGSAPGTSESATP ESGPGSPAGSPTSTE EGSPAGSPTSTEEG S PAGSPTSTEEGTSES ATPESGPGTSTEPSE GSAPGTSESATPES G PGSEPATSGSETPG T SESATPESGPGSEPA TSGSETPGTSESATP ESGPGTSTEPSEGS A PGSPAGSPTSTEEG T SESATPESGPGSEPA TSGSETPGTSESATP ESGPGSPAGSPTSTE EGSPAGSPTSTEEG T STEPSEGSAPGTSES ATPESGPGTSESAT P ESGPGTSESATPES G PGSEPATSGSETPGS EPATSGSETPGSPA G SPTSTEEGTSTEPSE GSAPGTSTEPSEGS A PGSEPATSGSETPG T SESATPESGPGTSTE PSEGSAPGKATHHH H HHHH

[00455] Example 10: Host Strain and Promoter for Expression of XTEN for Conjugation

[00456] Plasmids pCW1054 expressing CBD-TEV site-XTEN_AE864 under the control of the T7/lac promoter, pLCW0968.003 expressing CBD-TEV site-XTEN_AE864-GFP under the control of the T7/lac promoter, and pLCW0970.030 expressing CBD-TEV site-XTEN_AE864-

GFP under the control of the PhoA promoter, were transformed into both *E. coli* BL21 DE3 and *E. coli* BL21 DE3 rne-131 (Lopez, P. J., et al. (1999) Mol. Microbiol. 33, 188-199). The rne-131 mutation disrupts the 3' endoribonucleolytic activity of RNase E (Kido, M., et al. (1996) Journal of Bacteriology, 178: 3917-3925). Starter cultures of all six tranformants were prepared by picking single colonies to inoculate 2 mL of LB Broth media containing the appropriate selective antibiotic. The starter cultures were grown overnight and 0.5mL was used to inoculate, in quadruplicate, 25 mL of 2xYT broth, for cells containing pCW1054 and pLCW0968.003, or 25mL of PhoA induction broth (Amunix recipe 136-1) for cells containing pLCW0970.030. The cultures were shaken for 3 hours at 37°C. The temperature was then reduced to 26°C for all of the cultures; and for cells containing pCW1054 and pLCW0968.003 protein expression was induced with IPTG at 1.0 mM final concentration. Induction of the PhoA promoter in pLCW070.030 is auto-induced upon depletion of phosphate from the culture media. The cultures were then shaken overnight at 26°C. Samples of each culture were lysed and 20 µl of each lysate were subjected to non-reducing SDS-PAGE using NuPAGE 4-12% Bis-Tris gel from Invitrogen, according to manufacturer's specifications, with Coomassie staining. The results (FIG. 43) showed that when either CBD-TEV site-XTEN_AE864-GFP or CBD-TEV site-XTEN_AE864 is expressed under the control of the T7/lac promoter the yield of the recombinant protein is significantly higher in the E. coli BL21 DE3 rne-131 compared to the E. coli BL21 DE3 cells. Cells were also measured for GFP fluorescence using a fluorescent plate reader. The results (FIG. 44) showed that expression in E. coli BL21 DE3 cells of CBD-TEV site-XTEN_AE864-GFP under the control of the PhoA promoter is nearly three times greater than the expression of CBD-TEV site-XTEN_AE864-GFP under the control of the T7/lac promoter. In the E. coli BL21 DE3 rne-131 both the T7/lac and PhoA promoters yielded similar levels of expression. Therefore, only upon inhibition of Rnase E 3' riboendocleolytic activity does T7/lac induction yield titers similar to that obtained using PhoA induction. Likely the faster rate of T7 RNAP transcription (Studier, W., et al. (1986) Journal of Molecular Biology 189: 113–130), relative to translation results in mRNA susceptible to endonucleolytic attack, while in the case of PhoA induction where transcription is mediated by the native E. coli RNA polymerase II, the rate of transcription is closely coupled to the rate of translation protecting the mRNA from endonucleolytic attack.

[00457] Example 11: Construction of 1xAmino-XTEN288

[00458] A pair of primers AE278BsaIfor-AACG and AE278-RH8HindIIIrev were used to PCR the plasmid containing XTEN_AE864_003 in order to obtain the PCR product XTEN_AE278. Gel-purification of the band of the right size was performed, followed by digestion with BsaI/HindIII as the insert of XTEN_AE278-R-H8. A digestion of plasmid pCW1161, which encodes the gene of N-term-RP11-R-AE432_3Cys-R-H8 (construct AC763), with BsaI/HindIII was performed to remove the fragment of AE432_3Cys-R-H8 and gel-purify the large fragment

as the vector. Ligation of the vector with the insert was performed and was used to transform BL21 competent cells to obtain the construct of N-term-RP11-R-AE288-R-H8. The XTEN length between the two trypsin digestion sites (R, Arginine) was calculated by XTEN_AE278 plus some flanking amino acids and equaled exactly 288 amino acids. Thus, the construct is designed to produce the precursor N-term-RP11-R-AE288-R-H8 (sequence in Table 29, below) and generate 1xAmino-XTEN288 (Seg 178 of Table 3, with an N-terminal amino group for conjugation) after removal of the N-term-RP11 tag and C-term 8xHis-tag by trypsin digestion.

Table 29: DNA and amino acid sequence for 1xAmino-XTEN288

Clone Name	DNA Sequence	Amino Acid Sequence
N-term-RP11-R-AE288-R-H8	ATGAAAAACCCAGAGCAAGCAGAAGAACAAGCTGAAGAACA GCGCGAAGAAACACGTCCGCGTCCTCGCCCACGTCCACGTCCG CGTCCACGCCCTCGTCCTCGTCCGCGCCCTCGTCCGagcgcgtctcgtt ccgctGGGTCTCCAAcgGGCCCAGGTTCTGAACCAGCAACTTCTG GCTCTGAGACTCCAGGCACTTCTGAGTCCGCAACGCCTGAATC CGGTCCTGGTTCTGAACCAGCTACTTCCGGCAGCGAAACCCCA GGTACCTCTGAGTCTGCGACTCCAGAGTCTGGTCCTGGTACTT CCACTGAGCCTAGCGAGGGTTCCGCACCAGGTTCTCCGGCTGG TAGCCCGACCAGCACGGAGGAGGGTACGTCTGAATCTGCAAC GCCGGAATCGGGCCCAGGTTCGGAGCCTGCAACGTCTGGCAG CGAAACCCCGGGTACCTCCGAATCTGCTACACCGGAAAGCGG TCCTGGCAGCCCTGCTGGTTCTCCAACCTCTACCGAGGAGGGT TCACCGGCAGGTAGCCCGACTAGCACTGAAGAAGGTACTAGC ACGGAGCCGAGCGAGGGTAGTGCTCCGGGTACGAGCGAGAGC GCAACGCCAGAGAGCGGTCCAGGCACCAGCGAATCGGCCACC CCTGAGAGCGGCCCAGGTACTTCTGAGAGCGCCACTCCTGAAT CCGGCCCTGGTAGCGAGCCGGCAACCTCCGGCTCAGAAACTCC TGGTTCGGAACCAGCGACCAGCGGTTCTGAAACTCCGGGTAGC CCGGCAGGCAGCCCAACGAGCACCGAAGAGGGTACCAGCACG GAACCGAGCGAGGGTTCTGCCCCGGGTACTTCCACCGAACCAT CGGAGGGCTCTGCACCTGGTAGCGAACCTGCGACGTCTGGTTC TGAAACGCCGGGTACCAGCGAAAGCGCTACCCCAGAATCCGG TCCGGGCACTAGCACCGAGCCATCGGAGGGCTCCGCACCAagcg cctctcgctccgcaCATCACCATCACCACCATCATCACTAA	MKNPEQAEEQAEEQ REETRPRPRPRPRPRP RPRPRPRPRPSASRSA GSPTGPGSEPATSGSE TPGTSESATPESGPGS EPATSGSETPGTSESA TPESGPGTSTEPSEGS APGSPAGSPTSTEEGT SESATPESGPGSEPAT SGSETPGTSESATPES GPGSPAGSPTSTEEGS PAGSPTSTEEGTSTEP SEGSAPGTSESATPES GPGTSESATPESGPGT SESATPESGPGSEPAT SGSETPGSEPATSGSE TPGSPAGSPTSTEEGT STEPSEGSAPGTSTEP SEGSAPGSEPATSGSE TPGTSESATPESGPGT STEPSEGSAPSASRSA HHHHHHHH

[00459] Example 12: Optimization for expression of XTEN constructs with RP11 affinity tag

[00460] 1. 1. Design and construction of constructs encoding N-term-RP11-AE864-GFP and MalEss-AE48-RP11-AE864

[00461] A group of highly expressed native E. coli proteins described by Ishihama Y. et al, BMC Genomics 2008, 9:102 were used to generate a list of the first 20 N-terminal amino acids (column 3 of Table 30), from which the hydrophobic amino acids F, I, W, L, V, M, C were converted to alanine or serine, or were deleted in order to generate candidates to create helper sequences containing at least 11 amino acids (column 4 of Table 30). For comparative purposes, the first 20 amino acis of a known CBD sequence from a well expressed construct built at Amunix (AC616) was also included as a control.

Table 30: List of N-terminal helpers designed in the study

Plasmid	Protein description	1st 20aa	N-term Helpers
pSD0107	30S ribosomal protein S9	MAENQYYGTGRRKSSAARVF	MAENQYYGTGRRKSSAAR
pSD0108	50S ribosomal protein L32	MAVQQNKPTRSKRGMRRSHD	MAAQQNKPTRSKRGARRSHD
pSD0109	30S ribosomal protein S20	MANIKSAKKRAIQSEKARKH	MANAKSAKKRAAQSEKARKH
pSD0110	GrpE protein HSP-70 cofactor	MSSKEQKTPEGQAPEEIIMD	MSSKEQKTPEGQAPEE
pSD0111	30S ribosomal protein S14	MAKQSMKAREVKRVALADKY	MAKQSAKAREAKRAASADKY
pSD0112	30S ribosomal protein S12	MATVNQLVRKPRARKVAKSN	MATANQAARKPRARKAAKSN
pSD0113	Elongation factor Tu (EF-Tu) (P-43)	MSKEKFERTKPHVNVGTIGH	MSKEKAERTKPHANAGT
pSD0114	30S ribosomal protein S15	MSLSTEATAKIVSEFGRDAN	MSASTEATAKAASEAGRDAN
pSD0115	Superoxide dismutase [Mn] (EC 1.15.1.1) (MnSOD)	MSYTLPSLPYAYDALEPHFD	MSYTAPSAPYAYDAAEPH
pSD0116	rraB ribonuclease E inhibitor protein B	MANPEQLEEQREETRLIIEE	MANPEQAEEQREETR
pSD0117	Cellulose Binding Protein (CBD)	MANTPVSGNLKVEFYNSNPS	MANTPASGNAKAEAYNSNPS
pSD0118	CBD (from previous construct AC616)	MANTPVSGNLKVEFYNSNPS	MANTPVSGNLKVEFYNSNPS

[00462] DNA oligonucleotides for the 107N-F&R to 119N-F&R series and RP11F&R sequences of Table 31 were synthesized at Elim Biopharm (Hayward, CA). Solutions of each DNA pair (107N-F and 107N-R, 108N-F and 108N-R, etc) was mixed at a 1:1 molar ratio, were denatured at 95oC for 3 min, followed by cooling to 25oC at 0.1oC/min to allow double strand DNA annealing. The base vector LCW0970.030 (encoding CBD-AE864-GFP) was digested with NdeI/BsaI and the larger fragment was gel-purified as the vector. The vector was ligated with the annealed oligos 107-118N-F&R and PNK treated annealed RP11F&R oligos, and the ligation products were transformed into *E. coli* BL21 competent cells (New England Biolabs) to obtain the colonies designated pSD0107 to pSD118. The clones pSD0107-109, pSD0111-112, and pSD0114-118 were obtained and verified by DNA sequencing; clone pSD0110.001 had one mutation of frame-shift and was used as the stuffer vector.

[00463] The plasmid construct pCW1110 (encoding RP11-AE864) was digested with BsaI/NotI and the smaller band of corresponding to the nucleotides encoding AE864 was gel-purified as the insert. pCW1139 (encoding MalEss-AE48-payload-AE864) was digested by XhoI/BstXI/NotI and the larger fragment was gel-purified as the vector. The annealed product of oligos of 119-AEN-F&R was ligated with the insert and vector, and then transformed into E. coli BL21 to obtain colonies with the plasmid, designated pSD0119. The clones were sequence verified.

[00464] 2. Construction of N-term helper libraries based on pSD0116

[00465] DNA oligonucleotide pairs of Stuffer-RP5for & Stuffer-RP5revP, RP6-SASRSAforP & RP6-SASRSArev, L2for & L2rev, L3for & L3rev, L4for & L4rev, L5for & L5rev, L6for & L6rev, L7for & L7rev, L8for & L8rev, L9for & L9rev, L10for & L10rev, L11for & L11rev, L12for & L12rev, and L13for & L13rev (Table 31) were synthesized at Elim Biopharm (Hayward, CA) and each pair was annealed as described above (Section 1) to generate double strand DNA.

[00466] Plasmid pSD0110 was digested with NdeI/BsaI and the larger fragment was gel-purified as the vector. The vector was ligated with annealed oligos of Stuffer-RP5for&revP and RP6-SASRSAforP&rev, and then transformed into E. coli BL21 to obtain the colonies with the stuffer vector plasmid pCW1146 (Stuffer-RP11-XTEN_AE864_003-GFP). The clone was sequence verified.

[00467] The NdeI/BsaI digested pSD0110 vector was ligated with L5for&rev annealed oligos to obtain colonies of LCW1160 (L5).

[00468] The stuffer vector pCW1146 was digested with NdeI/BsaI and the larger fragment was gel-purified as the vector. The vector was ligated with annealed oligos of L2-4, and L6-13 for&rev as in Table 31, and then transformed into E. coli BL21 to obtain the colonies of constructs LCW1157 (L2), LCW1158 (L3), LCW1159 (L4), LCW1163 (L6), LCW1171 (L7), LCW1172 (L8), LCW1203 (L9), LCW1204 (L10), LCW1208 (L11), LCW1209 (L12), and LCW1210 (L13).

Table 31: List of DNA oligonucleotides

Name	DNA Sequence
RP11F	CGTCCGCGTCCTCGCCCACGTCCACGTCCGCGTCCACGCCCTCGTCCTCGTCCGCG CCCTCGTCCGagcgcgtctcgttccgctGGGTCTCC
RP11R	ACCTGGAGACCCAGCGGAACGAGACGCGCTCGGACGAGGGCGCGGACGAGGACG AGGGCGTGGACGCGGACGTGGACGTGGGCGAGGACGCG
107N-F	TATGGCTGAAAATCAATATTATGGTACGGGGCGCCGGAAGAGTTCGGCCGCC
107N-R	GACGGGCGGCCGAACTCTTCCGGCGCCCCGTACCATAATATTGATTTTCAGCCA
108N-F	TATGGCAGCTCAGCAGAATAAGCCTACACGAAGTAAAAGAGGCGCGCCGGTC GCACGAT
108N-R	GACGATCGTGCGACCGGCGCGCGCCTCTTTTACTTCGTGTAGGCTTATTCTGCTGA GCTGCCA
109N-F	TATGGCAAATGCTAAGAGTGCAAAGAAACGGGCGGCACAAAGCGAAAAAGCTCG GAAACAT
109N-R	GACGATGTTTCCGAGCTTTTTCGCTTTGTGCCGCCCGTTTCTTTGCACTCTTAGCAT TTGCCA
110N-F	TATGTCCAGCAAAGAACAGAAGACTCCGGAAGGTCAAGCGCCAGAGGAG
110N-R	GACGCTCCTCTGGCGCTTGACCTTCCGGAGTCTTCTGTTCTTTGCTGGACA
111N-F	TATGGCCAAACAAAGCGCTAAAGCCCGCGAGGCGAAACGTGCAGCCTCTGCGGA CAAATAT
111N-R	GACGATATTTGTCCGCAGAGGCTGCACGTTTCGCCTCGCGGGCTTTAGCGCTTTGT TTGGCCA
112N-F	TATGGCTACTGCAAATCAGGCCGCCCGTAAACCTCGAGCACGAAAGGCTGCTAAA TCAAAT

Name	DNA Sequence
112N-R	GACGATTTGATTTAGCAGCCTTTCGTGCTCGAGGTTTACGGGCGGCCTGATTTGCA GTAGCCA
113N-F	TATGTCCAAAGAAAAAGCCGAACGGACCAAACCTCATGCTAACGCTGGCACG
113N-R	GACGCGTGCCAGCGTTAGCATGAGGTTTGGTCCGTTCGGCTTTTTCTTTGGACA
114N-F	TATGTCAGCGTCTACGGAGGCAACCGCAAAAGCTGCTAGTGAAGCGGGCCGTGAT GCGAAT
114N-R	GACGATTCGCATCACGGCCCGCTTCACTAGCAGCTTTTGCGGTTGCCTCCGTAGAC GCTGACA
115N-F	TATGAGCTATACTGCACCGAGCGCACCGTATGCTTATGATGCAGCCGAACCTCAC
115N-R	GACGGTGAGGTTCGGCTGCATCATAAGCATACGGTGCGCTCGGTGCAGTATAGCT CA
116N-F	TATGGCAAACCCCGAACAGGCTGAGGAACAGAGAGAAGAAACA
116N-R	GACGTGTTTCTTCTCTCTGTTCCTCAGCCTGTTCGGGGTTTGCCA
117N-F	TATGGCTAATACCCCTGCGAGCGGGAACGCCAAGGCGGAAGCTTACAACAGTAAT CCAAGC
117N-R	GACGGCTTGGATTACTGTTGTAAGCTTCCGCCTTGGCGTTCCCGCTCGCAGGGGTA TTAGCCA
118N-F	TATGGCAAATACACCGGTATCAGGCAATTTGAAGGTTGAATTCTACAACAGCAAT CCTTCA
118N-R	GACGTGAAGGATTGCTGTTGTAGAATTCAACCTTCAAATTGCCTGATACCGGTGTA TTTGCCA
119-AEN-F	TCGAGCACGGGCAGCCCA
119-AEN-R	GACGTGGGCTGCCCGTGC
Stuffer-RP5for	TATGggctgaGGGTCTCaCGTCCGCGTCCTCGCCCACGTCCACGTCCGCGT
Stuffer-RP5revP	GGACGTGGACGTGGGCGAGGACGCGGACGtGAGACCCtcagccCA
RP6-SASRSAforP	CCACGCCCTCGTCCTCGTCCGCGCCCTCGTCCGagcgcgtctcgttccgc
RP6-SASRSArev	ACCTgcggaacgagacgcgctCGGACGAGGGCGCGGACGAGGACGAGGGCGTGGACGC
L2for	tATGaaaAAYCCNGARCARGCNGARGARCARMGYGARGARACa
L2rev	GACGTGTYTCYTCRCKYTGYTCYTCNGCYTGYTCNGGRTTTTTCA
L3for	tATGGCNAAYCCNGARCARGCNGARGARCARMGYGARGARACa
L3rev	GACGTGTYTCYTCRCKYTGYTCYTCNGCYTGYTCNGGRTTNGCCA
L4for	tATGaaaAAcCCVGARCARGCDGARGAaCARGCDGARGAaCAgMGYGAaGARACa
L4rev	GACGTGTYTCTTCRCKCTGTTCYTCHGCYTGTTCYTCHGCYTGYTCBGGGTTTTTC A
L5for	tATGaRaCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNCCNCGNC CNCGNCCNCGNCCNGGGTCTCC
L5rev	ACCTGGAGACCCNGGNCGNGGNCGNGGNCGNGGNCGNGGNCGNGGNCGNGGNC GNGGNCGNGGNCGNGGNCGNGGTYTCA
L6for	tATGaaaAAHMMVGARCARGCWGARGAaCARGCDGARGAaCAgMGYGAaGARACa
L6rev	GACGTGTYTCTTCRCKCTGTTCYTCHGCYTGTTCYTCWGCYTGYTCBKKDTTTTTC A
L7for	tATGAAAAAWCAMRARMARRMWRAARAAMAARMDRAARAACAGMGCGAAGAR ACA
L7rev	GACGTGTYTCTTCGCKCTGTTYTTYHKYTTKTTYTTYWKYYTKYTYKTGWTTTTTC A

Name	DNA Sequence
L8for	tATGAAAAAWCAMRARMARRMWRAARAAMAAGCDGAAGAACAGMGCGAAGARACA
L8rev	GACGTGTYTCTTCGCKCTGTTCTTCHGCTTKTTYTTYWKYYTKYTYKTGWTTTTTCA
L9for	tATGAAAAANCMMGAACAAGAARAARAAMAAGCNGAAGAACARCGYGARGARACA
L9rev	GACGTGTYTCYTCRCGYTGTTCTTCNGCTTKTTYTTYTTCTTGTTCKKGNTTTTTCA
L10for	tATGAAAAANCMMGAACAAGAARAARAAMAAGCNGAAGAAMARMRHRARRARAMA
L10rev	GACGTKTYTYYTYDYKYTKTTCTTCNGCTTKTTYTTYTTCTTGTTCKKGNTTTTTCA
L11for	tATGAAAAAACAAGAACAAGAAAAAGAACAAGCGGAAGAACAAKCNVARKCNVARCGTGAGGAGACA
L11rev	GACGTGTCTCCTCACGYTBNGMYTBNGMTTGTTCTTCCGCTTGTTCTTTTTCTTGTTCTTGTTTTTTCA
L12for	tATGAAAAAACAAGAACAAGAAAAAGAACAAGCGGAAGAACAAKCVVAAKCVVAAKCVVAAKCVVAACGTGAGGAGACA
L12rev	GACGTGTCTCCTCACGTTBBGMTTBBGMTTBBGMTTBBGMTTGTTCTTCCGCTTGTTCTTTTTCTTGTTCTTGTTTTTTCA
L13for	tATGAAAAAACAAGAACAAGAAAAAGAACAAGCGGAAGAACAANNNNNNNNNNNNNCGTGAGGAGACA
L13rev	GACGTGTCTCCTCACGNNNNNNNNNNNNTTGTTCTTCCGCTTGTTCTTTTTCTTGTTCTTGTTTTTTCA

[00469] 3. Screening and analysis of the N-terminal helper libraries LCW1157-1159

[00470] E. coli hosts transformed with the plasmids pSD0107 to pSD0118 were expressed in shake flasks and the expression levels in each were evaluated by measuring the fluorescence from the C-terminal GFP reporter. Briefly, an overnight culture was grown for each construct in SB media (with 12.5 µg/ml tetracycline), which was then used to inoculate a 200 ml culture of PhoA phosphate depletion autoinduction media with 12.5 µg/ml tetracycline (3 shake flasks were grown for each construct). After growing at 26 oC with 225 rpm for 48 h, 100 µl aliquot was taken from each culture and the GFP expression level was measured with a fluorescence plate reader with excitation wavelength of 395 nm and emission wavelength of 510 nm. Two readings were taken for each shake flask. Among the constructs tested, pSD0116 had the highest fluorescence signal, followed by pSD0114 (FIG. 81), but the expression levels of these two constructs were significantly lower than the LCW0970.030 (pLCW970) positive control.

[00471] In order to further improve expression, three libraries (LCW1157, 1158, and 1159) were built based on pSD0106, and were screened in a high through-put format. Large numbers of colonies from these libraries (Table 32) were picked to grow individually in 500 µl SB media (with 12.5 µg/ml tetracycline) in 96 deep well plates overnight at 37oC shaking with 300 rpm. 20 µl of the saturated culture was used to inoculate 500 µl of PhoA phosphate depletion autoinduction media (with 12.5 µg/ml tetracycline) in 96 deep well plates that were incubated at 26oC shaking with 300 rpm for 22-24 h. Expression was then determined by placing 100 µl of the culture into a 96 well plate measuring the fluorescence from the C-terminal GFP reporter.

Table 32: Libraries LCW1157-1159

Library	Description	N-terminal helper sequence (DNA)	Diversity	Number Screened
LCW 1157	Codon optimize helper sequence, Change 2nd codon to Lys (AAA)	ATGaaaAAY(C/T)CCN(A/G/C/T)GAR(A/G)CAR(A/G)GCN(A/C/T/G)GAR(A/G)GAR(A/G)CAR(A/G)M(A/C)GY(C/T)GAR(A/G)GAR(A/G)ACa	98304	406
LCW 1158	Codon optimize helper sequence	ATGGCN(A/G/C/T)AAY(C/T)CCN(A/G/C/T)GAR(A/G)CAR(A/G)GCN(A/G/C/T)GAR(A/G)GAR(A/G)CAR(A/G)M(A/C)GY(C/T)GAR(A/G)GAR(A/G)ACa	393216	85
LCW 1159	Insert AEEQ into helper sequence, Use fewer codons than LCW1157 to keep diversity manageable	ATGaaaAAcCCV(A/G/C)GAR(A/G)CAR(A/G)GCD(A/G/T)GAR(A/G)GAaCAR(A/G)GCD(A/G/T)GAR(A/G)GAaCAgM(A/C)GY(C/T)GAaGAR(A/G)ACa	20736	146

[00472] After evaluation of the fluorescence signal, the six highest expression clones and two low expression clones were chosen from each 96 deep well plate tested and the expression of these clones were tested again with 4 replicates. For all three libraries, clones having higher expression than the pSD0116 construct were identified (FIG. 82A-C), and the correlation between the original tests and retests was good (FIG. 82D-F). Among the 3 libraries tested, library LCW1159 gave higher expression level in general, and the highest expression construct from this round of screening (LCW1159.004) came from this library.

[00473] The 8 constructs with the highest expression levels from these three libraries and controls were treated with Pop Culture (EMD Millipore), were heat treated, and the resulting lysates were analyzed with SDS-PAGE/Coomassie staining (FIG. 83). Expression levels of the 8 constructs were confirmed to be higher than controls (negative control, LSD0114 and LSD0116), and full-length proteins were produced from these constructs. Lysates of 4 top expression constructs (after Pop Culture and heat treatment) and a negative control (AP32, a purified XTEN-GFP protein without RP11 tag) were each loaded onto a MacroCap SP column at pH of 8 and conductivity of 6.5 mS/cm. The column was washed with 20mM sodium phosphate, pH 8, 100mM NaCl, and the protein was eluted with 20mM sodium phosphate, pH 8, 500mM NaCl. The samples of the load, flow through, wash and elutate were analyzed by SDS-PAGE gel (FIG. 84). The results demonstrated that the expression protein of the four, which came from all three libraries, can be captured by MacroCap SP; thus the binding was contributed to the presence of the RP11 tag in the protein since the negative control (not containing the RP11 tag) didn't bind to the MacroCap SP column.

[00474] The plasmids of the clones chosen for retests were minipreped and the DNA sequences of the N-terminal helpers were analyzed. Codon bias was observed at several locations (Table 33). For example, the 3rd amino acid of LCW1157, N, is encoded by AAC or AAT. Most of the high expression clones (77%) in LCW1157 are encoded by AAT at the 3rd amino acid, while most of the low expression clones (88%) are encoded by AAC, indicating AAT is preferred over AAC at this position for high expression. Similarly, CCG is preferred at the 4th amino acid, while GCG at the 7th amino acid is accumulated in low expression clones. These trends were also observed in libraries LCW1158 and LCW1159, as well.

Table 33: Analysis of sequence results of high and low expression clones in libraries LCW1157-1159*

LCW1157															
amino acid#		2	3	4	5	6	7	8	9	10	11		12	13	14
		K(AAA)	N(AA+)	P(CC+)	E(GA+)	Q(CA+)	A(GC+)	E(GA+)	E(GA+)	Q(CA+)	R or S(+G+)		E(GA+)	E(GA+)	T(AC+)
codon			3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	1st	3rd	3rd	3rd	
high	A		0%	10%	57%	67%	33%	80%	70%	50%	30%	0%	63%	57%	
total:30	G		0%	43%	43%	33%	7%	20%	30%	50%	0%	0%	37%	43%	
	C		23%	23%	0%	0%	13%	0%	0%	0%	70%	67%	0%	0%	
	T	K(AAA)	77%	23%	0%	0%	47%	0%	0%	0%	0%	33%	0%	0%	T(ACA)
low	A		0%	13%	88%	50%	25%	38%	63%	25%	63%	0%	75%	63%	
total:8	G		0%	13%	13%	50%	63%	63%	38%	75%	0%	0%	25%	38%	
	C		88%	0%	0%	0%	0%	0%	0%	0%	38%	38%	0%	0%	
	T		13%	75%	0%	0%	13%	0%	0%	0%	0%	63%	0%	0%	

LCW1158															
amino acid#		2	3	4	5	6	7	8	9	10	11		12	13	14
		A(GC+)	N(AA+)	P(CC+)	E(GA+)	Q(CA+)	A(GC+)	E(GA+)	E(GA+)	Q(CA+)	R or S(+G+)		E(GA+)	E(GA+)	T(AC+)
codon		3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	1st	3rd	3rd	3rd	
high	A	83%	0%	33%	17%	67%	50%	83%	50%	83%	83%	0%	67%	50%	
total:6	G	0%	0%	0%	83%	33%	0%	17%	50%	17%	0%	0%	33%	50%	
	C	0%	33%	33%	0%	0%	33%	0%	0%	0%	17%	100%	0%	0%	
	T	17%	67%	33%	0%	0%	17%	0%	0%	0%	0%	0%	0%	0%	T(ACA)
low	A	0%	0%	0%	100%	0%	0%	0%	0%	0%	0%	0%	0%	100%	
total:2	G	100%	0%	100%	0%	100%	100%	100%	100%	100%	0%	0%	100%	0%	
	C	0%	0%	0%	0%	0%	0%	0%	0%	0%	100%	100%	0%	0%	
	T	0%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	

LCW1159																				
amino acid#		2	3	4	5	6	7	8	9	10	11	12	13	14	15		16	17	18
		K(AAA)	N(AA+)	P(CC+)	E(GA+)	Q(CA+)	A(GC+)	E(GA+)	E(GA+)	Q(CA+)	A(GC+)	E(GA+)	E(GA+)	Q(CA+)	R or S(+G+)		E(GA+)	E(GA+)	T(AC+)
codon			3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	3rd	1st	3rd	3rd	3rd	
high	A			42%	67%	67%	50%	75%		67%	50%	58%			25%	0%		58%	
total:12	G			17%	33%	33%	0%	25%		33%	17%	42%			0%	0%		42%	
	C			42%	0%	0%	0%	0%		0%	0%	0%			75%	75%		0%	
	T	K(AAA)	N(AAC)	0%	0%	0%	50%	0%	E(GAA)	0%	33%	0%	E(GAA)	Q(CAG)	0%	25%	E(GAA)	0%	T(ACA)
low	A			33%	100%	67%	0%	67%		67%	100%	100%			33%	0%		33%	
total:3	G			33%	0%	33%	100%	33%		33%	0%	0%			0%	0%		67%	
	C			33%	0%	0%	0%	0%		0%	0%	0%			67%	67%		0%	
	T			0%	0%	0%	0%	0%		0%	0%	0%			0%	33%		0%	

* The total numbers of high and low expression clones analyzed are specified for each library, and the percentages of A, G, C, or T in each of the location where the codon was varied were analyzed.

[00475] 4. Screening and analysis of the N-terminal helper library LCW1163

[00476] Since library LCW1159 had generally higher expression than LCW1157 and LCW1158, the next library design was based on LCW1159, with the introduction of more variants in the N-terminal helper domain coding region. A total of 672 clones from this library

(theoretical diversity of 55296) was screened and retested in the same way as libraries LCW1157-1159. Clones with higher expression than LCW1159.004 (the highest from the previous round of screening) were observed (FIG. 85). The top expression clone, LCW1163.029, achieved a 40% improvement from LCW1159.004, while its expression level was 27% lower than the CBD control. The sequence of the high and low expression clones were analyzed, and the preferred nucleotides for expression were identified and summarized (see Table 34). Most of the locations have shown a preference of codon A for high expression, while others have a preference for C.

Table 34: Analysis of sequence results of high and low expression clones in the library LCW1163*

		Expression (Percentage)													
nucleotide number		#9	#10	#11	#12	#15	#18	#21	#24	#30	#33	#36	#43	#45	#51
high expression	A	74	17	74	40	37	40	66	77	60	43	66	40	0	34
	C	17	83	26	49	0	0	0	0	0	0	0	60	83	0
	T	9	0	0	0	0	0	34	0	0	29	0	0	17	0
	G	0	0	0	11	63	60	0	23	40	29	34	0	0	66
low expression	A	20	70	3	20	40	20	60	50	30	10	20	50	0	60
	C	60	30	70	30	0	0	0	0	0	0	0	50	50	0
	T	20	0	0	0	0	0	40	0	0	40	0	0	50	0
	G	0	0	0	50	60	80	0	50	70	50	80	0	0	40
preferred		A	C	A	A/C				A	A		A		C	

[00477] * The percentages of A, G, C, or T in each of the location where the codon was varied were analyzed, and the identified preferred nucleotides were summarized in the bottom row

[00478] 5. Screening and analysis of the RP11 library LCW1160

[00479] At the same time, 168 colonies from library LCW1160 (the library varying the coding region of RP11 tag without any N-terminal helper domain (total theoretical diversity of $8.8X10^{12}$) were screened and analyzed. However, this library had very low expression level in general (FIG. 86), and the one outlier with high expression was found to encode a truncated RP11 tag after performing plasmid miniprep and DNA sequencing analysis. The screening results of the library, under these experimental conditions, strongly suggest that an N-terminal helper is required to achieve high expression levels.

[00480] 6. Screening of the N-terminal helper libraries LCW1171, LCW1172, LCW1203, and LCW1204.

[00481] More N-terminal libraries (LCW1171, LCW1172, LCW1203, and LCW1204) were screened and analyzed in the same way as those described above. LCW1171 and 1172 were designed similarly, while LCW1171 allowed more amino acid changes in the helper sequence than LCW1172. The screening results showed that LCW1171 in general had much lower

expression level than LCW1172 (FIGS. 94A and B). LCW1203 and 1204 were designed similarly, focusing on randomizing a different region of the helper sequence compared with LCW1171 and 1172. LCW1204 allowed more amino acid changes than LCW1203, which resulted in lower expression than LCW1203 in general (FIGS 94C and D). These results suggest that the expression level is sensitive to amino acid changes in the helper domain sequences.

[00482] 7. Screening of the N-terminal helper libraries LCW1208, LCW1209, and LCW1210.

[00483] Three new N-terminal libraries (LCW1208, LCW1209, and LCW1210) were designed to investigate the effect of further elongation the N-terminal helper sequence (Table 35). LCW1208 and LCW1210 introduced 4 more residues to the helper domain, while LCW1209 introduced 8 more residues. The screening results showed a general trend that LCW1209 had highest expression, followed by LCW1208, and then LCW1210 (FIG.95), which confirmed the beneficial effect of adding more amino acid in the helper sequence.

Table 35: Libraries LCW1208-1210

Library	N-terminal Helper Sequence (amino acid)	Diversity	Number Screened
LCW1208	MKKQEQEKEQAEEQ*BXBX*REET (B=A/S; X=E/K/Q)	2304	336
LCW1209	MKKQEQEKEQAEEQ*BXBXBXBX*REET (B=A/S; X=E/K/Q)	104976	336
LCW1210	MKKQEQEKEQAEEQ*ZZZZ*REET (Z=any amino acid)	262144	336

[00484] Additional residues in the helper sequences were underlined.

[00485] Three new N-terminal libraries (LCW1208, LCW1209, and LCW1210) were designed to investigate the effect of further elongation the N-terminal helper sequence (Table 36). LCW1208 and LCW1210 introduced 4 more residues to the helper domain, while LCW1209 introduced 8 more residues. The screening results showed a general trend that LCW1209 had highest expression, followed by LCW1208, and then LCW1210 (FIG. 95), which confirmed the beneficial effect of adding more amino acids in the helper sequence for improving expression.

[00486] The 4 top constructs with the highest expression levels from the three libraries were chosen from the retest and the sequence of their N-terminal helper sequences were analyzed (Table 36). The current highest expressed construct (LCW 1209.029) achieved 90% of the expression level of the CBD control by comparing the average florescence after subtracting the negative control.

Table 36: Constructs with the highest expression levels from Libraries LCW1208-1210 and controls.

Sample name	Avg. Fluorescence	Helper sequence*

LCW1208.009	9070	MKKQEQEKEQAEEQ*AESE*REET
LCW 1208.007	8870	MKKQEQEKEQAEEQ*AESE*REET
LCW 1208.008	8800	MKKQEQEKEQAEEQ*SQSQ*REET
LCW 1208.010	8740	MKKQEQEKEQAEEQ*SESE*REET
LCW 1209.029	10010	MKKQEQEKEQAEEQ*AKAESEAE*REET
LCW 1209.015	9440	MKKQEQEKEQAEEQ*SKSQAEAE*REET
LCW 1209.023	8980	MKKQEQEKEQAEEQ*AQAQAEDE*REET
LCW 1209.010	8580	MKKQEQEKEQAEEQ*SKSKAEDE*REET
LCW 1210.030	8650	MKKQEQEKEQAEEQ*PEVQ*REET
LCW 1210.032	8310	MKKQEQEKEQAEEQ*VENP*REET
LCW 1210.025	8100	MKKQEQEKEQAEEQ*ELCE*REET
LCW 1210.009	8030	MKKQEQEKEQAEEQ*GIDT*REET
CBD control	10940	n/a
Negative control	1630	n/a

*Additional residues in the helper sequences were underlined.

[00487] In summary, the screening results, under these experimental conditions, strongly suggest that an N-terminal helper contributes in achieving high expression levels.

[00488] Example 13: Fermentation of XTEN using PhoA induction- Evaluation of Expression Yields

[00489] *E. coli* BL21 carrying the plasmids encoding Helper_LCW1159.004-RP11-AE288-His8 (AC767), Helper_LCW1172.033-RP11-AE576-His8 (AC780), and Helper_LCW1172.033-RP11-AE864-His8 (AC786) were transformed into the *E. coli* BL21 strain. Three 10L fermentations were run for each of the 3 strains. Glycerol stocks were used to inoculate 125 mL of LB broth media containing 10 µg/mL tetracyclin. The starter cultures were then shaken overnight at 37°C. The starter culture was used to inoculate 4L of fermentation batch media containing -20 g ammonium sulfate, 10.4 g potassium phosphate dibasic anhydrous, 5 g sodium citrate dihydrate; 4.6 g sodium phosphate monobasic monohydrate; 106 g NZ BL4 soy peptone (Kerry Bioscience #5X00043); 54 g yeast extract (Teknova #Y9020); 3.6 L water; 0.05 mL polypropylene glycol; 5.2 mL trace elements solution (Amunix recipe 144-1); 35mL 1M magnesium sulfate; and 4 mL Kanamycin (50mg/mL)- in 10 L glass jacketed vessel with a B. Braun Biostat B controller. The fermentation control settings were: pH = 6.9 +/- 0.1; dO_2 = 10%; dissolved oxygen cascade in stirrer only mode with a range of 125 – 1180 rpm; air flow of 5 liters per minute of 90% oxygen; initial temperature 37°C; base control 13% ammonium hydroxide; and no acid control. After 6 hours of culture a 70% glycerol feed was initiated at a rate of 40 g/hr. Upon the cultures reaching an OD600 of 50 +/- 10 OD the culture temperature was lowered to 26°C, 54 mL of 1M magnesium sulfate was added, and a salt feed consisting of: 10 g/l ammonium sulfate, 26 g/l potassium phosphate dibasic anhydrous, 2 g/l sodium citrate dihydrate; 13 g/l sodium phosphate monobasic monohydrate; 15 g/l potassium phosphate monobasic anhydrous; 0.08% trace elements solution, was started at a rate of 33 g/L and continued for 6 hours. After a total fermentation run time of 64-70 hours the culture was harvested by centrifugation yielding cell pellets between 1.6-2.3 kilograms in wet weight. The

pellets were stored frozen at -80°C until further use. For titer analysis, end of run fermentation whole broth samples were frozen in a 0.2mL volume, then later thawed, then 0.2mL of water was added, then to lyse and flocculate host proteins the samples were incubated at 85oC for 15 minutes, then transferred to 4°C for 15 minutes, followed centrifugation for 10 minutes at 20,000g. The resulting flocculated soluble lysates were assayed by C18 reversed phased HPLC, and the A214 absorbance area corresponding of the peaks representing the Helper-RP11-XTEN-His8 was compared to that of purified reference standard. Next, to determine the dry cell weight (DCW), aliquots of cells were pelleted and the supernatant discarded. The cell pellet was washed once with water, and was then dried in an oven at 80° C for 3 days. The tubes containing cell pellets were weighed, the weight of the tube was subtracted from the measured weights, and the remaining weight was divided by the initial volume of each sample (0.0002 L) to obtain the DCW. The results of the fermentation growth, titer analysis, and dry cell weight are summarized in Table 37 below. In 96-well plate screening assays, when a library of RP11-XTEN-His8 constructs without an N-terminal helper, LCW1160 were screened (Example 12, FIG. 86) the expression level of the LCW1160.006, the highest expression construct, was only 50% of the expression of LCW1159.004 or LCW1172.033; constructs with helper sequences. Therefore, it is expected that XTEN constructs with N-terminal helper sequences will result in significantly higher expression titers compared to XTEN constructs not having helper sequences.

Table 37: Measured expression parameters

XTEN Series	Fermentation #	Final O.D.	Total Run Time (hours)	Dry cell weight per Liter of Ferm (g/L)	Titer by culture volume (g/L)	Average titer (micromoles/L)	Titer / Dry weight ferm (mg of XTEN / g of *E. coli*)	MW (g/mol)	Titer (micromoles /L)	Average titer (micromoles/L)	Std error of the mean (micromoles/L)
Helper_ LCW1159.004-RP11-AE288-His8 (AC767)	EC846	140	67.5	95	0.5	0.7	5.6	26399	212	271	76
	EC888	140	64	85	0.8		9.4	26399	357		
	EC903	136	69	103	0.7		6.4	26399	243		
Helper LCW1172.033-RP11-AE576-His8 (AC780)	EC850	125	66	107	1.1	2.0	10.0	52929	189	388	182
	EC869	140	70	90	2.1		22.8	52929	430		
	EC883	170	67	102	2.9		28.8	52929	545		
Helper LCW1172.033-RP11-AE864-His8 (AC786)	EC873	135	68	91	2.0	2.1	22.2	79284	280	272	41
	EC889	145	65.5	95	2.3		24.4	79284	308		
	EC913	108	67	108	2.0		18.1	79284	228		

[00490] Example 14: Purification of XTEN with RP11 and His8 tags

[00491] 1. Expression, lysis and clarification

[00492] The fusion protein MKNPEQAEEQAEEQREET-RP11-SASRSA-XTEN_AE432(C12,C217,C422)-SASRSA-His(8)], with the N-terminal helper sequence from the library member LCW1159.004 described in Example 10, with two affinity tags linked to XTEN at the N- and C-terminus, respectively, was expressed in *E.coli* using a 4 L fermenter using conditions described herein. After growth, the cells were harvested by centrifugation and frozen at -80°C until use. The cell pellet was resuspended in lysis buffer (20 mM sodium phosphate, 50 mM NaCl, 2 mM EDTA pH 8.0, 3 ml buffer per gram cell paste). The cells were lysed by passing through an APV homogenizer three times at a pressure of 830-900 bar. Lysis buffer (1 ml buffer per gram cell paste) was used as a chase to retrieve hold up volume from the homogenizer. The homogenized lysate was incubated in a water bath at 85°C for 20 minutes, followed by quick cooling in ice water bath for 20 minutes. After the heating and cooling treatment, the lysate was centrifuged at 11000 RPM for 90 minutes in a SORVALL centrifuge. After centrifugation, the supernatant was filtered through two CUNO Bio cap 25 (BC0025L90SP08A) filters. The clarified supernatant was stored at 4°C overnight.

[00493] 2. Capture Step: Toyopearl IMAC Chromatography

[00494] IMAC affinity chromatography was used as a capture step for binding the XTEN with an intact C-terminal His-tag. Briefly, the chromatography column BPG140/12 (GE Life Sciences) was packed with 2000 ml Toyopearl IMAC 650 M resin (TOSOH Biosciences). The column was equilibrated with 2 column volumes (CVs) of equilibrium buffer (20 mM sodium phosphate, 500 mM NaCl, pH 8.0). Clarified cell lysate was adjusted to a final NaCl concentration of 500 mM using 5 M NaCl stock solution, and then was loaded onto the IMAC resin. The column was washed with 2 column volumes of equilibrium buffer, and then 2 column volumes of 20 mM sodium phosphate, 500 mM NaCl, 5 mM Imidazole pH 8.0, followed by 2 column volumes of 20 mM sodium phosphate, 5 mM imidazole pH 8.0 to remove salt. Elution was performed with 2 column volumes of 20 mM sodium phosphate, 100 mM imidazole, pH 8.0. The flow through, wash and elution fractions were analyzed by non-reducing 4 -12% Bis-Tris SDS-PAGE/Coomassie staining and the fractions with the desired product were pooled.

[00495] 3. Polishing/Capture Step: MacroCap SP Chromatography

[00496] Cation exchange chromatography was used as a polishing step to ensure the N-terminal integrity of the product. MacroCap SP resin (GE Life Sciences) was selected among several cation exchange media due to its superior capacity and selectivity for the product. 1000 ml of MacroCap SP resin was packed in a BPG100/13 (GE Life Sciences) chromatography column and equilibrated with 20 mM sodium phosphate pH 8.0, 20 mM NaCl. The IMAC pool was loaded

onto the column and the resin was washed with 2 column volumes of 20 mM sodium phosphate, 50 mM NaCl, pH 8.0 and 2 column volumes of 20 mM sodium phosphate pH 8.0, 150 mM NaCl. The protein was eluted with 5 column volumes of linear gradient from 150 to 500 mM NaCl in 20 mM sodium phosphate pH 8.0. Fractions were collected and analyzed by 4-12% Bis-Tris SDS/PAGE. Fractions the with desired product were combined for the next step.

[00497] 4. Trypsin digestion of Macrocap SP elution pool

[00498] Trypsin (Sigma, Trypsin from Bovine Pancreas) digestion of the SP elution pool was performed at 1:200 m/m enzyme/protein ratio overnight at 37°C.

[00499] 5. Polishing Step: Macrocap Q Chromatography

[00500] After trypsin digestion, the cleaved tags were separated from the final product using Macrocap Q chromatography. The BPG100/19 column (GE Life Sciences) was packed with 1500 ml column volume of Macrocap Q resin (GE Life Sciences). The trypsin digested Macrocap SP elution pool was incubated for 15 min at 80o C with 20 mM DTT and 2 mM EDTA to reduce disulfide bonds and to inactivate trypsin. The cooled protein solution was diluted to a conductivity below 5 mS/cm with Milli-Q water and loaded onto the Macrocap Q column equilibrated with 20 mM HEPES, 50 mM NaCl, pH 7.0. The column was washed with 2 column volumes of 20 mM HEPES, 50 mM NaCl, pH 7.0, then 2 column volumes of 20 mM HEPES, 2 mM TCEP, 150mM NaCl pH7.0. The protein was eluted with a linear gradient from 150mM NaCl to 500 mM NaCl in 20 mM HEPES, pH 7.0 in 20 column volumes. Fractions were analyzed by SDS-PAGE/silver staining.

[00501] 6. Concentration and Diafiltration (Final Formulation)

[00502] Selected MacroCap Q fractions were combined and concentrated and using 10 KD Pellicon mini (Millipore) at a feed pressure < 20 psi and retentate < 8 psi, followed by 10X diafiltratiion with 20 mM HEPES, 50 mM NaCl, pH 7.0 to achieve a final protein concentration of > 5 mg/ml.

[00503] 9. Purity analysis of proteins purified with different methods

[00504] One batch (Batch 1) was purified through three purification steps as described above. Another batch (Batch 2) was purified from the same fermented material but the MacroCap SP polishing step was omitted. Truncated species of XTEN were detected by SDS-PAGE/silver staining in MacroCap Q elution fractions for Batch 2 (FIG. 87A), while the MacroCap Q elution fractions for Batch 1 were essentially free from truncations (FIG. 87B). These results support that, under the conditions employed, the MacroCap SP step based on the RP11 tag is essential to ensure N-terminal integrity and overall product quality.

[00505] Example 15: Construction of 1xAmino, 9xThiol-XTEN432

[00506] The following sets of primers 5Afor&CI1BbsIrev-TGGC, CI1BsaIfor-TGGC&CI2-AE38BbsIrev, and CI2-AE38BsaIfor&AatIICI3-2P were used to PCR plasmid pCW1164

containing XTEN_AE432 (C422) in order to obtain the PCR products of AE-CI1, CI1-2 and CI2-3, respectively. CI1, 2&3 were designated Cysteine Island1, 2&3, having the same amino acid sequence TAEAAGCGTAEAA but with different codon usages. Gel-purification of the PCR products was performed to obtain bands of the right sizes, which were digested with restriction enzymes SbfI/BbsI, BsaI/BbsI and BsaI/AatII, respectively, as the inserts. Digestion of the plasmid pCW1164, which encodes the gene of N-term-RP11-R-XTEN_AE432 (C422)-R-H8, was performed with SbfI/AatII to remove the fragment of about 290 amino acids within XTEN_AE432 and gel-purification was performed on the remaining large fragment as the vector. Ligation of the vector with the three inserts of PCR products, above, was performed and used to transform BL21 competent cells in order to obtain the construct N-term-RP11-R-XTEN_AE432 (C319, C370, C422)-R-H8. PCR was performed on this construct with primers CI1BsaIfor-TGGC&AatIICI3-2P to obtain a PCR product of around 360 bp in length. Gel-purification of the band of the right size was performed, followed by digestion with BsaI/AatII as the insert XTEN_AE120-3Cys, which contains three Cysteine Islands.

[00507] Simultaneously, the codon-optimized DNA fragment of XTEN_AE313-6Cys, containing six Cysteine Islands, was designed and synthesized (Genscript). The fragment was digested by the flanking restriction enzymes BsaI/BbsI and gel-purified as the insert containing the first six Cysteine Islands of XTEN_AE432. Digestion of the plasmid pCW1161, which encodes the gene of N-term-RP11-R-XTEN_AE432_3Cys-R-H8, with BsaI/AatII was performed to remove the fragment of XTEN_AE432_3Cys and gel-purification was performed to obtain the large fragment as the vector. Ligation of the vector with the BsaI/BbsI digested insert of XTEN_AE313-6Cys and BsaI/AatII digested insert of XTEN_AE120-3Cys, above, was performed. The ligated product was used to transform BL21 competent cells in order to obtain the construct N-term-RP11-R-XTEN_AE432 (C12, C63, C114, C165, C217, C268, C319, C370, C422)-R-H8. The construct was designed to produce the precursor N-term-RP11-R-AE432_9Cys-R-H8 (sequence in Table 38, below), the product of which was used to generate 1xAmino, 9-Thio-XTEN432 after removal of the N-term-RP11 tag and C-term 8xHis-tag by trypsin digestion. The final product contains nine cysteines in the XTEN432 sequence (Seg 177).

Table 38: DNA and amino acid sequence for 1xAmino, 9-Thio-XTEN432

Clone Name	DNA Sequence	Amino Acid Sequence
N-term-RP11-R-AE432_9Cys-R-H8	ATGAAAAACCCAGAGCAAGCAGAAGAACAAGCTGAAGA ACAGCGCGAAGAAACACGTCCGCGTCCTCGCCCACGTCC ACGTCCGCGTCCACGCCCTCGTCCTCGTCCGCGCCCTCGT CCGagcgcgtctcgttccgctGGGTCTCCAACGGCAGAGGCAGCAG GTTGTGGTACAGCAGAAGCAGCTCCGGGTAGCGAGCCTG CAACCAGCGGTTCTGAGACGCCGGGCACTTCCGAATCTG CGACCCCGGAGTCCGGTCCAGGTTCAGAGCCGGCGACGA GCGGTTCGGAAACGCCGGGTACTGCTGAAGCGGCTGGTT	MKNPEQAEEQAE E QREETRPRPRPRP RPRPRPRPRPRPR PSASRSAGSPTAE AAGCGTAEAAPG S EPATSGSETPGTS

Clone Name	DNA Sequence	Amino Acid Sequence
	GTGGTACTGCTGAAGCTGCATCGACCGAACCAAGCGAAG GTTCGGCACCGGGTACTAGCGAGAGCGCAACCCCTGAAA GCGGTCCGGGCAGCCCGGCAGGTTCTCCAACCAGCACCG AAGAAGGTTCCCCTGCTACTGCCGAAGCTGCAGGCTGCG GTACTGCGGAGGCGGCGTCCCCAACTTCTACTGAGGAAG GTACTTCTGAGTCCGCTACCCCAGAAAGCGGTCCTGGTAC CTCCACTGAACCGTCTGAAGGCTCTGCACCAGGCACTTCT GAGTCTGCTACTACCGCCGAAGCCGCTGGTTGTGGTACCG CAGAAGCTGCATCTGAGACTCCAGGCACTTCTGAGTCCG CAACGCCTGAATCCGGTCCTGGTTCTGAACCAGCTACTTC CGGCAGCGAAACCCCAGGTACCTCTGAGTCTGCGACTCC AGAGTCTGGTACCGCGGAAGCGGCTGGTTGTGGTACTGC AGAGGCAGCTGGTTCTCCGGCTGGTAGCCCGACCAGCAC GGAGGAGGGTACGTCTGAATCTGCAACGCCGGAATCGGG CCCAGGTTCGGAGCCTGCAACGTCTGGCAGCGAAACCCC GGGTACCACGGCGGAAGCGGCAGGTTGTGGCACCGCGGA GGCAGCAGCTGGTTCTCCAACCTCTACCGAGGAGGGTTC ACCGGCAGGTAGCCCGACTAGCACTGAAGAAGGTACTAG CACGGAGCCGAGCGAGGGTAGTGCTCCGGGTACGAGCGA GAGCACGGCAGAAGCCGCTGGCtgcGGTACTGCTGAAGCG GCAACCCCTGAGAGCGGCCCAGGTACTTCTGAGAGCGCC ACTCCTGAATCCGGCCCTGGTAGCGAGCCGGCAACCTCC GGCTCAGAAACTCCTGGTTCGGAACCAGCGACCAGCGGT ACCGCTGAAGCCGCAGGTtgtGGCACTGCGGAAGCTGCAA CCGAAGAGGGTACCAGCACGGAACCGAGCGAGGGTTCTG CCCCGGGTACTTCCACCGAACCATCGGAGGGCTCTGCAC CTGGTAGCGAACCTGCGACGTCTGGTTCTGAAACGCCGA CTGCAGAAGCGGCTGGTtgtGGCACCGCCGAAGCAGCTagcg cctctcgctccgcaCATCACCATCACCACCATCATCACTAA	ESATPESGPGSEP ATSGSETPGTAEA AGCGTAEAASTE P SEGSAPGTSESAT PESGPGSPAGSPT STEEGSPATAEAA GCGTAEAASPTS T EEGTSESATPESG PGTSTEPSEGSAP GTSESATTAEAA G CGTAEAASETPG T SESATPESGPGSE PATSGSETPGTSE SATPESGTAEAA G CGTAEAAGSPAG S PTSTEEGTSESAT PESGPGSEPATSG SETPGTTAEAAG C GTAEAAAGSPTS T EEGSPAGSPTSTE EGTSTEPSEGSAP GTSESTAEAAGC G TAEAATPESGPGT SESATPESGPGSE PATSGSETPGSEP ATSGTAEAAGCG T AEAATEEGTSTEP SEGSAPGTSTEPS EGSAPGSEPATSG SETPTAEAAGCG T AEAASASRSAHH H HHHHH

[00508] Example 16: Construction of 1xAmino, 9xThiol-XTEN864

[00509] The primers PhoAfor&RP11-SASRSABsaIrevAGGT were used to PCR the plasmid containing N-term-RP11 tag to obtain the PCR product of N-term-RP11-R. Gel-purification of the band of the right size was performed and was digested with NdeI/BsaI as the first insert. Another PCR was performed with primers AE432BsaIforAGGT&AE432_001BbsIrev-AACG on the plasmid containing XTEN_AE864_003 in order to obtain the PCR product of XTEN_AE432. Gel purification was performed on the band of the right size, which was digested with BsaI/BbsI as the second insert. Digestion of the construct N-term-RP11-R-AE432_9Cys-R-H8 from

Example 10 was performed with NdeI/BsaI to remove the N-term-RP11-R fragment and gel purification was performed to obtain the large fragment as the vector. Ligation of the vector with the first and second inserts, above, was performed and the product was used to transform BL21 competent cells in order to obtain the construct N-term-RP11-R-XTEN_AE864 (C444, C495, C546, C597, C649, C700, C751, C802, C854)-R-H8. The resulting construct was designed to produce the precursor N-term-RP11-R-AE864_9Cys-R-H8 (sequence in Table 39, below) the product of which would generate 1xAmino, 9-Thio-XTEN864 after removal of the N-term-RP11 tag and C-term 8xHis-tag by trypsin digestion. The resulting product contains an N-terminal amino group and nine cysteines in the XTEN864 sequence for conjugation (Seg 175).

Table 39: DNA and amino acid sequence for 1xAmino, 9-Thio-XTEN864

Clone Name	DNA Sequence	Amino Acid Sequence
N-term-RP11-R-AE864_9Cys-R-H8	ATGAAAAACCCAGAGCAAGCAGAAGAACAAGCTGAAGA	MKNPEQAEEQAE
	ACAGCGCGAAGAAACACGTCCGCGTCCTCGCCCACGTCC	E
	ACGTCCGCGTCCACGCCCTCGTCCTCGTCCGCGCCCTCGT	QREETRPRPRPRP
	CCGagcgcgtctcgttccgctGGGTCTCCAGGTAGCCCAGCTGGTA	RPRPRPRPRPRPR
	GCCCAACCTCTACCGAAGAAGGTACCTCTGAATCCGCTA	PSASRSAGSPGSP
	CTCCAGAATCCGGTCCTGGTACTAGCACTGAGCCAAGCG	AGSPTSTEEGTSE
	AAGGTTCTGCTCCAGGCTCCCCGGCAGGTAGCCCTACCTC	SATPESGPGTSTE
	TACCGAAGAGGGCACTAGCACCGAACCATCTGAGGGTTC	PSEGSAPGSPAGS
	CGCTCCTGGCACCTCCACTGAACCGTCCGAAGGCAGTGCT	PTSTEEGTSTEPS
	CCGGGTACTTCCGAAAGCGCAACTCCGGAATCCGGCCCT	EGSAPGTSTEPSE
	GGTTCTGAGCCTGCTACTTCCGGCTCTGAAACTCCAGGTA	GSAPGTSESATPE
	GCGAGCCAGCGACTTCTGGTTCTGAAACTCCAGGTTCACC	SGPGSEPATSGSE
	GGCGGGTAGCCCGACGAGCACGGAGGAAGGTACCTCTGA	TPGSEPATSGSET
	GTCGGCCACTCCTGAGTCCGGTCCGGGCACGAGCACCGA	PGSPAGSPTSTEE
	GCCGAGCGAGGGTTCAGCCCCGGGTACCAGCACGGAGCC	GTSESATPESGPG
	GTCCGAGGGTAGCGCACCGGGTTCTCCGGCGGGCTCCCC	TSTEPSEGSAPGT
	TACGTCTACGGAAGAGGGTACGTCCACTGAACCTAGCGA	STEPSEGSAPGSP
	GGGCAGCGCGCCAGGCACCAGCACTGAACCGAGCGAAG	AGSPTSTEEGTST
	GCAGCGCACCTGGCACTAGCGAGTCTGCGACTCCGGAGA	EPSEGSAPGTSTE
	GCGGTCCGGGTACGAGCACGGAACCAAGCGAAGGCAGC	PSEGSAPGTSESA
	GCCCCAGGTACCTCTGAATCTGCTACCCCAGAATCTGGCC	TPESGPGTSTEPS
	CGGGTTCCGAGCCAGCTACCTCTGGTTCTGAAACCCCAGG	EGSAPGTSESATP
	TACTTCCACTGAACCAAGCGAAGGTAGCGCTCCTGGCAC	ESGPGSEPATSGS
	TTCTACTGAACCATCCGAAGGTTCCGCTCCTGGTACGTCT	ETPGTSTEPSEGS
	GAAAGCGCTACCCCTGAAAGCGGCCCAGGCACCTCTGAA	APGTSTEPSEGSA
	AGCGCTACTCCTGAGAGCGGTCCAGGCTCTCCAGCAGGT	PGTSESATPESGP
	TCTCCAACCTCCACTGAAGAAGGCACCTCTGAGTCTGCTA	GTSESATPESGPG
	CCCCTGAATCTGGTCCTGGCTCCGAACCTGCTACCTCTGG	SPAGSPTSTEEGT
	TTCCGAAACTCCAGGTACCTCGGAATCTGCGACTCCGGA	SESATPESGPGSE
	ATCTGGCCCGGGCACGAGCACGGAGCCGTCTGAGGGTAG	PATSGSETPGTSE
	CGCACCAGGTACCAGCACTGAGCCTTCTGAGGGCTCTGC	SATPESGPGTSTE
	ACCGGGTACCTCCACGGAACCTTCGGAAGGTTCTGCGCC	PSEGSAPGTSTEP
	GGGTACCTCCACTGAGCCATCCGAGGGTTCAGCACCAGG	SEGSAPGTSTEPS
	TACTAGCACGGAACCGTCCGAGGGCTCTGCACCAGGTAC	EGSAPGTSTEPSE
	GAGCACCGAACCGTCGGAGGGTAGCGCTCCAGGTAGCCC	GSAPGTSTEPSEG
	AGCGGGCTCTCCGACAAGCACCGAAGAAGGCACCAGCAC	SAPGTSTEPSEGS
	CGAGCCGTCCGAAGGTTCCGCACCAACGGCAGAGGCAGC	APGSPAGSPTSTE
	AGGTTGTGGTACAGCAGAAGCAGCTCCGGGTAGCGAGCC	EGTSTEPSEGSAP
	TGCAACCAGCGGTTCTGAGACGCCGGGCACTTCCGAATC	TAEAAGCGTAEA

Clone Name	DNA Sequence	Amino Acid Sequence
	TGCGACCCCGGAGTCCGGTCCAGGTTCAGAGCCGGCGAC GAGCGGTTCGGAAACGCCGGGTACTGCTGAAGCGGCTGG TTGTGGTACTGCTGAAGCTGCATCGACCGAACCAAGCGA AGGTTCGGCACCGGGTACTAGCGAGAGCGCAACCCCTGA AAGCGGTCCGGGCAGCCCGGCAGGTTCTCCAACCAGCAC CGAAGAAGGTTCCCCTGCTACTGCCGAAGCTGCAGGCTG CGGTACTGCGGAGGCGGCGTCCCCAACTTCTACTGAGGA AGGTACTTCTGAGTCCGCTACCCCAGAAAGCGGTCCTGGT ACCTCCACTGAACCGTCTGAAGGCTCTGCACCAGGCACTT CTGAGTCTGCTACTACCGCCGAAGCCGCTGGTTGTGGTAC CGCAGAAGCTGCATCTGAGACTCCAGGCACTTCTGAGTC CGCAACGCCTGAATCCGGTCCTGGTTCTGAACCAGCTACT TCCGGCAGCGAAACCCCAGGTACCTCTGAGTCTGCGACT CCAGAGTCTGGTACCGCGGAAGCGGCTGGTTGTGGTACT GCAGAGGCAGCTGGTTCTCCGGCTGGTAGCCCGACCAGC ACGGAGGAGGGTACGTCTGAATCTGCAACGCCGGAATCG GGCCCAGGTTCGGAGCCTGCAACGTCTGGCAGCGAAACC CCGGGTACCACGGCGGAAGCGGCAGGTTGTGGCACCGCG GAGGCAGCAGCTGGTTCTCCAACCTCTACCGAGGAGGGT TCACCGGCAGGTAGCCCGACTAGCACTGAAGAAGGTACT AGCACGGAGCCGAGCGAGGGTAGTGCTCCGGGTACGAGC GAGAGCACGGCAGAAGCCGCTGGCtgcGGTACTGCTGAAG CGGCAACCCCTGAGAGCGGCCCAGGTACTTCTGAGAGCG CCACTCCTGAATCCGGCCCTGGTAGCGAGCCGGCAACCT CCGGCTCAGAAACTCCTGGTTCGGAACCAGCGACCAGCG GTACCGCTGAAGCCGCAGGTtgtGGCACTGCGGAAGCTGC AACCGAAGAGGGTACCAGCACGGAACCGAGCGAGGGTT CTGCCCCGGGTACTTCCACCGAACCATCGGAGGGCTCTGC ACCTGGTAGCGAACCTGCGACGTCTGGTTCTGAAACGCC GACTGCAGAAGCGGCTGGTtgtGGCACCGCCGAAGCAGCTa gcgcctctcgctccgcaCATCACCATCACCACCATCATCACTAA	A PGSEPATSGSETP GTSESATPESGPG SEPATSGSETPGT AEAAGCGTAEAA S TEPSEGSAPGTSE SATPESGPGSPAG SPTSTEEGSPATA EAAGCGTAEAAS P TSTEEGTSESATP ESGPGTSTEPSEG SAPGTSESATTAE AAGCGTAEAASE T PGTSESATPESGP GSEPATSGSETPG TSESATPESGTAE AAGCGTAEAAGS P AGSPTSTEEGTSE SATPESGPGSEPA TSGSETPGTTAEA AGCGTAEAAAGS P TSTEEGSPAGSPT STEEGTSTEPSEG SAPGTSESTAEAA GCGTAEAATPES G PGTSESATPESGP GSEPATSGSETPG SEPATSGTAEAA G CGTAEAATEEGT S TEPSEGSAPGTST EPSEGSAPGSEPA TSGSETPTAEAAG CGTAEAASASRS A HHHHHHHH

[00510] Example 17: Fermentation of XTEN for Conjugation

[00511] Starter cultures were prepared by inoculating glycerol stocks of *E. coli* carrying the plasmid containing the appropriate XTEN for conjugation protein sequences into 125 mL of LB Broth media containing 50 µg/mL kanamycin. The cultures were then shaken overnight at 37°C. The starter culture was used to inoculate 2L of fermentation batch media containing -12.5g ammonium sulfate, 15g potassium phosphate dibasic anhydrous, 2.5g sodium citrate dihydrate; 8.5g sodium phosphate monobasic monohydrate; 50g NZ BL4 soy peptone (Kerry Bioscience #5X00043); 25g yeast extract (Teknova #Y9020); 1.8L water; 0.5mL polypropylene glycol;

2.5mL trace elements solution (Amunix recipe 144-1); 17.5mL 1M magnesium sulfate; and 2mL Kanamycin (50mg/mL)- in 5L glass jacketed vessel with a B. Braun Biostat B controller. The fermentation control settings were: pH = 6.9 +/- 0.1; dO2 = 10%; dissolved oxygen cascade in stirrer only mode with a range of 125 – 1180 rpm; air flow of 5 liters per minute of 90% oxygen; initial temperature 37°C; base control 13% ammonium hydroxide; and no acid control. After 6 hours of culture a 50% glucose feed was initiated at a rate of 30g/hr. After 20 hours of culture, 25mL of 1M magnesium sulfate and 3mL of 1M IPTG were added. After a total fermentation run time of 45 hours the culture was harvested by centrifugation yielding cell pellets between 0.45-1.1 kilograms in wet weight for all constructs. The pellets were stored frozen at -80°C until further use. Culture samples at multiple time points in the fermentation were taken, the cells were lysed, then cell debris was flocculated with heat and rapid cooling, clarified soluble lysates were prepared by centrifugation and analyzed by a regular non-reducing SDS-PAGE using NuPAGE 4-12% Bis-Tris gel from Invitrogen according to manufacturer's specifications with Coomassie staining. An example of the accumulation of XTEN fusion protein as a function of fermentation run time is shown in FIG. 45. The results showed that the XTEN fusion protein constructs were expressed at fermentation scale with titers > 1g/L, with an apparent MW of about 160 kDa (note: the actual molecular weight are 100 kDa. The observed migration in SDS-PAGE was comparable to that observed for other XTEN-containing fusion proteins).

[00512] Example 18: Purification of 1xThiol-XTEN (Cysteine-engineered XTEN) Reagent with CBD and His8 tags

[00513] The example describes the purification of a cysteine-engineered XTEN comprising a single cysteine residue.

[00514] Materials and Methods:

[00515] 1. Clarification

[00516] 20 gm of cell paste from the fermentation was resuspended in 100 ml of 20 mM sodium phosphate, pH 8.0 (Lysis Buffer). Cell lysate was homogenized between 800 - 900 bars three times in a homogenizer. 50 ml of lysis buffer was used as a chase to retrieve hold-up volume from the homogenizer. The homogenized lysate was incubated in a water bath at 85°C for 20 minutes, followed by quick cooling in an ice water bath for 20 minutes. After the heating & cooling treatment, the lysate was centrifuged at 11000 RPM for 90 minutes in SORVALL centrifuge. After centrifugation, the supernatant was filtered through two CUNO Bio cap 25 (BC0025L90SP08A) filters. Filters were chased with 40 ml of lysis buffer. The final volume of clarified material was 230 ml. The clarified supernatant was stored at 4^0C overnight.

[00517] 2. Capture Step: Hydrophobic Interaction Chromatography

[00518] Hydrophobic interaction chromatography was used as a first step using hydrophobic CBD tag of XTEN to ensure the capture of N-terminal intact protein. Toyopearl Phenyl 650M

(Part # 0014783, TOSOH Bioscience) was used to pack XK16 to 15 cm bed height (30 ml column volume). The chromatography was performed using AKTA FPLC (GE Biosciences). Toyopearl Phenyl resin was equilibrated with 2 column volume of 20 mM Sodium Phosphate, 1M Sodium Sulfate, pH 8.0 prior to loading. HIC load was prepared by adding Sodium Sulfate to 1 M concentration to above clarified lysate (final volume ~ 250 ml). The sample was loaded on HIC resin (~ 4 mg/ml resin load) at 2 ml/min. Load was completed by chasing with ~ 9 column volume of equilibrium buffer (20 mM Sodium Phosphate, 1M Sodium Sulfate, pH 8.0) till UV215 was stable. Protein was step eluted with 100% B (20 mM Sodium Phosphate, pH 8.0). A total of 7 column volumes of elution buffer was applied to confirm complete elution (FIG. 46).

[00519] Samples were analyzed by 4 -12% Bis -Tris SDS-PAGE (non-reducing) to determine elution pool (FIG. 47). Based on the following gel elution, fractions E1, E2, E3 & E4 were pooled for further processing. The total protein was estimated to be 85 mg in HIC elution pool, with a 65% step yield determined by running another quantitation gel.

[00520] 3. Polishing/Capture Step: Toyopearl IMAC Chromatography

[00521] IMAC affinity chromatography was used as a capture step for binding to intact C-terminal His-tag of XTEN. A chromatography column XK26 was packed with Toyopearl IMAC 650 M (Part # 0014907, TOSOH Biosciences) with 15 cm bed height (85 ml Column volume). The column was equilibrated with 2 column volume of 20 mM sodium phosphate, 10 mM imidazole, 0.25 M NaCl, pH 8.0 (equilibrium buffer). IMAC load was prepared by adding 5M NaCl to the HIC elution pool to make 0.25 M NaCl in the final volume. The sample was loaded on IMAC resin at 4 ml/min flow rate. The load was completed by 2 column volumes of equilibrium buffer. Resin was washed with 2 column volumes of 20 mM Sodium Phosphate, 10 mM Imidazole, pH 8.0 to remove salt. A linear elution was performed from 0 to 100%B in 7 column volume with buffer A (20 mM Sodium Phosphate, 10 mM Imidazole, pH 8.0) and buffer B (20 mM Sodium Phosphate, 200 mM imidazole, pH 8.0) followed by 2 CV of 100% B. Presence of imidazole maintained UV 215 absorbance above 3500 mAu with AKTA FPLC, so an elution peak was not observed. The flow through, wash and elution fractions were analyzed by 4 -12% Bis-Tris non-reducing SDS-PAGE gel (FIG. 48). The gel shows the successful removal of host cell protein and truncated XTEN species (FIG. 48A). Based on the second gel (FIG. 48B), fractions C5, C6 & C7 were pooled. A total of 70 mg of protein was estimated in the IMAC elution pool.

[00522] 4. Trypsin digestion of IMAC elution pool

[00523] Trypsin digestion of IMAC elution pool was performed at a 1:200 m/m ratio. 0.35 mg of bovine trypsin from pancreas (Sigma, cat # T1426) was incubated with 70 mg of Protein (IMAC elution pool) overnight at 37°C. Non-reducing 4-12% Bis-Tris SDS-PAGE analysis was performed to confirm that cleavage of the CBD tag was completed as shown in FIG. 49.

[00524] 5. Polishing Step: MacroCap Q Chromatography

[00525] After trypsin digestion, cleaved tags were separated using MacroCap Q chromatography. An XK 16 column was packed with 18 cm bed height with MacroCap Q (GE Life Sciences, Cat# 17-5469-02). Trypsin digested IMAC elution pool was incubated for 1 hour at 37°C with 2 mM TCEP to reduce dimers of XTEN prior to loading on MacroCap Q column. Column was equilibrated with 20 mM HEPES, pH 7.0. The sample was loaded at 4 ml/min (~ 2 mg/ml resin load). Column loading was completed with additional 2 column volume of 20 mM HEPES, 2 mM TCEP pH 7.0. The column was washed with 2 column volumes of (20 mM HEPES, 2 mM TCEP, 150 mM NaCl pH 7.0). A linear gradient elution from 150 mM NaCl to 500 mM NaCl in 20 mM HEPES, 2 mM TCEP, pH 7.0 buffer was performed over 20 column volumes. UV 215 was observed at a high level during the entire chromatography (FIG. 50) due to presence of TCEP, but the elution peak was observed between 22 to 30 mS/cm. All samples were analyzed by SDS-PAGE, silver staining and C18 RP-HPLC. Removal of cleaved CBD was observed in the flow through (FIG. 51A), while very faint bands of XTEN were observed in elution fractions (FIG. 51B) in elution fractions E11, E12, F12, F11, F10… F6). Separation of truncation species of XTEN were observed by silver staining in earlier elution fractions E11, E12, F12 & F11 as species migrating faster than the main XTEN polypeptide (FIG. 51C). Based on the above results, elution fractions were further analyzed by C18 RP-HPLC. FIG. 52 shows the stacked chromatography profiles of the RP-HPLC analysis. Earlier elution fractions had wide leading shoulder indicating significant presence of truncated species. Also, these earlier fractions (E12, F12 & F11) were enriched with proteolysis tags. Based on the above analysis, elution fractions F10, F9, F8, F7 and F6 were pooled. The elution pool was analyzed again by C18 RP-HPLC (FIG. 53). The purified protein was found to be 97.5% pure.

[00526] 6. Concentration and Diafiltration (Final Formulation)

[00527] The above MacroCap Q pool was concentrated using Amicon Ultracel-15 (MWCO 10k) centrifugal device to 5 ml followed by 7X diafiltration with 20 mM HEPES pH 7.0 to a final protein concentration of 8.13 mg/ml. Total of 43 mgs of protein was purified from 20 gm of cell pellet. The overall recovery for three step chromatography was estimated at ~ 33%.

[00528] Example 19: Purification of 1xAmino-XTEN Reagent with CBD and His8 tags

[00529] Purification of amino-XTEN was performed essentially as described for the purification of the 1xThiol-XTEN containing one cysteine (see Example 15 for details). 20 gm of cell paste from fermentation was homogenized in 100 ml of 20 mM sodium phosphate, pH 8.0 (Lysis Buffer), heat treated and clarified by centrifugation and filtration. Hydrophobic interaction chromatography was used as a first step to capture N-terminal intact protein (FIG. 54). Fractions E2, E3, & E4 were pooled for further processing. IMAC affinity chromatography was used as a capture step to bind intact C-terminal His-tag of XTEN (FIG. 55). Fractions E2 and E3 were

pooled. Trypsin digestion of IMAC elution pool was performed at1:200 m/m ratio overnight at 37°C. After trypsin digestion cleaved tags were separated using MacroCap Q chromatography. Fractions were analyzed by SDS-PAGE followed by silver staining (FIG. 56) and C18 RP-HPLC (FIG. 57). Based on above analysis elution fractions C10, C11 and C12 were pooled. Elution pool was analyzed again by C18 RP-HPLC (FIG. 58). Protein was found to be >98% pure. MacroCap Q pool was concentrated using Amicon Ultracel-15 (MWCO 10k)centrifugal device at 3000 RPM to 5 ml followed by 7X diafiltration with 20 mM HEPES pH 7.0 to final protein concentration to 5.35 mg/ml.

[00530] Example 20: Purification and Assessment of RP11/His8-XTEN Two-tag System

[00531] Using expression vectors as described above, two-tagged XTEN proteins were constructed to encode fusion proteins with the following amino acid sequences or components: MKIKTGARILALSALTTMMFSASALAAPTTAGAG-Tag-XTEN_AE869(Am1)-RHHHHHHHH, where: MKIKTGARILALSALTTMMFSASALA is a MalE recognition sequence that is cleaved from the polypeptide expressed and transported to the host cell periplasm, APTTAGAG is a spacer, and Tag is from the following (tag name followed by sequence in parentheses): RP5 (RPRPRPRPRPGR); RP7 (RPRPRPRPRPRPRPGR); KP5 (KPKPKPKPKPGR); RP9 (RPRPRPRPRPRPRPRPRPGR); RP11 (RPRPRPRPRPRPRPRPRPRPRPGR); P5K4P9 (RPRPKPRPKPRPKPRPKPGR); and R6K5P11 (RPRPKPRPKPRPKPRPKPRPKPGR). All variations of the contructs with tags were made and the proteins were expressed in *E.coli* using the methods as described in Example 15. Soluble extracts were prepared from the host cell for SDS-PAGE/Coomassie staining analysis. By analysis, the N-terminal tag length and amino acid composition did not affect protein expression noticeably (see FIG. 59) for expression of constructs with RP7, RP9, RP11 and R6K5P11 tags. Expressed proteins with the RP5, RP7, RP9 and RP11 tags proteins were further tested for binding to MacroCap SP resin. Proteins with longer tags bound more efficiently to cation exchange resin, and remained bound under more stringent wash conditions. Thus RP11 tag was selected as N-terminal tag for purification of XTEN using cation exchange chromatography. An additional experiment showed that RP11-XTEN-His8 polypeptide was efficiently expressed in fermenter and most of the expressed protein was found in the cell pellet fraction (FIG. 60).

[00532] Example 21: Purification of 1xAmino-XTEN reagent with RP11/H8 two-tag system

[00533] 1. Expression

[00534] The RP11-XTEN-His8 precursor of 1xAmino-XTEN was produced by expression in transformed *E. coli* using a 4 L fermention reaction as described. Cells were harvested by centrifugation and frozen at -80°C until use.

[00535] 2. Lysis and clarification

[00536] 25 g of cell paste was resuspended in 75 mL of 20 mM sodium phosphate pH 8.0, 50 mM NaCl, 2 mM EDTA. Lysis was performed by passing the resuspended paste through a homogenizer at 800-900 bar three times. Homogenate was held at 85°C in a water bath for 15 min before it was quickly cooled down using an ice/water bath until the temperature dropped to below 10°C. The treated homogenate was then centrifuged at 10, 000 rpm in SLA-3000 rotor for 60 minutes. Supernatant was collected and filtered using a 0.22 μm bottletop filter.

[00537] 3. Cation exchange capture step

[00538] Cation exchange chromatography was used as a capture step to ensure N-terminal integrity of the product. MacroCap SP resin (GE Healthcare) was selected among several cation exchange media due to its superior capacity and selectivity for the product. A 20 mL MacroCap SP column was packed in a Redi-Sep housing and equilibrated with 20 mM sodium phosphate (pH 8.0), 20 mM NaCl buffer. The lysate was loaded onto the column by gravity. Three column volumes (CV) of 20 mM sodium phosphate pH 8.0, 100 mM NaCl was applied as the wash step before protein was step-eluted with 3 CVs of 20 mM sodium phosphate pH 8.0, 500 mM NaCl. Half CV fractions (10 mL) were collected for elutions and analyzed by 4-12% Bis-Tris SDS/PAGE (FIG. 61). Elution fractions 2-4 were combined for the subsequent chromatography step.

[00539] 4. IMAC polishing step

[00540] A 20-mL ToyoPearl AF-Chelate column was packed in a Redi-Sep column housing and charged with 100 mM nickel sulfate. The column was equilibrated with 20 mM sodium phosphate pH 8.0, 500 mM NaCl before the MacroCap SP pool was loaded onto the column by gravity. Two wash steps were applied using 20 mM sodium phosphate (pH 8.0), 500 mM NaCl, 5 mM imidazole buffer followed by 20 mM sodium phosphate (pH 8.0), 5 mM imidazole. Product was then eluted from the column using 20 mM sodium phosphate, 100 mM imidazole and half CV (10 mL) fractions were collected for 4 CVs of elution. Samples from each step were examined by 4-12% Bis-Tris SDS/PAGE (FIG. 62). Based on the gel, elutions 2 and 3 were pooled for further processing. The overall yield was 30%.

[00541] 5. Trypsin digestion of IMAC elution pool

[00542] Trypsin digestion of the IMAC pool was performed at 1:200 and 1:500 m/m ratio by adding 1 mg/mL bovine trypsin (Sigma, Cat # T1426, Trypsin from Bovine Pancreas) to the IMAC pool. The reaction mixtures were held at 37°C overnight and the completion of digestion was confirmed by MALDI-TOF mass spectrometry. Pre- and post-digest samples were analyzed by 4-12% Bis-Tris SDS/PAGE stained by both Coomassie and silver stain (FIG. 63). Fainter staining on Coomassie-stained gel as well as the shifting of the molecule weight for the post-digestion samples, when compared to pre-digestion sample, indicates the successful removal of both N- and C-terminal tags. A silver stained gel showed homogeneous bands after digestion,

suggesting the absence of truncated species in the sample, supporting the conclusion that the RP11/H8 two-tag system and purification methods provides a homogeneous final XTEN product.

[00543] Example 22: Purification of XTEN with RP11 and His8 affinity tags

[00544] 1. Expression

[00545] The fusion protein RP11-XTEN-His8, with two affinity tags linked to XTEN at the N- and C-terminus, respectively, was expressed in E.coli using a 4 L fermention reaction using conditions described.

[00546] 2. Lysis and clarification

[00547] After growth, the cells were harvested by centrifugation and frozen at -80°C until use. The cell pellet was resuspended in lysis buffer (20 mM sodium phosphate, 50 mM NaCl, 2 mM EDTA pH 8.0, 3 ml buffer per gram cell paste). The cells were lysed by passing through an APV homogenizer three times at a pressure of 830-900 bar. Lysis buffer (1 ml buffer per gram cell paste) was used as a chase to retrieve hold up volume from the homogenizer. The homogenized lysate was incubated in a water bath at 85°C for 20 minutes, followed by quick cooling in ice water bath for 20 minutes. After the heating and cooling treatment, the lysate was centrifuged at 11000 RPM for 90 minutes in a SORVALL centrifuge. After centrifugation, the supernatant was filtered through two CUNO Bio cap 25 (BC0025L90SP08A) filters. The clarified supernatant was stored at 4°C overnight.

[00548] 3. Capture Step: Toyopearl IMAC Chromatography

[00549] IMAC affinity chromatography was used as a capture step for binding the XTEN with an intact C-terminal His-tag. Briefly, the chromatography column BPG140/12 (GE Life Sciences) was packed with 2000 ml Toyopearl IMAC 650 M resin (TOSOH Biosciences). The column was equilibrated with 2 column volumes (CVs) of equilibrium buffer (20 mM sodium phosphate, 500 mM NaCl, pH 8.0). Clarified cell lysate was adjusted to a final NaCl concentration of 500 mM using 5 M NaCl stock solution, and then was loaded onto the IMAC resin. The column was washed with 2 column volumes of equilibrium buffer, and then 2 column volumes of 20 mM sodium phosphate, 500 mM NaCl, 5 mM Imidazole pH 8.0, followed by 2 column volumes of 20 mM sodium phosphate, 5 mM Imidazole pH 8.0 to remove salt. Elution was performed with 2 column volumes of 20 mM sodium phosphate, 100 mM Imidazole, pH 8.0. The flow through, wash and elution fractions were analyzed by non-reducing 4 -12% Bis-Tris SDS-PAGE/Coomassie staining and the fractions with the desired product were pooled.

[00550] 4. Polishing/Capture Step: MacroCap SP Chromatography

[00551] Cation exchange chromatography was used as a polishing step to ensure the N-terminal integrity of the product. MacroCap SP resin (GE Life Sciences) was selected among several cation exchange media due to its superior capacity and selectivity for the product. 1000 ml of MacroCap SP resin was packed in a BPG100/13 (GE Life Sciences) chromatography column and

equilibrated with 20 mM sodium phosphate pH 8.0, 20 mM NaCl. The IMAC pool was loaded onto the column and the resin was washed with 2 column volumes of 20 mM sodium phosphate, 50 mM NaCl, pH 8.0 and 2 column volumes of 20 mM sodium phosphate pH 8.0, 150 mM NaCl. The protein was eluted with 5 column volumes of linear gradient from 150 to 500 mM NaCl in 20 mM sodium phosphate pH 8.0. Fractions were collected and analyzed by 4-12% Bis-Tris SDS/PAGE. Fractions the with desired product were combined for the next step.

[00552] 5. Trypsin digestion of Macrocap SP elution pool

[00553] Trypsin (Sigma, Trypsin from Bovine Pancreas) digestion of the SP elution pool was performed at 1:200 m/m enzyme/protein ratio overnight at 37°C.

[00554] 6. Polishing Step: Macrocap Q Chromatography

[00555] After trypsin digestion, the cleaved tags were separated from the final product using Macrocap Q chromatography. The BPG100/19 column (GE Life Sciences) was packed with 1500 ml column volume of Macrocap Q resin (GE Life Sciences). The trypsin digested Macrocap SP elution pool was incubated for 15 min at 80o C with 20 mM DTT and 2 mM EDTA to reduce disulfide bonds and to inactivate trypsin. The cooled protein solution was diluted to a conductivity below 5 mS/cm with Milli-Q water and loaded onto the Macrocap Q column equilibrated with 20 mM HEPES, 50 mM NaCl, pH 7.0. The column was washed with 2 column volumes of 20 mM HEPES, 50 mM NaCl, pH 7.0, then 2 column volumes of 20 mM HEPES, 2 mM TCEP, 150mM NaCl pH7.0. The protein was eluted with a linear gradient from 150mM NaCl to 500 mM NaCl in 20 mM HEPES, pH 7.0 in 20 column volumes. Fractions were analyzed by SDS-PAGE/silver staining.

[00556] 7. Concentration and Diafiltration (Final Formulation)

[00557] Selected MacroCap Q fractions were combined and concentrated and using 10 KD Pellicon mini (Millipore) at a feed pressure < 20 psi and retentate < 8 psi, followed by 10X diafiltratiion with 20 mM HEPES, 50 mM NaCl, pH 7.0 to achieve a final protein concentration of > 5 mg/ml.

[00558] 8. Purity analysis of proteins purified with different methods

[00559] One batch (Batch 1) was purified through three purification steps as described above. Another batch (Batch 2) was purified from the same fermented material but the MacroCap SP polishing step was omitted. Truncated species of XTEN were detected by SDS-PAGE/silver staining in MacroCap Q elution fractions for Batch 2 (FIG. 87A), while the MacroCap Q elution fractions for Batch 1 were essentially free from truncations (FIG. 87B). These results support that, under the conditions employed, the MacroCap SP step based on the RP11 tag is essential to ensure N-terminal integrity and overall product quality and that the RP11/H8 two-tag system and purification methods provides a homogeneous final XTEN product.

[00560] Example 23: Conjugation of the DBCO-Mal Linker to 3xThiol-XTEN to Make an XTEN Precursor

[00561] A 3x-Thiol-XTEN (XTEN_AE905(Am1,C8,C453,C898, Seg 174)) cysteine-engineered XTEN segment was prepared for reaction as a 193 uM (16 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. DBCO-Maleimide (Click Chemistry Tools, Inc., cat. # A108) was dissolved in DMF to a final concentration of 50 mM. An aliquot of the 3xThiol-XTEN (5.1 mg, 320 µl) was reduced with 10mM freshly reconstituted DTT at 70°C for 20 minutes. The protein sample was diluted to 600 µl total volume with water. 1200 µl of 100% acetonitrile was added and the mixture was centrifuged at 13,000 rpm for 5 minutes. The supernatant was removed, 1000 µl of 80% acetonitrile was added and the mixture was centrifuged at 13,000 rpm for 1 minute. The wash step was repeated once more. The pellet was dissolved in 300 µl 100 mM HEPES pH 7.0. A 7.7 µl 50 mM solution of DBCO-Mal in DMF was added (1:6 molar ratio of 3xThiol-XTEN to DBCO-Maleimide) and was incubated for 2 hours at 25°C. Completion of modification was monitored by C18 RP-HPLC analysis (FIG. 64A). The protein mixture was purified by hydrophobic interaction chromatography (HIC) using a 1.6 ml Toyopearl butyl column. Elution was performed with a 30 column volume descending gradient of ammonium sulfate from 1.05 M to 0.3M in 20 mM Phosphate, pH 7.0 buffer at 0.5ml/min flow rate (FIG.64B). Chromatographic fractions were analyzed by C18 RP-HPLC (FIG. 64C).

[00562] Example 24: Trypsin cleavage and purification of double tagged precursor.

[00563] Trypsin digestion

[00564] A double-tagged (CBD/His8) precursor of XTEN_AE870_Am1,C1 stains well with Coomassie due to the presence of CBD sequence, while a no-tagged version of XTEN_AE870_Am1,C1 stains poorly with Coomassie, but can be detected by silver staining. Therefore, trypsin digestion completeness was monitored using both Coomassie staining (FIG. 65A) and silver staining (FIG. 65B) techniques. The double tagged precursor of XTEN_AE870_Am1,C1 was digested with different ratios of bovine trypsin and proteomics grade porcine trypsin (positive control) in 20 mM phosphate buffer, pH 8:. Overnight incubation at 37°C allowed more complete digestion than overnight incubation at 25°C based on detection of remaining Coomassie stained 160 kDa band of double tagged precursor (FIG. 65A: all ratios refer to mass/mass ratio of trypsin to substrate). FIG. 65B shows that 1:100, 1:200 and 1:500 ratio digests with bovine trypsin and 1:100 digests with porcine trypsin resulting in efficient digestion of the XTEN precursor.

[00565] MacroCap Q purification of trypsin digested double tagged precursor

[00566] 1:200 ratio of bovine trypsin to double tagged precursor (mass/mass) was used for digestion at 37°C overnight. FIG. 66A shows >90% conversion of double tagged precursor to

digested product. This was demonstrated by disappearance of the Coomassie stained band at ~160kDa after digestion and appearance of 20 kDa CBD fragment.

[00567] Trypsin digested material was subjected to step purification using MacroCap Q anion exchange resin and following buffers: A: 20mM HEPES, 50mM NaCl, pH 7.5 and B: 20mM HEPES, 500mM NaCl, pH 7.5. Digested material was loaded by gravity and eluted in a stepwise manner using 3 column volume washes of 0%, 20%, 40%, 60%, 80% and 100% Buffer B consecutively. XTEN_AE870 eluted in 60%B. FIG. 66B shows that cleaved CBD fragment did not bind to MacroCap Q under used conditions and was completely separated from XTEN. Stepwise elution of XTEN from MacroCap Q only partially separated truncated polypeptides. Better separation was achieved by gradient elution of XTEN (FIG. 66C).

[00568] Test for residual trypsin activity

[00569] To test the presence of residual trypsin activity in the final formulated XTEN preparations, a protein sample was mixed with synthetic [G2]GLP2 peptide at 10:1 mass/mass ratio. A positive control for digestion contained [G2]GLP2 peptide and bovine trypsin; A negative control contained [G2]GLP2 peptide only. All samples were incubated overnight at 37°C. After incubation samples were quenched with 1% TFA and subjected to C18 RP-HPLC analysis using Phenomenex Jupiter C18 5um 300A analytical column. Buffer A contained 0.1%TFA, 99.9% HPLC grade H_2O; Buffer B contained 0.1%TFA, 99.9% HPLC grade Acetonitrile. Analysis was performed using a gradient of 5% B to 50% B over 45min elution time. FIG. 67 shows the results of RP-HPLC analyses of residual trypsin activity in the XTEN_AE869(Am1,C2) final preparation. FIG. 67A shows the intact GLP2 peptide (41 min retention time). FIG. 67B shows tryptic digest of GLP2 peptide with two characteristic tryptic fragments(33.5 min and 34 min retention time). FIG. 67C shows that GLP2 peptide remained intact after overnight incubation with XTEN and no tryptic fragments were observed. This result indicates that final MacroCap Q purified preparations do not contain any residual trypsin activity.

[00570] Example 25: Fermentation and Purification of Cysteine-engineered XTEN for Conjugation

[00571] *E. coli* containing AC292 on a plasmid was grown to saturation overnight in 2xYT and then 200 ml of this culture was used to inoculate a 25L culture of 2xYT media in a wavebag. Both cultures were in the presence of 50 μg/ml kanamycin. The second culture was grown to an OD600 of ~1.0 at 37°C, chilled to 26°C, and induced with 12 ml of 1M IPTG overnight. The cell pellet was harvested at 4000 rpm in a SLA-3000 rotor spinning for 20 minutes. The cell pellet (184g) was resuspended in 736 ml of 20 mM Tris pH 6.8, 50 mM NaCl. The resuspended cells were lysed with a microfluidizer at 20,000 psi and then heated to 75°C for 15 minutes, followed by rapid cooling on ice for 30 minutes. The lysate was then clarified by centrifugation. The clarified lysate was then loaded on to a DE52 column, previously sanitized with NaOH and

equilibrated with 20 mM Tris pH 6.8, 50 mM NaCl. The column was washed with 5 column volumes of 20 mM Tris pH 6.8, 50 mM NaCl, 5 column volumes of 20 mM Tris pH 6.8, 150 mM NaCl and eluted with 5 column volumes of 20 mM Tris pH 6.8, 250 mM NaCl. The pooled elution fractions. were then loaded on to a macrocapQ column, previously sanitized with NaOH and equilibrated with 20 mM Tris pH 6.8, 50 mM NaCl. The column was washed with 9 column volumes of 20 mM Tris pH 6.8, 50 mM NaCl, 9 column volumes of 20 mM Tris pH 6.8, 100 mM NaCl and eluted with 9 column volumes of 20 mM Tris pH 6.8, 250 mM NaCl. The pooled elution fractions were adjusted to a 15% w/v sodium sulfate and then loaded on to a octyl sepharose FF column column, previously sanitized with NaOH and equilibrated with Tris pH 7.5. The column was washed with 4 column volumes of 20 mM Tris pH 7.5 15% w/v sodium sulfate, and eluted with 4 column volumes of 20 mM Tris pH 7.5, 5% w/v sodium sulfate. The sample was stored at 4°C and given the lot # AP197. The purified cysteine-engineered XTEN could then serve as a suitable reactant for conjugation with a payload, such as a drug from Table 11, resulting in an XTEN-drug conjugate.

[00572] Example 26: Conjugation of GLP2-Cys to 1xAmino-XTEN to result in XTEN-payload of GLP2-XTEN

[00573] A 1xAmino-XTEN (XTEN_AE869(Am1)) was prepared as 67 uM (5.35 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. Sulfo-SMCC (Thermo Scientific, cat. # 22322) was prepared fresh as 100 mM solution in DMSO. 10 mg of amino-XTEN (1.87 ml) was mixed with 15-molar excess of sulfo-SMCC (18.7ul) and incubated for 1 hr at 25°C. Excess cross-linker was removed by centrifugal filtration using Amicon Ultra-15, MWCO 5k centrifugal device. A volume of 1.8 ml reaction mixture was mixed with 8 ml 20 mM HEPES pH 7.0, 50 mM NaCl and centrifuged for 20 min in Sorvall RT6000 centrifuge at 3000rpm, 4°C. The procedure was repeated two more times. Final volume of recovered retentate was 1.8 ml. The GLP2-Cys peptide (CSBio, custom synthesis) was dissolved in 20 mM HEPES pH 7.0, 50 mM NaCl to the final concentration 3 mg/ml. N-Maleimide-XTEN was mixed with 2.3-fold molar excess of GLP2-Cys peptide and was incubated for 1 hr at 25°C. Completion of the modification was monitored by C18 RP-HPLC. 20 µg protein samples were loaded on Phenomenex Jupiter C18 5uM 300A 4.6mm x 150mm column. Proteins were eluted with 5-50% gradient of acetonitrile in 0.1% trifluoroacetic acid and detected by absorbance at 214 nm. Essentially all N-maleimide-XTEN was converted into GLP2-Cys-XTEN conjugate, as demonstrated by HPLC and electrospray mass spectrometry (ESI-MS analysis of samples performed on 100 µg protein samples desalted using NanoSep 3K Omega centrifugal devices (Pall Corp.). Protein solutions in 50% acetonitrile, 0.5% formic acid were infused into high-resolution mass spectometer at flow rate 10ul/min. Spectra were acquired in 800-1600 amu range and reconstructed into zero-charge spectra using Bayesian Protein Reconstruction Software) (FIG. 68). Unreacted XTEN and GLP2

peptide were separated from the conjugate by consecutive anion exchange (MacroCap Q) and hydrophobic interaction (Toyopearl Phenyl) chromatographies. The results of RP-HPLC and MS analyses demonstrated the high yield and purity of the reactants and final product (FIG. 68).

[00574] Example 27: Conjugation of GLP2-N-Mal to 1xThiol-XTEN (cysteine-engineered XTEN)

[00575] 1xThiol-XTEN (XTEN_AE880(Am1,C8)(Seg 181) was prepared as 122 uM (9.84 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. GLP2-N-Maleimide peptide (CSBio, custom synthesis) was dissolved in DMSO to the final concentration 3 mg/ml. 1xThiol-XTEN (8.8 mg in 900 µl) was mixed with 3-fold molar excess of GLP2-N-Mal peptide and incubated for 1 hr at 25°C. Completion of the modification and the resulting conjugate was monitored by C18 RP-HPLC (20 µg protein samples were loaded on Phenomenex Jupiter C18 5uM 300A 4.6mm x 150 mm column. Proteins were eluted with 5-50% gradient of acetonitrile in 0.1% trifluoroacetic acid and detected by absorbance at 214 nm) and electrospray ionization mass spectrometry (ESI-MS analysis of samples was performed on100 µg protein samples desalted using NanoSep 3K Omega centrifugal devices (Pall Corp.). Protein solutions in 50% acetonitrile, 0.5% formic acid were infused into high-resolution mass spectrometer at flow rate 10 µl/min. Spectra were acquired in 800-1600 amu range and reconstructed into zero-charge spectra using Bayesian Protein Reconstruction Software.) The results of the analysis are shown in FIG. 69. The GLP2-XTEN conjugate was purified by preparative C4 RP-HPLC (Vydac Protein C4 5µ 300A 10mm x 250mm column) using 5-50% gradient of acetonitrile in 0.1% TFA as mobile phase (see FIG. 70A).Final HPLC-purified GLP2-XTEN conjugate was analyzed using Phenomenex Jupiter C18 5uM 300A 4.6mm x 150 mm column (see FIG. 70B). Theield of purified GLP2-XTEN conjugate was 6.2 mg (70%).

[00576] Example 28: Conjugation of DBCO-Mal to 1xThiol-XTEN

[00577] 1xThiol-XTEN (XTEN_AE880(Am1,C8) (Seg 181) was prepared as a 150uM (12 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. DBCO-Maleimide (Click Chemistry Tools, Inc., cat. # A108) was dissolved in DMF to a final concentration of 50 mM. A volume of 200ul (2.4 mg) 1xThiol-XTEN was adjusted to 100mM HEPES pH 7.0 using a 1M stock solution. A 1.2 µl volume of 50 mM DBCO-Mal in DMF was added to the protein solution (1:2 molar ratio of 1xThiol-XTEN to DBCO-Maleimide reagent) and was incubated for 1 hr at 25°C. Completion of the modification reaction was monitored by C18 RP-HPLC (FIG. 71A). The protein mixture was purified by hydrophobic interaction chromatography (HIC) using a 1.6 ml Toyopearl Butyl column. Elution was performed with a 30 column volume of a descending gradient of ammonium sulfate from 1.05 M to 0.3M in 20 mM Phosphate, pH 7.0 buffer at 0.5ml/min flow rate (FIG. 71B). Chromatographic fractions were analyzed by C18 RP-HPLC (FIG. 71C).

[00578] Example 29: Preparation of A Bispecific Conjugate from Monospecific XTEN Precursors Linked by the N-termini.

[00579] The example describes the creation of an XTEN-payload composition by linking two different XTEN-payload precursors in an N- to N-terminus configuration; one with a payload A and one with a payload B, resulting in a bispecific conjugate.

[00580] As a first step, XTEN molecules containing multiple cysteines (cysteine-engineered XTEN) are prepared using a RP11-His8 two-tag purification system, described above, and are formulated in 20 mM HEPES, pH 7.0, 50 mM NaCl. A Payload A-maleimide is dissolved in aqueous solution 20 mM HEPES, pH 7.0, DMF or DMCO or any other appropriate solvent depending on reagent solubility. The Payload A-maleimide is added to the cysteine-engineered XTEN in a 2-6 molar excess over XTEN and incubated for 1 hr at 25°C. Completion of modification is monitored by C18 RP-HPLC. The resulting Payload A-XTEN conjugate is purified from contaminants and unreacted components using preparative C4-C18 RP-HPLC. The Payload A-XTEN conjugate is formulated in 20 mM HEPES, pH 7.0, 50 mM NaCl. Next, the Payload A-XTEN conjugate is further modified by adding dibenzylcyclooctyne (DBCO)-NHS ester or DBCO-sulfo-NHS ester in a 10-50 molar excess to the XTEN and incubating 1-2 hrs at 25°C. Completion of the modification is monitored by analytical C18 RP-HPLC. If the conjugation efficiency is low (for example, <90%) or multiple unspecific products are formed, the DBCO-Payload A-XTEN conjugate is purified using preparative C4-C18 RP-HPLC. If the efficiency of DBCO-NHS ester conjugation is high (>90%) with no significant side products, the DBCO-Payload A-XTEN conjugate is purified from excess reagent by buffer exchange using a 10-30 kDa MWCO centrifugal device, acetonitrile precipitation or anion exchange chromatography.

[00581] To create the second XTEN-payload precursor, a Payload B-maleimide is dissolved in aqueous solution 20 mM HEPES, pH 7.0, DMF or DMCO or any other appropriate solvent depending on reagent solubility. Payload B-maleimide is added to the second cysteine-containing XTEN in 2-6 molar excess over XTEN concentration and incubated for 1 hr at 25°C. Completion of modification is monitored by analytical C18 RP-HPLC. The resulting Payload B-XTEN conjugate is purified from contaminants and reactants using preparative C4-C18 RP-HPLC. The Payload B-XTEN conjugate is formulated in 20 mM HEPES, pH 7.0, 50 mM NaCl. Azide-PEG4-NHS ester is added in 10-50 molar excess to the Payload B-XTEN and incubated 1-2 hrs at 25°C. Completion of modification is monitored by C18 RP-HPLC. If the conjugation efficiency is low (for example <90%) or multiple unspecific products are formed, the azide-Payload B-XTEN conjugate is purified using preparative C4-C18 RP-HPLC. If the efficiency of DBCO-NHS ester conjugation is high (>90%) with no significant side products, the azide-Payload B-XTEN conjugate is purified from excess reagent by buffer exchange using a 10-30

kDa MWCO centrifugal device, acetonitrile precipitation or anion exchange chromatography. The final product is created by mixing purified and concentrated DBCO-Payload A-XTEN and azide-Payload B-XTEN proteins in an equilmolar ratio in 20 mM HEPES pH 7.0 buffer, 50 mM NaCl and incubated at 25°C for 1 hr or longer until the reaction is complete. Completion of modification is monitored by C4 or C18 RP-HPLC. If necessary, the bispecific conjugate Payload A-XTEN-Payload B is purified by preparatiove RP-HPLC, hydrophobic interaction chromatography or anion exchange chromatography.

[00582] Example 30: Preparation of A Trimeric Conjugate from Monospecific XTEN Precursors Linked by the N-termini.

[00583] Monospecific XTEN-payload precursors will be prepared as N-terminal fusions of a Payload A linked to an XTEN molecule; e.g. of lengths ranging from AE144 to AE890, containing a single cysteine at the C-terminus (prepared and purified as described in Example 25). Purified precursors are formulated in 20 mM HEPES, pH 7.0, 50 mM NaCl. Tris-(2-maleimidoethyl)amine (TMEA, Thermo Scientific, cat. # 33043) and dissolved in DMSO or DMF. Precursor (4-6 molar excess over cross-linker) and TMEA reagent are mixed and incubated for 1 hr at 25°C. Completion of the modification is monitored by C4 or C18 RP-HPLC or size exclusion chromatography. The resulting trivalent Payload A-XTEN conjugate is purified from protein reactants or partial product mixture by hydrophobic interaction chromatography (HIC), anion exchange chromatography or preparative C4-C18 RP-HPLC.

[00584] Example 31 : Conjugation and Purification of FITC-X-XTEN

[00585] Purified protein derived from AC272, lot # AP197, was labeled with FITC maleimide. The sample was reduced by incubating at room temperature with 5 mM TCEP for 1 hour. The sample was then desalted into PBS using DG-10 columns. The sample was labeled by adding a 25-fold molar excess of FITC-maleimide in DMSO and incubating at room temperature for 2 hours. Note that the volume adjusted such that the DMSO concentration was <5% of total solvent. The reaction was quenched by adding 2 mM DTT and then the sample was digested overnight with TEV protease. The sample was diluted two fold with 20 mM Tris pH 7.5 and loaded onto a macrocapQ column, previously sanitized with NaOH and equilibrated with 20 mM Tris pH 7.5. The column was washed with 5 column volumes of 20 mM Tris pH 7.5, 135 mM NaCl, 5 column volumes of 20 mM Tris pH 7.5, 175 mM NaCl and eluted with 5 column volumes of 20 mM Tris pH 7.5, 250 mM NaCl. The pooled elution fractions were then digested with TEV over 60 hours at 4C to complete the digestion. The digested samples were then twice passed over a 1 ml perloza column previously sanitized with NaOH and equilibrated with 20 mM Tris pH 7.5, 135 mM NaCl. To remove any free FITC the sample was then dialyzed against 20 mM Tris pH 7.5, 135 mM NaCl using a 10,000 MWCO membrane. Co-migration of the OD214 protein signal and OD495 FITC signal in a SEC column indicate successful conjugation of the

XTEN with the label, with minimal free dye contamination (FIG. 72B). The successful conjugation is also indicated by apparent large MW of the protein with FITC fluorescence in SDS PAGE (FIG. 72A).

[00586] Example 32: Purification of GFP-X-XTEN

[00587] GFP (AC219) was chemically cross-linked to XTEN by a bifunctional cross-linker with an amine reactive group to couple to the GFP lysines and a cysteine reactive group to couple to the free cysteine engineered into the XTEN in AC292. GFP was labeled with bi-functional cross-linker sulfo-SMCC by incubating at room temperature for 2 hours. The protein was desalted into PBS using DG-10 columns to remove free sulfo-SMCC. Purified protein derived from AC272, lot # AP197 was reduced and desalted into PBS on DG-10 columns and mixed with the labeled GFP to allow for cross-linking. The cross-linking reaction was quenched with 2 mM DTT and TEV added to remove the CBD domain in a overnight incubation at 4°C. The following day additional TEV was added to complete the digestion with an additional 60 hour 4°C incubation. Following TEV digestion the sample was dilute to 100 ml in 20 mM Tris pH 7.5 and loaded onto a macrocapQ column, previously sanitized with NaOH and equilibrated with 20 mM Tris pH 7.5. The column was washed with 5 column volumes of 20 mM Tris pH 7.5, 5 column volumes of 20 mM Tris pH 7.5, 50 mM NaCl, 5 column volumes of 20 mM Tris pH 7.5, 100 mM NaCl, 5 column volumes of 20 mM Tris pH 7.5, 150 mM NaCl, 5 column volumes of 20 mM Tris pH 7.5, 200 mM NaCl, 5 column volumes of 20 mM Tris pH 7.5, 250 mM NaCl, 5 column volumes of 20 mM Tris pH 7.5, 300 mM NaCl, and 5 column volumes of 20 mM Tris pH 7.5, 500 mM NaCl. The peak elution fractions were pooled and stored at 4°C. Cross-linking was confirm by co-migration of the OD214 protein signal and OD395 GFP signal in a SEC column, with the SEC output shown as overlays in FIG. 73.

[00588] Example 33: Pharmacokinetics of GFP-XTEN and FITC-XTEN Conjugates

[00589] The pharmacokinetics of the GFP-XTEN and FITC-XTEN cross-linked conjugates prepared as described in the Examples above were tested in cynomolgus monkeys. GFP-XTEN and FITC-XTEN were administered to male cynos IV at 2 mg/kg and dose volumes of 0.77 and 0.68 mL respectively. Blood samples (1.0 mL) were collected into prechilled heparinized tubes at predose, 2, 4, 8, 24, 48, 72, 96, 120, 168, 216, 264, 336, 388, 432, 504 hour time points, and processed into plasma. Quantitation was performed by ELISA assay using the anti-XTEN antibody for both capture and detection in the case of GFP-XTEN and anti-XTEN capture and anti-FITC detection in the case of FITC-XTEN. A non-compartmental analysis was performed in WinNonLin with all time points included in the fit to determine the PK parameters. The pharmacokinetic results are summarized in Table 40 and FIG. 74. The data show XTEN can extend the half-life of molecules to which it is chemically conjugated in a manner comparable to genetic fusions to payloads of similar size.

Table 40: PK parameters of conjugated XTEN-payload compositions.

Construct	Cmax (ng/mL)	AUC (hr*ng/mL)	T ½ (hrs)
GFP-X-XTEN (AP197d)	52800	8220000	107
FITC-X-XTEN AP197e	18900	3930000	84.2

[00590] The pharmacokinetics of GFP-L288, GFP-L576, GFP-XTEN_AF576, GFP-XTEN_Y576 and XTEN_AD836-GFP were tested in cynomolgus monkeys to determine the effect of composition and length of the unstructured polypeptides on PK parameters. Blood samples were analyzed at various times after injection and the concentration of GFP in plasma was measured by ELISA using a polyclonal antibody against GFP for capture and a biotinylated preparation of the same polyclonal antibody for detection. Results are summarized in FIG. 75. They show a surprising increase of half-life with increasing length of the XTEN sequence. For example, a half-life of 10 h was determined for GFP-XTEN_L288 (with 288 amino acid residues in the XTEN). Doubling the length of the unstructured polypeptide fusion partner to 576 amino acids increased the half-life to 20-22 h for multiple fusion protein constructs; i.e., GFP-XTEN_L576, GFP-XTEN_AF576, GFP-XTEN_Y576. A further increase of the unstructured polypeptide fusion partner length to 836 residues resulted in a half-life of 72-75 h for XTEN_AD836-GFP. Thus, increasing the polymer length by 288 residues from 288 to 576 residues increased in vivo half-life by about 10 h. However, increasing the polypeptide length by 260 residues from 576 residues to 836 residues increased half-life by more than 50 h. These results show that there is a surprising threshold of unstructured polypeptide length that results in a greater than proportional gain in in vivo half-life. Thus, fusion proteins comprising extended, unstructured polypeptides are expected to have the property of enhanced pharmacokinetics compared to polypeptides of shorter lengths.

[00591] Example 34: Preparation of 1xDBCO,3xLHRH-XTEN by conjugation

[00592] An aliquot of 1xAmino,3xThiol-XTEN432 (XTEN_AE432(Am1,C12,C217,C422)) was prepared as a 196 µM (7.7 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. FIG. 88A shows a C18 RP-HPLC and ESI-MS analysis of the protein. 2,2'-Dipyridyl disulfide (DPD, Sigma, cat. # D5767) was dissolved in dimethylformamide (DMF) to the final concentration 100 mM. 4 ml of 1xAmino,3xThiol-XTEN432 solution was mixed with 0.2 ml 1 M HEPES, pH 8.0 to adjust the pH to ~7.5 and with 78 µl DPD solution (10x molar excess over protein). The reaction mixture was incubated for 2 hours at 25°C and products of the reaction were analyzed by C18 RP-HPLC (FIG. 88B). DBCO-sulfo-NHS (Click Chemistry Tools, Inc., cat. # A124) was dissolved in anhydrous DMF to a final concentration of 10 mM. 0.865 ml of DBCO-sulfo-NHS solution was added to protein solution (11x molar excess over protein). The reaction mixture was incubated for 2 hours at 25°C and products of reaction were analyzed by C18 RP-HPLC (FIG. 88C). A solution of 1M ethanolamine pH 8.0 was added to a final concentration of 50 mM to

quench the unreacted DBCO-sulfo-NHS. The reaction mixture was incubated for 2 hours at 25°C and then overnight at 4°C. 500 mM Bond-Breaker™ TCEP Solution (Thermo Scientific, cat. # 77720) was added to a final concentration 20 mM. The reaction mixture was incubated for 1 hour at 25°C and the products of reaction were analyzed by C18 RP-HPLC (FIG. 88D). The reaction mixture was diluted to 15mL with 0.01% TFA and pH adjusted to ~3 using 10% TFA solution. The protein solution was loaded on a preparative C4 RP-HPLC column Vydac C4 250 x 22 mm (Grace Davison Discovery Sciences, cat. # 214TP1022). The protein was eluted with 1200 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 15 ml/min flow rate. Fractions containing 1xDBCO,3xThiol-XTEN432 were adjusted to pH ~ 7 with 1 M HEPES pH 8 and were concentrated by vacuum evaporation. A Glp-His-Trp-Ser-Tyr-D-Lys-Leu-Arg-Pro-Gly-NH2 peptide modified with 3-maleimidopropionic acid at ε-amino group of D-Lys (LHRH-Mal) was synthesized by CSBio Co. (Menlo Park, CA). The peptide was dissolved to a final concentration 25 mg/ml in anhydrous DMF and was added to 1xDBCO,3xThiol-XTEN432 solution in a 5x molar excess over protein. The reaction mixture was incubated for 1 hr at 25°C and the products of the reaction were analyzed by C18 RP-HPLC (FIG. 88E). The reaction mixture was diluted to 15mL with 0.01% TFA and the pH adjusted to ~3 using a 10% TFA solution. The protein solution was loaded on preparative C4 RP-HPLC column Vydac C4 250 x 22 mm. The protein was eluted with 1200 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 15 ml/min flow rate. Fractions containing 1xDBCO,3xLHRH-XTEN432 were adjusted to ~pH 7 with 1 M HEPES pH 8 and concentrated to 2 ml by vacuum evaporation to yield the final product.

[00593] Example 35: Preparation of 1xAzide,3xMMAE-XTEN by conjugation

[00594] An aliquot of the fusion protein 1xAmino,3xThiol-XTEN432 (XTEN_AE432(Am1,C12,C217,C422)) was prepared as 196 µM (7.7 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. FIG. 89A shows a C18 RP-HPLC and ESI-MS analysis of the protein. MA6-Val-Cit-PAB-MMAE (MMAE-Mal, custom synthesis by Concortis Biosystems, Inc.) was dissolved in dimethylsulfoxide (DMSO) to a final concentration 1 mg/ml. A 2.2 ml volume of 1xAmino,3xThiol-XTEN432 solution was mixed with 2.5 ml of MMAE-Mal (3.5x molar excess over protein). The reaction mixture was incubated for 1 hr at 25°C and the products of the reaction were analyzed by C18 RP-HPLC (FIG. 89B). Azide-PEG4-NHS ester (Click Chemistry Tools, Inc., cat. # A103) was dissolved in anhydrous DMF to a final concentration of 500 mM. The reaction mixture (4.7 ml) was mixed with 0.235 ml 1 M HEPES, pH 8.0 and with 9.75ul 500 mM azide-PEG4-NHS (10x molar excess over protein). The reaction mixture was incubated for 2 hr at 25°C and the products of reaction were analyzed by C18 RP-HPLC (FIG. 89C). The conjugation mixture was diluted to 15 ml with 0.01% TFA and the pH was adjusted to ~3 using 10% TFA. The protein solution was loaded onto a preparative C4 RP-HPLC column Vydac C4 250 x 22 mm (Grace Davison Discovery Sciences, cat. # 214TP1022). The protein

was eluted with 1200 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 15 ml/min flow rate. Fractions containing 1xAzide,3xMMAE-XTEN432 were adjusted to ~pH7 with 1 M HEPES pH 8 and concentrated by vacuum evaporation to yield the final product.

[00595] Example 36: Preparation of 3xLHRH,3xMMAE-XTEN by conjugation

[00596] An aliquot of the fusion protein 1xDBCO,3xLHRH-XTEN432 was prepared as 143 µM (6.26 mg/ml) solution in 20 mM HEPES, pH 7.0. 1xAzide,3xMMAE-XTEN432 was prepared as a 135 µM (5.90 mg/ml) solution in 20 mM HEPES, pH 7.0. The two protein reactants were mixed in solution to yield a 1.1 molar excess of 1xDBCO,3xLHRH-XTEN432. The reaction mixture was incubated overnight at 25°C. Completion of the click chemistry reaction was analyzed by SDS-PAGE (FIG. 90A) and RP-HPLC (FIG. 90B). The conjugation mixture was diluted to 15 ml with 0.01% TFA and pH adjusted to ~3 using 10% TFA. The protein solution was loaded onto a preparative C4 RP-HPLC column Vydac C4 250 x 10 mm (Grace Davison Discovery Sciences, cat. # 214TP510). The protein was eluted with 180 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 2 ml/min flow rate. Fractions containing 3xLHRH,3xMMAE-XTEN were adjusted to ~pH7 with 1 M HEPES pH 8 and concentrated by vacuum evaporation to yield the final product.

[00597] Example 37: Preparation of 1xLHRH,3xMMAE-XTEN by conjugation

[00598] An aliquot of the fusion protein 1xAmino,3xThiol-XTEN905 (XTEN_AE905(Am1,C8,C453,C898, Seg 174)) was prepared as a 131 µM (10.9 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. FIG. 91A shows a C18 RP-HPLC and ESI-MS analysis of the protein. 2,2'-Dipyridyl disulfide (DPD, Sigma, cat. # D5767) was dissolved in dimethylformamide (DMF) to the final concentration 100 mM. The 1xAmino,3xThiol-XTEN905 solution was adjusted pH to ~7.5 using 1 M HEPES pH 8 and mixed with DPD solution (10x molar excess over protein). The reaction mixture was incubated for 2 hr at 25°C and the products of the reaction were analyzed by C18 RP-HPLC (FIG.91B). DBCO-sulfo-NHS (Click Chemistry Tools, Inc., cat. # A124) was dissolved in anhydrous DMF to a final concentration 10 mM. DBCO-sulfo-NHS solution was added to the protein solution (10x molar excess over protein). The reaction mixture was incubated for 2 hr at 25°C and the products of the reaction analyzed by C18 RP-HPLC (FIG. 91C). 1M ethanolamine pH 8.0 was added to a final concentration of 50 mM to quench unreacted DBCO-sulfo-NHS. The reaction mixture was incubated for 2 hr at 25°C and then overnight at 4°C. A 500 mM Bond-Breaker™ TCEP Solution (Thermo Scientific, cat. # 77720) was added to a final concentration 20 mM. The reaction mixture was incubated for 1 hour at 25°C and the products of the reaction were analyzed by C18 RP-HPLC (FIG.91D). The reaction mixture was diluted to 15 mL with 0.01% TFA and the pH adjusted to ~3 using 10% TFA solution. The protein solution was loaded onto preparative C4 RP-HPLC column Vydac C4 250 x 22 mm (Grace Davison Discovery Sciences, cat. # 214TP1022). The protein was eluted

with 1200 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 15 ml/min flow rate. Fractions containing 1xDBCO,3xThiol-XTEN905 were adjusted to ~ pH7 with 1 M HEPES pH 8 and concentrated by vacuum evaporation. MA6-Val-Cit-PAB-MMAE (MMAE-Mal, custom synthesis by Concortis Biosystems, Inc.) was dissolved in dimethylsulfoxide (DMSO) to a final concentration 1 mg/ml. 1xDBCO,3xThiol-XTEN905 solution was mixed with a 3.5x molar excess of MMAE-Mal. The reaction mixture was incubated for 1 hr at 25°C and products of the reaction were analyzed by C18 RP-HPLC. The Glp-His-Trp-Ser-Tyr-D-Lys-Leu-Arg-Pro-Gly-NH2 peptide was modified with azido-hexanoic acid at the ε-amino group of D-Lys (LHRH-Mal, custom synthesis by CS Bio Co., Menlo Park, CA). The peptide was dissolved to a final concentration 25 mg/ml in anhydrous DMF and added to 1xDBCO,3xMMAE-XTEN905 solution in 1.5-5x molar excess over protein. The reaction mixture was incubated at 25°C and the products of the reaction were analyzed by C18 RP-HPLC. The final reaction mixture was diluted to 15 mL with 0.01% TFA and pH adjusted to ~3 using 10% TFA solution. The protein solution was loaded on preparative C4 RP-HPLC column Vydac C4 250 x 22 mm. The protein was eluted with 1200 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 15 ml/min flow rate. Fractions containing 1xDBCO,3xLHRH-XTEN432 were adjusted to ~pH7 with 1 M HEPES pH 8 and concentrated by vacuum evaporation to yield the final product.

[00599] Example 38: Preparation of 1xDBCO,3xFolate(γ)-XTEN by conjugation

[00600] An aliquot of the fusion protein 1xAmino,3xThiol-XTEN432 (XTEN_AE432(Am1,C12,C217,C422)) was prepared as a 203 μM (8.0 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. FIG. 107A shows a C18 RP-HPLC and ESI-MS analysis of the protein. Folate-γ-aminopentyl-maleimide (FA(γ)-Mal, custom synthesis by CPC Scientific) was dissolved in dimethylformamide (DMF) to a final concentration 21 mg/ml (9.8 mM). A 1.1 ml volume of 1xAmino,3xThiol-XTEN432 solution was mixed with 0.08 ml of FA(γ)-Mal (3.5 molar excess over protein). The reaction mixture was incubated for 2 hrs at 25°C and the products of the reaction were analyzed by C18 RP-HPLC (FIG. 107B). pH of the reaction mixture was adjusted with 0.06 ml of 1 M HEPES pH 8.0 buffer. DBCO-sulfo-NHS (Click Chemistry Tools, Inc., cat. # A124) was dissolved in anhydrous DMF to a final concentration of 50 mM. 0. 53 ml of DBCO-sulfo-NHS solution was added to protein solution (11x molar excess over protein). The reaction mixture was incubated for 2 hours at 25°C and products of reaction were analyzed by C18 RP-HPLC (FIG. 107C). A solution of 1M ethanolamine pH 8.0 was added to a final concentration of 50 mM to quench the unreacted DBCO-sulfo-NHS. The reaction mixture was incubated for 2 hours at 25°C and then overnight at 4°C. The reaction mixture was diluted to 15mL with 0.01% TFA and pH adjusted to ~3 using 10% TFA solution. The protein solution was loaded on a preparative C4 RP-HPLC column Vydac C4 250 x 10 mm (Grace Davison Discovery Sciences, cat. # 214TP510). The protein was eluted with 180 ml linear 5-50%

gradient of acetonitrile in 0.01% TFA at 2 ml/min flow rate. Fractions containing 1xDBCO,3xFA(γ)-XTEN432 were adjusted to pH ~ 7 with 1 M HEPES pH 8 and were concentrated by vacuum evaporation to yield the final product.

[00601] The 1xDBCO,3xFolate(α)-XTEN conjugate was prepared essentially as described above using folate-alpha-Maleimide (FA(α)-Mal, custom synthesis by CPC Scientific).

[00602] Example 39: Preparation of 3xFA(γ),3xMMAE-XTEN by conjugation

[00603] An aliquot of the fusion protein 1xDBCO,3xFA(γ)-XTEN432 was prepared as 191 µM (8.8 mg/ml) solution in 20 mM HEPES, pH 7.0. 1xAzide,3xMMAE-XTEN432 (prepared as described in Example 32) was prepared as a 242 µM (11.1 mg/ml) solution in 20 mM HEPES, pH 7.0. The two protein reactants were mixed in solution to yield a 1.1 molar excess of 1xDBCO,3xFA(γ)-XTEN432. The reaction mixture was incubated overnight at 25°C. Completion of the click chemistry reaction was analyzed by RP-HPLC (FIG. 108). The conjugation mixture was diluted to 15 ml with 0.01% TFA and pH adjusted to ~3 using 10% TFA. The protein solution was loaded onto a preparative C4 RP-HPLC column Vydac C4 250 x 10 mm (Grace Davison Discovery Sciences, cat. # 214TP510). The protein was eluted with 180 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 2 ml/min flow rate. Fractions containing 3xFA(γ),3xMMAE-XTEN were adjusted to ~pH7 with 1 M HEPES pH 8 and concentrated by vacuum evaporation to yield the final product. The final product was analyzed by size exclusion chromatography (SEC-HPLC) (FIG. 109A), RP-HPLC (FIG. 109B) and ESI-MS (FIG. 109C).

[00604] The 3xFA(α),3xMMAE-XTEN conjugate was prepared essentially as described above using click reaction between 1xDBCO,3xFA(α)-XTEN432 and 1xAzide,3xMMAE-XTEN432.

[00605] Example 40: Comparison of viscosity in solutions of branched versus linear XTEN

[00606] The viscosity of linear and branched XTENs (the latter as trimeric or tetrameric configurations) can be measured using various types of viscometers and rheometers. For example one can measure the time required to draw 1 mL of liquid into a syringe through a 30G needle as described by Miller, M. A., et al. (2010) Langmuir, 26:1067. In order to compare monomeric linear versus trimeric or tetrameric configurations of XTENs to be for viscosity, constructs having equivalent molecular weights for the XTEN amino acid component are prepared and then solutions are made at fixed, equivalent concentrations of protein at 20, 50, 100 mg/ml each. The solutions are then are evaluated using the method of Miller. Using the method, data are obtained with known standards to prepare a standard curve, and then the XTEN solutions are measured. It is expected that results will show that the viscosity of equimolar solutions of XTENs with similar molecular weight will be significantly decrease with increasing branching; a conjugate of 3 arms of XTEN288 will have significantly lower viscosity compared to an equal concentration of linear XTEN864, even though they have equivalent numbers of amino acids. Similarly, it is expected

that a configuration with 4 arms of XTEN216 will have even lower viscosity than a conjugate with 3 arms of XTEN288.

[00607] Example 41: Preparation of Her2-XTEN-PTX by conjugation

[00608] An aliquot of the fusion protein 1xAmino,3xThiol-XTEN432 (XTEN_AE432(Am1,C12,C217,C422)) is prepared as 196 µM (7.7 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. Paclitaxel-Mal (PTX-Mal) is custom synthesized by modification of paclitaxel with succinic anhydride followed by conjugation to aminoethylmaleimide. PTX-Mal is dissolved in dimethylformamide (DMF) and added to the protein in a 3.5-5x molar excess. The reaction mixture is incubated for 1-2 hr at 25°C and the products of the reaction are analyzed by C18 RP-HPLC. Sulfo-SMCC (Thermo Scientific, cat. #22122) is dissolved in anhydrous DMF to a final concentra tion 50 mM and added to the protein solution in a 10x molar excess over protein. The reaction mixture is incubated for 2 hr at 25°C and the products of the reaction analyzed by C18 RP-HPLC (see FIG. 92). The reaction mixture is diluted to 15 mL with 0.01% TFA and pH adjusted to ~3 using 10% TFA solution. The protein solution is loaded on a preparative C4 RP-HPLC column Vydac C4 250 x 22 mm (Grace Davison Discovery Sciences, cat. # 214TP1022). The protein is eluted with a 1200 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 15 ml/min flow rate. Fractions containing 1xMal,3xPTX-XTEN432 are adjusted to ~pH 7 with 1 M HEPES pH 8 and concentrated by vacuum evaporation. Herceptin (Trastuzumab, Roche) antibody is reconstituted in water according to the instructions and is buffer exchanged into PBS pH 7.2 containing 5 mM EDTA. DTT is added to the protein solution to a 1-10 mM final concentration and incubated for 5-30 min at 37°C. Excess DTT is removed by gel filtration or cut-off membrane filtration. 1xMal,3xPTX-XTEN432 is added to partially reduced antibody in a 3-4x molar excess. The reaction mixture is incubated for 1 hr at 25°C and the final products of the reaction are analyzed by SDS-PAGE and size exclusion chromatography under non-reducing and reducing conditions.

[00609] Example 42: Preparation of iodoacetyl-XTEN by conjugation

[00610] An aliquot of the fusion protein 1xAmino-XTEN869 (XTEN_AE869(Am1) was prepared as a 164 µM (13.1 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. A 1/20 volume of 1M HEPES pH 8 was added to the protein solution to adjust the pH of the protein solution to ~7.5. N-succinimidyl iodoacetate (SIA, Thermo Scientific, cat. # 22349) was dissolved in anhydrous dimethylformamide (DMF) to a final concentration 100 mM and was added in a 10x molar excess over the protein. The reaction mixture was incubated for 1 hr at 25°C and the products of the reaction are analyzed by C18 RP-HPLC (Fig. 93A). The excess SIA was removed by buffer exchange using Vivaspin 500 ultracentrifugal device (5,000 MWCO, VivaScience, cat. # VS0112). Modification of the N-terminal amino group by iodoacetyl group did not change the retention time of the modified XTEN (FIG. 93A), therefore the covalent

modification was confirmed by ESI-MS (FIG. 93B). Also, the IA-XTEN conjugate efficiently reacted with the cysteine-containing peptide HCKFWW (Bachem, cat. # H-3524) (FIG93C).

[00611] Example 43: In vitro cell-based screening of LHRH-XTEN-drug conjugates for activity and specificity

[00612] LHRH-XTEN-drug conjugates are assessed for *in vitro* activity and selectivity. Each LHRH-XTEN-drug conjugate, its corresponding non-targeting XTEN-drug molecule and its respective free drug control are tested in a CellTiter-Glo anti-proliferation assay against a panel of LHRH receptor positive and negative cell lines listed in Table 41. Appropriate assay conditions, including optimal cell density and incubation time are determined using the respective free drug as control. LHRH-XTEN-drug conjugates are tested as follows: cells in log-phase are collected, counted and plated at pre-determined cell density in a 96-well microtiter assay plate. Adherent cells are allowed to attach to the plate by an overnight incubation at 37°C with an atmosphere of 5% CO_2. The LHRH-XTEN-drug conjugates and corresponding controls are introduced using appropriate dose range dilutions, in duplicate, and the plates are incubated for an additional 2-5 days. After the appropriate incubation period, CellTiter-Glo reagent is added to each well, mixed for 2 minutes on an orbital shaker. The plate is then centrifuged at 90 x g and incubated at room temperature for an additional 10 minutes to stabilize the luminescent signal. Luminescence signals are then read on a luminometer and the IC_{50} (half maximal inhibitory concentration) values are calculated with GraphPad Prism or equivalent software. Quantitative comparisons of the IC_{50} values will enable ranking of the constructs' activity for inhibition of cell growth and selectivity against LHRH receptor positive versus negative cell lines. It is expected that the results would support the finding that the LHRH-XTEN-drug conjugates will show highly selective potent killing on LHRH receptor positive cells but not on LHRH receptor negative cells. This will be in contrast to the free drug moiety whereby no discrimination in cytotoxicity is expected between LHRH receptor positive and negative cell lines. The XTEN-drug control is expected to yield poor cytotoxic activity. LHRH-XTEN-drug conjugates with favorable activity and cell line selectivity relative to controls will be further verified for LHRH receptor association by the addition of free competitive LHRH peptide in the assay, resulting in impaired LHRH-XTEN-drug cytotoxicity, further verifying the selective activity of the constructs.

Table 41: LHRH receptor positive and negative cell lines

Cell line	Tissue	LHRHR status
MCF-7	Breast	Positive
MDA-MB-231	Breast (HER2-/ER-/PR-)	Positive
HCC1806	Breast (HER2-/ER-/PR-)	Positive
HCC1937	Breast (HER2-/ER-/PR-)	Positive
OV-1063	Ovarian	Positive

Cell line	Tissue	LHRHR status
EFO-21	Ovarian	Positive
EFO-27	Ovarian	Positive
NIH:OVCAR-3	Ovarian	Positive
BG-1	Ovarian	Positive
HEC-1A	Endometrial	Positive
HEC-1B	Endometrial	Positive
Ishikawa	Endometrial	Positive
KLE	Endometrial	Positive
AN-3-CA	Endometrial	Positive
MiaPaCa	Pancreatic	Positive
Panc-1	Pancreatic	Positive
rat Dunning R-3327-H	Prostate (androgen-dep)	Positive
PC-82	Prostate (androgen-dep)	Positive
MDA-PCa-2b	Prostate (androgen-indep)	Positive
C4-2 (derivative of LNCaP)	Prostate (androgen-dep)	Positive
A549	Lung	Positive
UCI-107	Ovarian	Negative
SK-OV-3	Ovarian	Negative
SW 626	Ovarian	Negative
MFE-296	Endometrial	Negative

ER: estrogen receptor; PR: progesterone receptor

[00613] Example 44: *In vitro* cell-based screening of folate-XTEN-drug conjugates for activity and specificity

[00614] Folate-XTEN-drug conjugates are first subjected to an *in vitro* activity and selectivity screen. Each folate-XTEN-drug conjugate, its corresponding non-targeting XTEN-drug molecule and respective free drug control are tested in a CellTiter-Glo anti-proliferation assay against a panel of folate receptor positive and negative cell lines listed in Table 42. As culture media contain high folic acid content, cells will be grown and the assay performed in folic acid free-media containing 5-10% heat-inactivated fetal calf serum (FCS) at 37°C, in an atmosphere of 5% CO_2 (heat-inactivated FCS contains endogenous level of folic acid sufficient for folate receptor expressing cells to survive and proliferate). Appropriate assay conditions are established, including optimal cell density and incubation times, using folate-free media containing 5-10% FCS using the respective free drug as control. Folate-XTEN-drug conjugates are then tested as follows: cells in log-phase are collected, counted and plated at pre-determined cell density in 96-well microtiter assay plates. Adherent cells are allowed to attach to the plate by an overnight incubation at 37°C, 5% CO_2. Folate-XTEN-drug conjugates and corresponding controls are introduced using appropriate dose range dilutions, in duplicate, and the plates are incubated for an additional 2-5 days. After the appropriate incubation period, CellTiter-Glo reagent is added to

each well and is mixed for 2 minutes on an orbital shaker. The plate is then centrifuged at 90 x g and incubated at room temperature for an additional 10 minutes to stabilize the luminescent signal. Luminescence signals are then read on a luminometer and the IC_{50} (half maximal inhibitory concentration) values are calculated with GraphPad Prism or equivalent software. Quantitative comparisons of the IC_{50} values will enable ranking of the constructs' activity for inhibition of cell growth and selectivity against folate receptor positive versus negative cell lines. It is expected that the results would support the finding that the folate-XTEN-drug conjugates will show highly selective potent killing on folate receptor positive cells but not on folate receptor negative cells. This will be in contrast to the free drug moiety where no discrimination in cytotoxicity is expected between folate receptor positive and negative cell lines. The XTEN-drug control is expected to yield poor cytotoxic activity. Folate-XTEN-drug conjugates with favorable activity and cell line selectivity relative to controls will be further verified for folate receptor association by the addition of free competitive folic acid in the assay, demonstrating impaired folate-XTEN-drug cytotoxicity, further verifying the selective activity of the constructs.

Table 42: Folate receptor positive and negative cell lines

Cell line	Tissue	Folate receptor status
KB	Nasopharyngeal	Positive
IGROV	Ovarian	Positive
SK-OV-3	Ovarian	Positive
HeLa	Cervical	Positive
LoVo	Colorectal	Positive
SW620	Colorectal	Positive
A549	Lung	Negative
A375	Multiple melanoma	Negative
LS-174T	Colorectal	Negative
SK-BR-3	Breast	Negative

[00615] Example 45: *In vitro* serum stability of LHRH-XTEN-drug conjugates

[00616] As a measure of stability, LHRH-XTEN-drug conjugates are incubated independently in normal human, cynomolgus monkey and mouse plasma at 37°C for up to 2 weeks with aliquots removed at periodic intervals and stored at -80°C till analysis. The stability of LHRH-XTEN-drug conjugate can be assessed either by the amount of free drug released or the integrity of the LHRH-XTEN-drug conjugate over time. Free drug is quantitated with RP-HPLC and/or LC-MS/MS whereas the amount of intact LHRH-XTEN-drug conjugate is determined using an XTEN/drug and/or an LHRH/drug ELISA.

[00617] For RP- HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated under vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV

absorption at wavelengths specific for the particular drug, compared to known drug standards. For example, doxorubicin is detected at 480 nm. For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated under vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected and quantitated by triple quadrupole tandem mass spectrometry, compared to known drug standards. Parental ion–daughter ion pairs will be determined experimentally for each drug. For quantitative ELISA, optimal concentrations of antibodies for LHRH-XTEN-drug conjugate in the ELISAs are determined using criss-cross serial dilution analysis. An appropriate capture antibody recognizing one component of the conjugate is coated onto a 96-well microtiter plate by an overnight incubation at 4°C. The wells are blocked, washed and serum stability samples added to the wells, each at varying dilutions to allow optimal capture of the LHRH-XTEN-drug conjugate by the coated antibody. After washing, detection antibody recognizing another component of the conjugate is added and allowed to bind to the conjugate captured on the plate. Wells are then washed again and either streptavidin-horseradish peroxidase (complementary to biotinylated version of detection antibody) or an appropriate secondary antibody-horseradish peroxidase (complementary to non-biotinylated version of detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and the plate read at 450nM. Concentrations of intact conjugate are then calculated for each time point by comparing the colorimetric response to a calibration curve prepared with LHRH-XTEN-drug in the relevant plasma type. The *t*1/2 of the decay of the conjugate in human, cyno and mouse serum is then defined using linear regression analysis of the log concentrations vs. time.

[00618] Example 46: *In vitro* serum stability of folate-XTEN-drug conjugates

[00619] As a measure of stability, folate-XTEN-drug conjugates are incubated independently in normal human, cynomolgus monkey and mouse plasma at 37°C for up to 2 weeks with aliquots removed at periodic intervals and stored at -80°C until analysis. The stability of folate-XTEN-drug conjugate is assessed either by the amount of free drug or the integrity of the folate-XTEN-drug conjugate over time. Free drug is quantitated with HPLC and/or LC-MS/MS whereas the amount of intact folate-XTEN-drug conjugate is determined using an XTEN/drug and/or folate/drug ELISA.

[00620] For RP- HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated under vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug, compared to known drug standards. For example, doxorubicin is detected at 480 nm. For LC-MS/MS analysis, plasma samples will be treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble

fractions will be evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes will be in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs will be determined experimentally for each drug. Calibration standards will be prepared by adding known amounts of free drug to corresponding plasma type and will be treated in parallel with experimental samples. For quantitative ELISA, optimal concentrations of antibodies for folate-XTEN-drug conjugate in the ELISAs is determined using criss-cross serial dilution analysis. An appropriate capture antibody recognizing one component of the conjugate is coated onto a 96-well microtiter plate by an overnight incubation at 4°C. The wells are blocked, washed and serum stability samples added to the wells, each at varying dilutions to allow optimal capture of the folate-XTEN-drug conjugate by the coated antibody. After washing, detection antibody recognizing another component of the conjugate is added and allowed to bind to the conjugate captured on the plate. Wells are then washed again and either streptavidin-horseradish peroxidase (complementary to biotinylated version of detection antibody) or an appropriate secondary antibody-horseradish peroxidase (complementary to non-biotinylated version of detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and the plate is read at 450nM. Concentrations of intact conjugate are then calculated for each time point by comparing the colorimetric response to a calibration curve prepared with folate-XTEN-drug in the relevant plasma type. The *t*1/2 of the decay of the conjugate in human, cyno and mouse serum is then defined using linear regression analysis of the log concentrations vs. time.

[00621] Example 47: *In Vivo* and *ex vivo* imaging of LHRH-XTEN-Cy5.5 conjugate

[00622] A Cy5.5 fluorescent tagged LHRH-XTEN molecule is used as a surrogate to investigate the targeting and biodistribution efficiency of LHRH-XTEN-drug conjugates. Experiments will be carried out in nude mice bearing subcutaneous grown xenografts of LHRH receptor positive tumor cells using *in vivo*, followed by *ex vivo*, fluorescence imaging with IVIS 50 optical imaging system (Caliper Life Sciences, Hopkinton, MA). In brief, female nu/nu mice bearing LHRH receptor positive tumor cells are given a single intravenous injection of high or low dose LHRH-XTEN-Cy5.5 and corresponding doses of non-targeting Cy5.5 tagged XTEN control. Whole body scans are acquired pre-injection and then at approximately 8, 24, 48 and 72 hours post-injection on live anesthetized animals using the IVIS 50 optical imaging system. After measuring the distribution of fluorescence in the entire animal at the last time point of 72h, tumor and healthy organs including liver, lung, heart, spleen and kidneys are excised and their fluorescence registered and processed by the imaging system. Cy5.5 excitation (615-665nm) and emission (695-770nm) filters are selected to match the fluorescence agents' wavelengths. Small and medium binning of the CCD chip is used and the exposure time optimized to obtain at least several thousand counts from the signals observable in each mouse in the image and to avoid

saturation of the CCD chip. To normalize images for quantification, a background fluorescence image is acquired using background excitation and emission filters for the Cy5.5 spectral region. The intensity of fluorescence is expressed as different colors with blue color reflecting the lowest intensity and red being indicative of the highest intensity, and the resulting images are used to assess the uptake of the conjugates and controls.

[00623] Example 48: *In Vivo* and *ex vivo* imaging of folate-XTEN-Cy5.5 conjugates

[00624] A Cy5.5 fluorescent tagged folate-XTEN molecule is used as a surrogate to investigate the targeting and biodistribution efficiency of folate-XTEN-drug conjugates. Experiments will be carried out in nude mice bearing subcutaneous grown xenografts of folate receptor positive tumor cells using *in vivo*, followed by *ex vivo*, fluorescence imaging with IVIS 50 optical imaging system (Caliper Life Sciences, Hopkinton, MA). As culture media contain high folate content, folate receptor positive tumor cells to be transplanted onto these mice will be grown in folate-free cell culture media containing 5-10% heat-inactivated FCS with no antibiotics. Similarly, normal rodent chow contains a high concentration of folic acid; nude mice used in this study will be maintained on folate-free diet 2 weeks prior to tumor implantation and for the duration of the imaging analysis to reduce serum folate concentration.

[00625] In brief, female nu/nu mice bearing folate receptor positive tumor cells are given a single intravenous injection of high or low dose folate-XTEN-Cy5.5 and corresponding doses of non-targeting Cy5.5 tagged XTEN control. Whole body scans are acquired pre-injection and then at approximately 8, 24, 48 and 72 hours post-injection on live anesthetized animals using the IVIS 50 optical imaging system. After measuring the distribution of fluorescence in the entire animal at the last time point of 72h, tumor and healthy organs including liver, lung, heart, spleen and kidneys are excised and their fluorescence registered and processed by the imaging system. Cy5.5 excitation (615-665nm) and emission (695-770nm) filters are selected to match the fluorescence agents' wavelengths. Small and medium binning of the CCD chip is used and the exposure time optimized to obtain at least several thousand counts from the signals that were observable in each mouse in the image and to avoid saturation of the CCD chip. To normalize images for quantification, a background fluorescence image is acquired using background excitation and emission filters for the Cy5.5 spectral region. The intensity of fluorescence is expressed as different colors with blue color reflecting the lowest intensity and red being indicative of the highest intensity, and the resulting images are used to assess the uptake of the conjugates and controls.

[00626] Example 49: Pharmacokinetic analysis of LHRH-XTEN-drug conjugates

[00627] The *in vivo* pharmacokinetics of LHRH-XTEN-drug constructs are assessed using standard methods for protein compositions using mice, rats, cynomolgus monkeys, and dogs. Compositions of LHRH-XTEN-drug constructs are provided in an aqueous buffer compatible

with in vivo administration (for example: phosphate-buffered saline, Tris-buffered saline or Hepes-buffered saline). The compositions are administered at appropriate doses and via multiple routes: most preferably via intravenous or subcutaneous routes. Blood samples are collected at appropriate time points ranging from 0.08 to 504 hours, and processed into plasma. Plasma samples are analyzed for concentration of LHRH-XTEN-drug conjugates by one of a variety of methods, including ELISA, HPLC and/or LC-MS/MS. ELISA analysis are performed using a sandwich ELISA format that can recognize 2 components of the LHRH-XTEN-drug conjugate, for instance, XTEN/LHRH, XTEN/drug moiety, LHRH/drug moiety and/or XTEN/XTEN combinations. Typically antibody recognizing one component of the LHRH-XTEN-drug conjugate is coated onto wells of a 96-well microtiter plate. The wells are blocked, washed and plasma samples are then added to the wells at varying dilutions to allow capture of the conjugate by the coated antibody. Wells are then washed extensively, and bound protein detected using either a biotinylated antibody or an appropriate secondary antibody against the second LHRH-XTEN-drug conjugate component. Wells are then washed again and streptavidin-horseradish peroxidase (complementary to the biotinylated detection antibody) or a secondary antibody-horseradish peroxidase (complementary to a non biotinylated detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and the plate is read at 450 nM. Concentrations of conjugate are then calculated for each time point by comparing the colorimetric response to a LHRH-XTEN-drug calibration curve. Pharmacokinetic parameters are calculated using the WinNonLin software package.

[00628] For RP-HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug. For example, doxorubicin is detected at 480 nm. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are assayed in parallel with experimental samples.

[00629] For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated under vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs are determined experimentally for each drug. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are assayed in parallel with experimental samples.

[00630] It is expected that the results would support the finding that addition of an XTEN to LHRH and drug moiety will greatly increase the terminal half-life and enhance the pharmacokinetic properties of targeting and drug moiety not linked to XTEN.

[00631] Example 50: Pharmacokinetic analysis of folate-XTEN-drug conjugates

[00632] The *in vivo* pharmacokinetics of folate-XTEN-drug constructs are assessed using standard methods for protein compositions using mice, rats, cynomolgus monkeys, and dogs. As normal feed contains a high concentration of folic acid (approx. 6mg/kg mouse chow), animals to be used in pharmacokinetic studies of folate conjugates will be maintained on folate-free diet for 2 weeks prior to study initiation and for the duration of the study. The compositions are administered at appropriate doses and via multiple routes: most preferably via intravenous or subcutaneous routes. Blood samples are collected at appropriate time points ranging from 0.08 to 504 hours, and processed into plasma. Plasma samples are analyzed for concentration of folate-XTEN-drug conjugates by a variety of methods including ELISA, HPLC and/or LC-MS/MS.

[00633] ELISA analysis are performed using a sandwich ELISA format that can recognize 2 components of the folate-XTEN-drug conjugate, for instance, XTEN/folate, XTEN/drug moiety, folate/drug moiety and/or XTEN/XTEN combinations. Typically antibody recognizing one component of the folate-XTEN-drug conjugate is coated onto wells of a 96-well microtiter plate. The wells are blocked, washed and plasma samples are then added to the wells at varying dilutions to allow capture of the conjugate by the coated antibody. Wells are then washed extensively, and bound protein detected using either a biotinylated antibody or an appropriate secondary antibody against the second folate-XTEN-drug conjugate component. Wells are then washed again and streptavidin-horseradish peroxidase (complementary to the biotinylated detection antibody) or a secondary antibody-horseradish peroxidase (complementary to a non biotinylated detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and the plate is read at 450 nM. Concentrations of conjugate are then calculated for each time point by comparing the colorimetric response to a folate-XTEN-drug calibration curve. Pharmacokinetic parameters are calculated using the WinNonLin software package.

[00634] For RP-HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug. For example, doxorubicin is detected at 480 nm. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are assayed in parallel with experimental samples.

[00635] For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated under vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs are

determined experimentally for each drug. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are assayed in parallel with experimental samples.

[00636] It is expected that the results would support the finding that addition of an XTEN to folate and drug moiety will greatly increase the terminal half-life and enhance the pharmacokinetic properties of targeting and drug moiety not linked to XTEN.

[00637] Example 51: In vivo efficacy and toxicity analysis of LHRH-XTEN-drug conjugates

[00638] LHRH-XTEN-drug conjugate is intended for targeted delivery of highly potent toxin to LHRH receptor positive tumor cells. As such, the *in vivo* pharmacologic activity of LHRH-XTEN-drug constructs can be assessed using human tumor cells expressing LHRH receptor transplanted into nude mice.

[00639] Prior to beginning the efficacy study, an initial assessment in nude mice is carried out to establish the maximum tolerated dose (MTD) of the LHRH-XTEN-drug candidates. The MTD, the highest dose that is tolerated by the animal for the study duration, will then be used to calculate the dose range for the efficacy and toxicity study in the standard xenograft model. Briefly, the MTD experiment is carried out with 5 mice per group evaluating the intravenous administration of LHRH-XTEN-drug conjugates at various dose level, interval and duration. The starting MTD dose and number of dose groups required is based on scientific literature, knowledge of the targeting LHRH moiety, the nature of the drug moiety conjugated, toxicological properties of closely related compounds, and data from the initial pharmacokinetic studies (see, above). Standard MTD parameters such as reduction in body weight, food and water consumption and signs of piloerection, hunched, behavior patterns, respiratory pattern, tremors, convulsions, prostration and self-mutilation are monitored on a daily basis. The highest dose of LHRH-XTEN-drug that does not cause unacceptable toxicity will be assigned as the MTD. The tumor xenograft study will include 3 to 4 dosing levels of LHRH-XTEN-drug conjugate and will depend on the results from the MTD study; with other parameters depending on the tumor cell line chosen. Table 42 provides examples of tumor lines that can be used in the xenograft study. Thus, an appropriate number of LHRH receptor positive cells from the relevant human tumor line are injected subcutaneously and allowed to form tumors, the size of which will be measured with calipers and the volume calculated as $0.5 \times L \times W^2$, where L = measurement of longest axis in millimeters and W = measurement of axis perpendicular to L in millimeters. Following randomization of mice containing tumor volume in the desired size range into groups of 8-10 animals, vehicle control, free drug control and LHRH-XTEN-drug conjugate is administered intravenously at the chosen doses and interval. Cessation or regression of tumor growth is determined by measuring the tumor size and volume at selected time points with

calipers. Body weights and food consumption are measured every 1to 2 days to assess gross toxicity. Survival of animals is monitored daily. At the end of the study, all animals are sacrificed and clinical pathology and histopathology on major organs is performed.

[00640] It is anticipated that the results would support the finding that the LHRH-XTEN-drug conjugate will produce a positive therapeutic index as exhibited by potent efficacy and low systemic toxicity. In contrast, the non-LHRH targeted free drug dosed at equimolar doses is expected to be less potent but highly more toxic. It is expected that the vehicle control will display uncontrolled tumor growth and severe toxicity.

[00641] Example 52: In vivo efficacy and toxicity analysis of folate-XTEN-drug conjugates

[00642] Folate-XTEN-drug conjugates are intended for targeted delivery of the toxin component to folate receptor positive tumor cells. The *in vivo* pharmacologic activity of folate-XTEN-drug constructs is assessed using human tumor cell expressing folate receptor xenograft onto nude mice. Prior to beginning the efficacy study, an initial assessment in nude mice is carried out to establish the maximum tolerated dose (MTD) of the folate-XTEN-drug candidates. The MTD, the highest dose that will be tolerated by the animal for the study duration, is then used to calculate the dose range for the efficacy and toxicity study in the standard xenograft model. As normal rodent chow contains a high concentration of folic acid (6mg/kg chow), mice to be used in these studies are maintained on a folate-free diet for 2 weeks prior to study initiation and for the duration of the study. The MTD experiment is carried out with 5 mice per group evaluating the intravenous administration of folate-XTEN-drug conjugates at various dose level, interval and duration. The starting MTD dose and number of dose groups required is based on scientific literature, knowledge of the targeting folate moiety, the nature of the drug moiety conjugated, toxicological properties of closely related compounds, and data from the initial pharmacokinetic studies (see PK Example above). Standard MTD parameters such as reduction in body weight, food and water consumption and signs of piloerection, hunched, behavior patterns, respiratory pattern, tremors, convulsions, prostration and self-mutilation are carefully monitored on a daily basis. The highest dose of folate-XTEN-drug that does not cause unacceptable toxicity is assigned as the MTD.

[00643] The tumor xenograft study includes 3 to 4 dosing levels of folate-XTEN-drug, depending on the results from the MTD study, with other parameters depending on the tumor cell line chosen. Table 42 describes examples of tumor lines that can be used in the xenograft study. To reduce folate content, folate receptor positive tumor cells to be transplanted onto nude mice are grown in folate-free cell culture media containing 5-10% heat-inactivated fetal calf serum with no antibiotics. Similarly, to reduce serum folate concentration, mice used in the xenograft studies are maintained on folate-free diet 2 weeks prior to tumor implantation and for the duration of the study. An appropriate number of folate receptor positive cells from the relevant

line are injected subcutaneously and allowed to form tumors, the size of which are measured with calipers and the volume calculated as 0.5 x L x W^2, where L = measurement of longest axis in millimeters and W = measurement of axis perpendicular to L in millimeters. Following randomization of mice containing tumor volume in the desired size range into groups of 8-10 animals, vehicle control, free drug control and folate-XTEN-drug is administered intravenously at the chosen doses and intervals. Cessation or regression of tumor growth is determined through measuring the tumor size and volume at selected time points with calipers. Body weight and food consumption is measured every 1 to 2 days to assess gross toxicity. Survival of animals is monitored daily. At the end of study, all animals are sacrificed and major organs will be removed for clinical pathology and histopathology examination.

[00644] It is anticipated that the targeted chemotherapeutic folate-XTEN-drug conjugate will be more effective and less toxic than free cytotoxic drug alone on folate receptor positive tumors in the mouse model.

[00645] Example 53: Human Clinical Trial Designs for Evaluating LHRH-XTEN-drug conjugates

[00646] Targeted chemotherapy is a modern approach aimed at increasing the efficacy of systemic chemotherapy and reducing side effects. LHRH is a peptide that functions in reproductive organs. Because its receptors are particularly concentrated on certain tumors but are not expressed in most normal tissue, the LHRH receptor is an ideal target for selective destruction of malignant tumors. Indeed, ~52% of breast, ~80% of ovarian and endometrial, and ~85% of prostate cancer specimens is targetable via the LHRH receptor. Of note, LHRH-dependent therapies would be especially useful for triple negative breast tumors, which do not overexpress estrogen or progesterone receptors or HER2 and are therefore unsuitable for treatment with many available targeted drugs. Patients with advanced endometrial, ovarian, or prostate cancer often have particularly poor outcomes, as these malignancies can be prone to recurrence and/or resistant to current treatments. Fusion of a XTEN carrying ≥1 copy of LHRH to a XTEN bearing ≥ 3 drug molecules to create a targeted peptide-drug conjugate is expected to have vastly improved therapeutic index and half-life that will enable dosing at levels way below MTD, reduce dosing frequency and cost (reduced drug required per dose).

[00647] Clinical evaluation of a LHRH-XTEN-drug composition is conducted in patients suffering from advanced breast, endometrial, ovarian, and prostate or bladder cancers, with trials designed to confirm the efficacy and safety of the LHRH-XTEN-drug conjugate in humans. Such studies in patients would comprise three phases. First, a Phase I safety and pharmacokinetics study would be conducted to determine the maximum tolerated dose (MTD) and to characterize the dose-limiting toxicity, pharmacokinetics and preliminary pharmacodynamics in humans. These initial studies could be performed in patients with

metastatic or unresectable cancers and for which standard curative or palliative measures could not be used or were no longer effective or tolerated, and LHRH receptor positive status in the patients would be an enrollment criteria. The scheme of the phase I study would be to use single escalating doses of LHRH-XTEN-drug conjugate and to measure the biochemical, PK, and clinical parameters, permiting the determination of the MTD and the threshold and maximum concentrations in dosage and in circulating drug that constitute the therapeutic window to be used in subsequent Phase II and Phase III trials, as well as defining potential toxicities and adverse events to be tracked in future studies.

[00648] Phase II clinical studies of human patients would be independently conducted in LHRH receptor positive advanced (stage 3 or 4) or recurrent breast, endometrial, ovarian, and prostate or bladder cancer patients. The trial would evaluate the efficacy and safety of LHRH-XTEN-drug conjugate alone and in combination with a current chemotherapy employed in the specific indication. Patients will receive intravenously administered LHRH-XTEN-drug clinical candidate at a dose level and regimen pre-determined in Phase I with or without the standard chemotherapeutic agent. A control arm comprising of the chemotherapeutic agent plus placebo would be included. The primary endpoint would be response rate as defined by the Response Evaluation Criteria in Solid Tumors (RECIST). Secondary endpoints will include safety and tolerability, time-to-progression and overall survival.

[00649] A phase III efficacy and safety study is conducted in LHRH receptor positive advanced (resistant, recurrent) breast, endometrial, ovarian, and prostate or bladder cancer patients to test ability to reach statistically significant clinical endpoints such as progression-free-survival as measured by RECIST. The trial will also be statistically powered for overall survival as a secondary endpoint with projected enrollment in excess of 400 patients. Efficacy outcomes are determined using standard statistical methods. Toxicity and adverse event markers are also followed in the study to verify that the compound is safe when used in the manner described.

[00650] Example 54: Human Clinical Trial Designs for Evaluating folate-XTEN-drug conjugates

[00651] Targeted chemotherapy is a modern approach aimed at increasing the efficacy of systemic chemotherapy and reducing its side effects. Folate, also known as folic acid, vitamin B_9, is a vital nutrient required by all living cells for nucleotide biosynthesis and function as cofactor in certain biological pathways. The folate receptor is a focus for the development of therapies to treat fast dividing malignancies; in particular ovarian cancer and non-small cell lung carcinoma. While folate receptor expression is negligible in normal ovary, ~90% of epithelial ovarian cancers overexpress the folate receptor, as do many lung adenocarinomas, thereby opening the possibility of directed therapies. Fusion of a XTEN carrying $\geq$1 copy of folate to a XTEN bearing $\geq$ 3 drug molecules to create a targeted peptide-drug conjugate is expected to

improve the therapeutic index and the extended half-life will enable dosing at levels way below maximum tolerated dose (MTD), reduce dosing frequency and cost (reduced drug required per dose).

[00652] Clinical evaluation of folate-XTEN-drug composition is conducted in patients with relapsed or refractory advanced tumors or in patients suffering from platinum-resistant ovarian cancer and non-small cell lung carcinoma who have failed using other chemotherapies. Clinical trials are designed to determine the efficacy and advantages of the folate-XTEN-drug conjugate over standard therapies in humans. Such studies in patients would comprise three phases. First, a Phase I safety and pharmacokinetics study is conducted to determine the MTD and to characterize the dose-limiting toxicity, pharmacokinetics and preliminary pharmacodynamics in humans. These initial studies could be performed in patients with folate receptor positive status that have relapsed or have refractory advanced tumors and for which standard curative or palliative measures could not be used or were no longer effective or tolerated. The phase I study would use single escalating doses of folate-XTEN-drug conjugate and would measure biochemical, PK, and clinical parameters to permit the determination of the MTD and establish the threshold and maximum concentrations in dosage and in circulating drug that constitute the therapeutic window to be used in subsequent Phase II and Phase III trials as well as defining potential toxicities and adverse events to be tracked in future studies.

[00653] Phase II clinical studies of human patients would be independently conducted in folate receptor positive platinum-resistant ovarian cancer patient population, non-small cell lung carcinoma patients having failed numerous chemotherapies, and patients suffering from relapsed or refractory advanced tumors. The trials would evaluate the efficacy and safety of folate-XTEN-drug conjugate alone and in combination with a current chemotherapy employed in the specific indication. Patients will receive intravenously administered folate-XTEN-drug conjugate at a dose level and regimen determined in the Phase I study with or without the standard chemotherapy agent. A control arm comprising of the chemotherapy agent plus placebo would be included. The primary endpoint would be response rate as defined by the Response Evaluation Criteria in Solid Tumors (RECIST). Secondary endpoints will include safety and tolerability, time-to-progression and overall survival.

[00654] A phase III efficacy and safety study is conducted in folate-receptor positive platinum-resistant ovarian cancer patients, non-small cell lung carcinoma patients, or advanced tumor relapsed or refractory patients cancer patients to test ability to reach statistically significant clinical endpoints such as progression-free-survival as measured by RECIST. The trial will also be statistically powered for overall survival as a secondary endpoint with projected enrollment in excess of 400 patients. Efficacy outcomes are determined using standard statistical methods.

Toxicity and adverse event markers are also followed in the study to verify that the compound is safe when used in the manner described.

[00655] Example 55: Serum stability of XTEN

[00656] A fusion protein containing XTEN_AE864 fused to the N-terminus of GFP was incubated in monkey plasma and rat kidney lysate for up to 7 days at 37°C. Samples were withdrawn at time 0, Day 1 and Day 7 and analyzed by SDS PAGE followed by detection using Western analysis and detection with antibodies against GFP as shown in FIG. 76. The sequence of XTEN_AE864 showed negligible signs of degradation over 7 days in plasma. However, XTEN_AE864 was rapidly degraded in rat kidney lysate over 3 days. The in vivo stability of the fusion protein was tested in plasma samples wherein the GFP_AE864 was immunoprecipitated and analyzed by SDS PAGE as described above. Samples that were withdrawn up to 7 days after injection showed very few signs of degradation. The results demonstrate the resistance of aaT-XTEN to degradation due to serum proteases; a factor in the enhancement of pharmacokinetic properties of the aaT-XTEN fusion proteins.

[00657] Example 56: Characterization of secondary structure of XTEN linked to exendin-4

[00658] The XTEN_AE864-Ex4 was evaluated for degree of secondary structure by circular dichroism spectroscopy. CD spectroscopy was performed on a Jasco J-715 (Jasco Corporation, Tokyo, Japan) spectropolarimeter equipped with Jasco Peltier temperature controller (TPC-348WI). The concentration of protein was adjusted to 0.2 mg/mL in 20 mM sodium phosphate pH 7.0, 50 mM NaCl. The experiments were carried out using HELLMA quartz cells with an optical path-length of 0.1 cm. The CD spectra were acquired at 5°, 25°, 45°, and 65°C and processed using the J-700 version 1.08.01 (Build 1) Jasco software for Windows. The samples were equilibrated at each temperature for 5 min before performing CD measurements. All spectra were recorded in duplicate from 300 nm to 185 nm using a bandwidth of 1 nm and a time constant of 2 sec, at a scan speed of 100 nm/min. The CD spectrum shown in FIG. 77 shows no evidence of stable secondary structure and is consistent with an unstructured polypeptide.

[00659] Example 57: Increasing solubility and stability of a peptide payload by linking to XTEN

[00660] In order to evaluate the ability of XTEN to enhance the physicochemical properties of solubility and stability, fusion proteins of glucagon plus shorter-length XTEN were prepared and evaluated. The test articles were prepared in Tris-buffered saline at neutral pH and characterization of the Gcg-XTEN solution was by reverse-phase HPLC and size exclusion chromatography to affirm that the protein was homogeneous and non-aggregated in solution. The data are presented in Table 43. For comparative purposes, the solubility limit of unmodified glucagon in the same buffer was measured at 60 μM (0.2 mg/mL), and the result demonstrate that for all lengths of XTEN added, a substantial increase in solubility was attained. Importantly,

in most cases the glucagon-XTEN fusion proteins were prepared to achieve target concentrations and were not evaluated to determine the maximum solubility limits for the given construct. However, in the case of glucagon linked to the AF-144 XTEN, the limit of solubility was determined, with the result that a 60-fold increase in solubility was achieved, compared to glucagon not linked to XTEN. In addition, the glucagon-AF144 was evaluated for stability, and was found to be stable in liquid formulation for at least 6 months under refrigerated conditions and for approximately one month at 37°C (data not shown).

[00661] The data support the conclusion that the linking of short-length XTEN polypeptides to a biologically active protein such as glucagon can markedly enhance the solubility properties of the protein by the resulting fusion protein, as well as confer stability at the higher protein concentrations.

Table 43: Solubility of Glucagon-XTEN constructs

Test Article	Solubility
Glucagon	60 μM
Glucagon-Y36	>370 μM
Glucagon-Y72	>293 μM
Glucagon-AF108	>145 μM
Glucagon-AF120	>160 μM
Glucagon-Y144	>497 μM
Glucagon-AE144	>467 μM
Glucagon-AF144	>3600 μM
Glucagon-Y288	>163 μM

[00662] Example 58: Analytical size exclusion chromatography of XTEN linked with diverse payloads

[00663] Size exclusion chromatography analyses were performed on fusion proteins containing various therapeutic proteins and unstructured recombinant proteins of increasing length. An exemplary assay used a TSKGel-G4000 SWXL (7.8mm x 30cm) column in which 40 μg of purified glucagon fusion protein at a concentration of 1 mg/ml was separated at a flow rate of 0.6 ml/min in 20 mM phosphate pH 6.8, 114 mM NaCl. Chromatogram profiles were monitored using OD214nm and OD280nm. Column calibration for all assays were performed using a size exclusion calibration standard from BioRad; the markers include thyroglobulin (670 kDa), bovine gamma-globulin (158 kDa), chicken ovalbumin (44 kDa), equine myoglobuin (17 kDa) and vitamin B12 (1.35 kDa). Representative chromatographic profiles of Glucagon-Y288, Glucagon-Y144, Glucagon-Y72, Glucagon-Y36 are shown as an overlay in FIG. 78. The data show that the molecular weight of each compound is proportional to the length of the attached

XTEN sequence. However, the data also show that the apparent molecular weight of each construct is significantly larger than that expected for a globular protein (as shown by comparison to the standard proteins run in the same assay). Based on the SEC analyses for all constructs evaluated, the apparent molecular weights, the apparent molecular weight factor (expressed as the ratio of apparent molecular weight to the calculated molecular weight) and the hydrodynamic radius (R_H in nm) are shown in Table 44. The results indicate that incorporation of different XTENs of 576 amino acids or greater confers an apparent molecular weight for the fusion protein of approximately 339 kDa to 760, and that XTEN of 864 amino acids or greater confers an apparent molecular weight greater than approximately 800 kDA. The results of proportional increases in apparent molecular weight to actual molecular weight were consistent for fusion proteins created with XTEN from several different motif families; i.e., AD, AE, AF, AG, and AM, with increases of at least four-fold and ratios as high as about 17-fold. Additionally, the incorporation of XTEN fusion partners with 576 amino acids or more into fusion proteins with the various payloads (and 288 residues in the case of glucagon fused to Y288) resulted with a hydrodynamic radius of 7 nm or greater; well beyond the glomerular pore size of approximately 3-5 nm. Accordingly, it is expected that fusion proteins comprising growth and XTEN have reduced renal clearance, contributing to increased terminal half-life and improving the therapeutic or biologic effect relative to a corresponding un-fused biologic payload protein.

Table 44: SEC analysis of various polypeptides

Construct Name	XTEN or fusion partner	Therapeutic Protein	Actual MW (kDa)	Apparent MW (kDa)	Apparent Molecular Weight Factor	R_H (nm)
AC14	Y288	Glucagon	28.7	370	12.9	7.0
AC28	Y144	Glucagon	16.1	117	7.3	5.0
AC34	Y72	Glucagon	9.9	58.6	5.9	3.8
AC33	Y36	Glucagon	6.8	29.4	4.3	2.6
AC89	AF120	Glucagon	14.1	76.4	5.4	4.3
AC88	AF108	Glucagon	13.1	61.2	4.7	3.9
AC73	AF144	Glucagon	16.3	95.2	5.8	4.7
AC53	AG576	GFP	74.9	339	4.5	7.0
AC39	AD576	GFP	76.4	546	7.1	7.7
AC41	AE576	GFP	80.4	760	9.5	8.3
AC52	AF576	GFP	78.3	526	6.7	7.6
AC398	AE288	FVII	76.3	650	8.5	8.2
AC404	AE864	FVII	129	1900	14.7	10.1
AC85	AE864	Exendin-4	83.6	938	11.2	8.9

Construct Name	XTEN or fusion partner	Therapeutic Protein	Actual MW (kDa)	Apparent MW (kDa)	Apparent Molecular Weight Factor	R_H (nm)
AC114	AM875	Exendin-4	82.4	1344	16.3	9.4
AC143	AM875	hGH	100.6	846	8.4	8.7
AC302	AE912 + AE144	hGH	119.1	2,287	19.2	11.0
AC227	AM875	IL-1ra	95.4	1103	11.6	9.2
AC228	AM1318	IL-1ra	134.8	2286	17.0	10.5
AC493	AE864	FIX	127.7*	3967	31.1	12.2
AC616	AE864	GLP2-2G	83.1	1427	17.2	10
AC647	AE864	Ghrelin	82.7	996	12	9.2
AC659	AE864	C-peptide	82.7	822	10	8.8
AC663	AE1296	C-peptide	122.2	2348	19.2	11.1
AC434	AE288	aaT	71.1	500	7.0	7.7
AC435	AE576	aaT	97.5	1,127	11.6	9.5
AC345	AM875	aaT	122.6	1,390	11.3	9.9
AC450	AE288	aHer2_scFv	56.2	312	5.5	6.7
AC451	AE576	aHer2_scFv	82.6	760	9.2	8.6
AC452	AE864	aHer2_scFv	109.1	1,390	12.7	9.9

* excluding glycosylation

[00664] Example 59: Analysis of sequences for secondary structure by prediction algorithms

[00665] Amino acid sequences can be assessed for secondary structure via certain computer programs or algorithms, such as the well-known Chou-Fasman algorithm (Chou, P. Y., *et al.* (1974) *Biochemistry*, **13**: 222-45) and the Garnier-Osguthorpe-Robson, or "GOR" method (Garnier J, Gibrat JF, Robson B. (1996). GOR method for predicting protein secondary structure from amino acid sequence. Methods Enzymol 266:540-553). For a given sequence, the algorithms can predict whether there exists some or no secondary structure at all, expressed as total and/or percentage of residues of the sequence that form, for example, alpha-helices or beta-sheets or the percentage of residues of the sequence predicted to result in random coil formation.

[00666] Several representative sequences from XTEN "families" have been assessed using two algorithm tools for the Chou-Fasman and GOR methods to assess the degree of secondary structure in these sequences. The Chou-Fasman tool was provided by William R. Pearson and the University of Virginia, at the "Biosupport" internet site, URL located on the World Wide Web at .fasta.bioch.virginia.edu/fasta_www2/fasta_www.cgi?rm=misc1 as it existed on June 19, 2009. The GOR tool was provided by Pole Informatique Lyonnais at the Network Protein Sequence Analysis internet site, URL located on the World Wide Web at .npsa-pbil.ibcp.fr/cgi-bin/secpred_gor4.pl as it existed on June 19, 2008.

[00667] As a first step in the analyses, a single XTEN sequence was analyzed by the two algorithms. The AE864 composition is a XTEN with 864 amino acid residues created from multiple copies of four 12 amino acid sequence motifs consisting of the amino acids G, S, T, E, P, and A. The sequence motifs are characterized by the fact that there is limited repetitiveness within the motifs and within the overall sequence in that the sequence of any two consecutive amino acids is not repeated more than twice in any one 12 amino acid motif, and that no three contiguous amino acids of full-length the XTEN are identical. Successively longer portions of the AF 864 sequence from the N-terminus were analyzed by the Chou-Fasman and GOR algorithms (the latter requires a minimum length of 17 amino acids). The sequences were analyzed by entering the FASTA format sequences into the prediction tools and running the analysis. The results from the analyses are presented in Table 45.

[00668] The results indicate that, by the Chou-Fasman calculations, short XTEN of the AE and AG families, up to at least 288 amino acid residues, have no alpha-helices or beta sheets, but amounts of predicted percentage of random coil by the GOR algorithm vary from 78-99%. With increasing XTEN lengths of 504 residues to greater than 1300, the XTEN analyzed by the Chou-Fasman algorithm had predicted percentages of alpha-helices or beta sheets of 0 to about 2%, while the calculated percentages of random coil increased to from 94-99%. Those XTEN with alpha-helices or beta sheets were those sequences with one or more instances of three contiguous serine residues, which resulted in predicted beta-sheet formation. However, even these sequences still had approximately 99% random coil formation.

[00669] The analysis supports the conclusion that: 1) XTEN created from multiple sequence motifs of G, S, T, E, P, and A that have limited repetitiveness as to contiguous amino acids are predicted to have very low amounts of alpha-helices and beta-sheets; 2) that increasing the length of the XTEN does not appreciably increase the probability of alpha-helix or beta-sheet formation; and 3) that progressively increasing the length of the XTEN sequence by addition of non-repetitive 12-mers consisting of the amino acids G, S, T, E, P, and A results in increased percentage of random coil formation. Based on the numerous sequences evaluated by these methods, it is concluded that XTEN created from sequence motifs of G, S, T, E, P, and A that have limited repetitiveness (defined as no more than two identical contiguous amino acids in any one motif) are expected to have very limited secondary structure. With the exception of motifs containing three contiguous serines, generally any order or combination of sequence motifs from Table 1 can be used to create an XTEN polypeptide that will result in an XTEN sequence that is substantially devoid of secondary structure, and that the effects of three contiguous serines is ameliorated by increasing the length of the XTEN. Such sequences are expected to have the characteristics described in the XTEN-containing composition embodiments of the invention disclosed herein.

Table 45: CHOU-FASMAN and GOR prediction calculations of polypeptide sequences

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
AE36: LCW0402_002	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP	36	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	94.44%
AE36: LCW0402_003	GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP	36	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	94.44%
AG36: LCW0404_001	GASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP	36	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	77.78%
AG36: LCW0404_003	GSSTPSGATGSPGSSPSASTGTGPGSSTPSGATGSP	36	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	83.33 %
AE42_1	TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGS	42	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	90.48%
AE42_1	TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGS	42	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	90.48%
AG42_1	GAPSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGPSGP	42	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	88.10%
AG42_2	GPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASP	42	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	88.10%
AE144	GSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGSEPATSGSETPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP	144	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	98.61%
AG144_1	PGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSS	144	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	91.67%
AE288	GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGP	288	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	99.31%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
	GTSESATPESGPGTSESATPESGPGSEP ATSGSETPGSEPATSGSETPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAP GSEPATSGSETPGTSESATPESGPGTST EPSEGSAP			
AG288_2	GSSPSASTGTGPGSSPSASTGTGPGTP GSGTASSSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGTPGSGTASS SPGSSTPSGATGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGASPGTSST GSPGTPGSGTASSSPGSSTPSGATGSP GSSPSASTGTGPGSSPSASTGTGPGSST PSGATGSPGSSTPSGATGSPGASPGTS STGSPGASPGTSSTGSPGASPGTSSTGS PGTPGSGTASSSP	288	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	92.71
AF504	GASPGTSSTGSPGSSPSASTGTGPGSSP SASTGTGPGTPGSGTASSSPGSSTPSG ATGSPGSNPSASTGTGPGASPGTSSTG SPGTPGSGTASSSPGSSTPSGATGSPGT PGSGTASSSPGASPGTSSTGSPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGAT GSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGSNPSASTGTGPGSS PSASTGTGPGSSTPSGATGSPGSSTPSG ATGSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGASP GTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATG SPGSSTPSGATGSPGSSPSASTGTGPG ASPGTSSTGSP	504	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	94.44%
AD 576	GSSESGSSEGGPGSGGEPSESGSSGSSE SGSSEGGPGSSESGSSEGGPGSSESGSS EGGPGSSESGSSEGGPGSSESGSSEGG PGESPGGSSGSESGSEGSSGPGESSGSS ESGSSEGGPGSSESGSSEGGPGSSESGS SEGGPGSGGEPSESGSSGESPGGSSGS ESGESPGGSSGSESGSGGEPSESGSSGS SESGSSEGGPGSGGEPSESGSSGSGGE PSESGSSGSEGSSGPGESSGESPGGSSG SESGSGGEPSESGSSGSGGEPSESGSSG SGGEPSESGSSGSSESGSSEGGPGESPG GSSGSESGESPGGSSGSESGESPGGSS GSESGESPGGSSGSESGESPGGSSGSES GSSESGSSEGGPGSGGEPSESGSSGSE GSSGPGESSGSSESGSSEGGPGSGGEP SESGSSGSSESGSSEGGPGSGGEPSESG SSGESPGGSSGSESGESPGGSSGSESGS SESGSSEGGPGSGGEPSESGSSGSSESG SSEGGPGSGGEPSESGSSGSGGEPSES GSSGESPGGSSGSESGSEGSSGPGESS GSSESGSSEGGPGSEGSSGPGESS	576	Residue totals: H: 7 E: 0 percent: H: 1.2 E: 0.0	99.65%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
AE576	GSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPA GSPTSTEEGTSESATPESGPGTSTEPSE GSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSE SATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSE SATPESGPGSPAGSPTSTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSPAGSPTSTEEGSP AGSPTSTEEGSPAGSPTSTEEGTSESAT PESGPGTSTEPSEGSAP	576	Residue totals: H: 2 E: 0 percent: H: 0.4 E: 0.0	99.65%
AG576	PGTPGSGTASSSPGSSTPSGATGSPGSS PSASTGTGPGSSPSASTGTGPGSSTPSG ATGSPGSSTPSGATGSPGASPGTSSTG SPGASPGTSSTGSPGASPGTSSTGSPGT PGSGTASSSPGASPGTSSTGSPGASPG TSSTGSPGASPGTSSTGSPGSSPSASTG TGPGTPGSGTASSSPGASPGTSSTGSP GASPGTSSTGSPGASPGTSSTGSPGSST PSGATGSPGSSTPSGATGSPGASPGTS STGSPGTPGSGTASSSPGSSTPSGATGS PGSSTPSGATGSPGSSTPSGATGSPGSS PSASTGTGPGASPGTSSTGSPGASPGT SSTGSPGTPGSGTASSSPGASPGTSSTG SPGASPGTSSTGSPGASPGTSSTGSPG ASPGTSSTGSPGTPGSGTASSSPGSSTP SGATGSPGTPGSGTASSSPGSSTPSGA TGSPGTPGSGTASSSPGSSTPSGATGSP GSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGASPGTSSTGSPGTPGSGT ASSSPGSSTPSGATGSPGSSPSASTGTG PGSSPSASTGTGPGASPGTSSTGS	576	Residue totals: H: 0 E: 3 percent: H: 0.4 E: 0.5	99.31%
AF540	GSTSSTAESPGPGSTSSTAESPGPGSTS ESPSGTAPGSTSSTAESPGPGSTSSTAE SPGPGTSTPESGSASPGSTSESPSGTAP GTSPSGESSTAPGSTSESPSGTAPGSTS ESPSGTAPGTSPSGESSTAPGSTSESPS GTAPGSTSESPSGTAPGTSPSGESSTAP GSTSESPSGTAPGSTSESPSGTAPGSTS ESPSGTAPGTSTPESGSASPGSTSESPS GTAPGTSTPESGSASPGSTSSTAESPGP GSTSSTAESPGPGTSTPESGSASPGTST PESGSASPGSTSESPSGTAPGTSTPESG SASPGTSTPESGSASPGSTSESPSGTAP GSTSESPSGTAPGSTSESPSGTAPGSTS STAESPGPGTSTPESGSASPGTSTPESG	540	Residue totals: H: 2 E: 0 percent: H: 0.4 E: 0.0	99.65

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
	SASPGSTSESPSGTAPGSTSESPSGTAP GTSTPESGSASPGSTSESPSGTAPGSTS ESPSGTAPGTSTPESGSASPGTSPSGES STAPGSTSSTAESPGPGTSPSGESSTAP GSTSSTAESPGPGTSTPESGSASPGSTS ESPSGTAP			
AD836	GSSESGSSEGGPGSSESGSSEGGPGESP GGSSGSESGSGGEPSESGSSGESPGGS SGSESGESPGGSSGSESGSSESGSSEGG PGSSESGSSEGGPGSSESGSSEGGPGES PGGSSGSESGESPGGSSGSESGESPGG SSGSESGSSESGSSEGGPGSSESGSSEG GPGSSESGSSEGGPGSSESGSSEGGPG SSESGSSEGGPGSSESGSSEGGPGSGG EPSESGSSGESPGGSSGSESGESPGGSS GSESGSGGEPSESGSSGSEGSSGPGESS GSSESGSSEGGPGSGGEPSESGSSGSE GSSGPGESSGSSESGSSEGGPGSGGEP SESGSSGESPGGSSGSESGSGGEPSESG SSGSGGEPSESGSSGSSESGSSEGGPGS GGEPSESGSSGSGGEPSESGSSGSEGSS GPGESSGESPGGSSGSESGSEGSSGPG ESSGSEGSSGPGESSGSGGEPSESGSSG SSESGSSEGGPGSSESGSSEGGPGESPG GSSGSESGSGGEPSESGSSGSEGSSGP GESSGESPGGSSGSESGSEGSSGPGSSE SGSSEGGPGSGGEPSESGSSGSEGSSG PGESSGSEGSSGPGESSGSEGSSGPGES SGSGGEPSESGSSGSGGEPSESGSSGES PGGSSGSESGESPGGSSGSESGSGGEP SESGSSGSEGSSGPGESSGESPGGSSGS ESGSSESGSSEGGPGSSESGSSEGGPGS SESGSSEGGPGSGGEPSESGSSGSSESG SSEGGPGESPGGSSGSESGSGGEPSES GSSGSSESGSSEGGPGESPGGSSGSES GSGGEPSESGSSGESPGGSSGSESGSG GEPSESGSS	836	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	98.44%
AE864	GSPAGSPTSTEEGTSESATPESGPGTST EPSEGSAPGSPAGSPTSTEEGTSTEPSE GSAPGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPA GSPTSTEEGTSESATPESGPGTSTEPSE GSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGTSE SATPESGPGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSE SATPESGPGSPAGSPTSTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGTST EPSEGSAPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSESATPESGPGSEPATS GSETPGTSESATPESGPGTSTEPSEGSA PGTSESATPESGPGSPAGSPTSTEEGSP	864	Residue totals: H: 2 E: 3 percent: H: 0.2 E: 0.4	99.77%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
	AGSPTSTEEGSPAGSPTSTEEGTSESAT PESGPGTSTEPSEGSAPGTSESATPESG PGSEPATSGSETPGTSESATPESGPGSE PATSGSETPGTSESATPESGPGTSTEPS EGSAPGSPAGSPTSTEEGTSESATPES GPGSEPATSGSETPGTSESATPESGPGS PAGSPTSTEEGSPAGSPTSTEEGTSTEP SEGSAPGTSESATPESGPGTSESATPES GPGTSESATPESGPGSEPATSGSETPGS EPATSGSETPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGSEPATSGSE TPGTSESATPESGPGTSTEPSEGSAP			
AF864	GSTSESPSGTAPGTSPSGESSTAPGSTS ESPSGTAPGSTSESPSGTAPGTSTPESG SASPGTSTPESGSASPGSTSESPSGTAP GSTSESPSGTAPGTSPSGESSTAPGSTS ESPSGTAPGTSPSGESSTAPGTSPSGES STAPGSTSSTAESPGPGTSPSGESSTAP GTSPSGESSTAPGSTSSTAESPGPGTST PESGSASPGTSTPESGSASPGSTSESPS GTAPGSTSESPSGTAPGTSTPESGSASP GSTSSTAESPGPGTSTPESGSASPGSTS ESPSGTAPGTSPSGESSTAPGSTSSTAE SPGPGTSPSGESSTAPGTSTPESGSASP GSTSSTAESPGPGSTSSTAESPGPGSTS STAESPGPGSTSSTAESPGPGTSPSGES STAPGSTSESPSGTAPGSTSESPSGTAP GTSTPESGPXXXGASASGAPSTXXXX SESPSGTAPGSTSESPSGTAPGSTSESP SGTAPGSTSESPSGTAPGSTSESPSGTA PGSTSESPSGTAPGTSTPESGSASPGTS PSGESSTAPGTSPSGESSTAPGSTSSTA ESPGPGTSPSGESSTAPGTSTPESGSAS PGSTSESPSGTAPGSTSESPSGTAPGTS PSGESSTAPGSTSESPSGTAPGTSTPES GSASPGTSTPESGSASPGSTSESPSGTA PGTSTPESGSASPGSTSSTAESPGPGST SESPSGTAPGSTSESPSGTAPGTSPSGE SSTAPGSTSSTAESPGPGTSPSGESSTA PGTSTPESGSASPGTSPSGESSTAPGTS PSGESSTAPGTSPSGESSTAPGSTSSTA ESPGPGSTSSTAESPGPGTSPSGESSTA PGSSPSASTGTGPGSSTPSGATGSPGSS TPSGATGSP	875	Residue totals: H: 2 E: 0 percent: H: 0.2 E: 0.0	95.20%
AG864	GASPGTSSTGSPGSSPSASTGTGPGSSP SASTGTGPGTPGSGTASSSPGSSTPSG ATGSPGSSPSASTGTGPGASPGTSSTG SPGTPGSGTASSSPGSSTPSGATGSPGT PGSGTASSSPGASPGTSSTGSPGASPG TSSTGSPGTPGSGTASSSPGSSTPSGAT GSPGASPGTSSTGSPGTPGSGTASSSP GSSTPSGATGSPGSSPSASTGTGPGSSP SASTGTGPGSSTPSGATGSPGSSTPSG ATGSPGASPGTSSTGSPGASPGTSSTG SPGASPGTSSTGSPGTPGSGTASSSPG ASPGTSSTGSPGASPGTSSTGSPGASP	864	Residue totals: H: 0 E: 0 percent: H: 0.0 E: 0.0	94.91%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
	GTSSTGSPGSSPSASTGTGPGTPGSGT ASSSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGSSTPSGATGSPGSS TPSGATGSPGASPGTSSTGSPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATG SPGSSTPSGATGSPGSSPSASTGTGPG ASPGTSSTGSPGASPGTSSTGSPGTPGS GTASSSPGASPGTSSTGSPGASPGTSST GSPGASPGTSSTGSPGASPGTSSTGSP GTPGSGTASSSPGSSTPSGATGSPGTP GSGTASSSPGSSTPSGATGSPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATG SPGSSPSASTGTGPGSSPSASTGTGPG ASPGTSSTGSPGTPGSGTASSSPGSSTP SGATGSPGSSPSASTGTGPGSSPSAST GTGPGASPGTSSTGSPGASPGTSSTGS PGSSTPSGATGSPGSSPSASTGTGPGA SPGTSSTGSPGSSPSASTGTGPGTPGSG TASSSPGSSTPSGATGSPGSSTPSGATG SPGASPGTSSTGSP			
AM875	GTSTEPSEGSAPGSEPATSGSETPGSPA GSPTSTEEGSTSSTAESPGPGTSTPESG SASPGSTSESPSGTAPGSTSESPSGTAP GTSTPESGSASPGTSTPESGSASPGSEP ATSGSETPGTSESATPESGPGSPAGSPT STEEGTSTEPSEGSAPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGTSESATPESGPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGTSE SATPESGPGTSTEPSEGSAPGSEPATSG SETPGSPAGSPTSTEEGSSTPSGATGSP GTPGSGTASSSPGSSTPSGATGSPGTS TEPSEGSAPGTSTEPSEGSAPGSEPATS GSETPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGASASGAPSTGGTS ESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGSTSSTAESPGPGSTSESPSGTA PGTSPSGESSTAPGTPGSGTASSSPGSS TPSGATGSPGSSPSASTGTGPGSEPAT SGSETPGTSESATPESGPGSEPATSGSE TPGSTSSTAESPGPGSTSSTAESPGPGT SPSGESSTAPGSEPATSGSETPGSEPAT SGSETPGTSTEPSEGSAPGSTSSTAESP GPGTSTPESGSASPGSTSESPSGTAPGT STEPSEGSAPGTSTEPSEGSAPGTSTEP SEGSAPGSSTPSGATGSPGSSPSASTGT GPGASPGTSSTGSPGSEPATSGSETPG TSESATPESGPGSPAGSPTSTEEGSSTP SGATGSPGSSPSASTGTGPGASPGTSS TGSPGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAP	875	Residue totals: H: 7 E: 3 percent: H: 0.8 E: 0.3	98.63%
AM1318	GTSTEPSEGSAPGSEPATSGSETPGSPA GSPTSTEEGSTSSTAESPGPGTSTPESG SASPGSTSESPSGTAPGSTSESPSGTAP GTSTPESGSASPGTSTPESGSASPGSEP	1318	Residue totals: H: 7 E: 0 percent: H: 0.7 E:	99.17%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
	ATSGSETPGTSESATPESGPGSPAGSPT STEEGTSTEPSEGSAPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGTSTEPSE GSAPGTSESATPESGPGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGTSE SATPESGPGTSTEPSEGSAPGSEPATSG SETPGSPAGSPTSTEEGSSTPSGATGSP GTPGSGTASSSPGSSTPSGATGSPGTS TEPSEGSAPGTSTEPSEGSAPGSEPATS GSETPGSPAGSPTSTEEGSPAGSPTSTE EGTSTEPSEGSAPGPEPTGPAPSGGSEP ATSGSETPGTSESATPESGPGSPAGSPT STEEGTSESATPESGPGSPAGSPTSTEE GSPAGSPTSTEEGTSESATPESGPGSPA GSPTSTEEGSPAGSPTSTEEGSTSSTAE SPGPGSTSESPSGTAPGTSPSGESSTAP GSTSESPSGTAPGSTSESPSGTAPGTSP SGESSTAPGTSTEPSEGSAPGTSESATP ESGPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSESATPESGPGTST EPSEGSAPGTSESATPESGPGTSTEPSE GSAPGTSPSGESSTAPGTSPSGESSTAP GTSPSGESSTAPGTSTEPSEGSAPGSPA GSPTSTEEGTSTEPSEGSAPGSSPSAST GTGPGSSTPSGATGSPGSSTPSGATGS PGSSTPSGATGSPGSSTPSGATGSPGA SPGTSSTGSPGASASGAPSTGGTSPSG ESSTAPGSTSSTAESPGPGTSPSGESST APGTSESATPESGPGTSTEPSEGSAPG TSTEPSEGSAPGSSPSASTGTGPGSSTP SGATGSPGASPGTSSTGSPGTSTPESG SASPGTSPSGESSTAPGTSPSGESSTAP GTSESATPESGPGSEPATSGSETPGTST EPSEGSAPGSTSESPSGTAPGSTSESPS GTAPGTSTPESGSASPGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGSPA GSPTSTEEGTSESATPESGPGSEPATSG SETPGSSTPSGATGSPGASPGTSSTGSP GSSTPSGATGSPGSTSESPSGTAPGTSP SGESSTAPGSTSSTAESPGPGSSTPSGA TGSPGASPGTSSTGSPGTPGSGTASSSP GSPAGSPTSTEEGSPAGSPTSTEEGTST EPSEGSAP		0.0	
AM923	MAEPAGSPTSTEEGASPGTSSTGSPGS STPSGATGSPGSSTPSGATGSPGTSTEP SEGSAPGSEPATSGSETPGSPAGSPTST EEGSTSSTAESPGPGTSTPESGSASPGS TSESPSGTAPGSTSESPSGTAPGTSTPE SGSASPGTSTPESGSASPGSEPATSGSE TPGTSESATPESGPGSPAGSPTSTEEGT STEPSEGSAPGTSESATPESGPGTSTEP SEGSAPGTSTEPSEGSAPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGT SESATPESGPGTSESATPESGPGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPES	924	Residue totals: H: 4 E: 3 percent: H: 0.4 E: 0.3	98.70%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
	GPGTSTEPSEGSAPGSEPATSGSETPGS PAGSPTSTEEGSSTPSGATGSPGTPGS GTASSSPGSSTPSGATGSPGTSTEPSEG SAPGTSTEPSEGSAPGSEPATSGSETPG SPAGSPTSTEEGSPAGSPTSTEEGTSTE PSEGSAPGASASGAPSTGGTSESATPE SGPGSPAGSPTSTEEGSPAGSPTSTEEG STSSTAESPGPGSTSESPSGTAPGTSPS GESSTAPGTPGSGTASSSPGSSTPSGA TGSPGSSPSASTGTGPGSEPATSGSETP GTSESATPESGPGSEPATSGSETPGSTS STAESPGPGSTSSTAESPGPGTSPSGES STAPGSEPATSGSETPGSEPATSGSETP GTSTEPSEGSAPGSTSSTAESPGPGTST PESGSASPGSTSESPSGTAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAP GSSTPSGATGSPGSSPSASTGTGPGAS PGTSSTGSPGSEPATSGSETPGTSESAT PESGPGSPAGSPTSTEEGSSTPSGATGS PGSSPSASTGTGPGASPGTSSTGSPGTS ESATPESGPGTSTEPSEGSAPGTSTEPS EGSAP			
AE912	MAEPAGSPTSTEEGTPGSGTASSSPGS STPSGATGSPGASPGTSSTGSPGSPAG SPTSTEEGTSESATPESGPGTSTEPSEG SAPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPG TSTEPSEGSAPGSPAGSPTSTEEGTSTE PSEGSAPGTSTEPSEGSAPGTSESATPE SGPGTSTEPSEGSAPGTSESATPESGPG SEPATSGSETPGTSTEPSEGSAPGTSTE PSEGSAPGTSESATPESGPGTSESATPE SGPGSPAGSPTSTEEGTSESATPESGPG SEPATSGSETPGTSESATPESGPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEG SAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGSPAGSPTSTEEGTSTE PSEGSAPGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGSEPATSGSETPG TSESATPESGPGTSTEPSEGSAPGTSES ATPESGPGSPAGSPTSTEEGSPAGSPTS TEEGSPAGSPTSTEEGTSESATPESGPG TSTEPSEGSAPGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPG SPAGSPTSTEEGTSESATPESGPGSEPA TSGSETPGTSESATPESGPGSPAGSPTS TEEGSPAGSPTSTEEGTSTEPSEGSAPG TSESATPESGPGTSESATPESGPGTSES ATPESGPGSEPATSGSETPGSEPATSGS ETPGSPAGSPTSTEEGTSTEPSEGSAPG TSTEPSEGSAPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAP	913	Residue totals: H: 8 E: 3 percent: H: 0.9 E: 0.3	99.45%

SEQ NAME	Sequence	No. Residues	Chou-Fasman Calculation	GOR Calculation
BC 864	GTSTEPSEPGSAGTSTEPSEPGSAGSEP ATSGTEPSGSGASEPTSTEPGSEPATS GTEPSGSEPATSGTEPSGSEPATSGTEP SGSGASEPTSTEPGTSTEPSEPGSAGSE PATSGTEPSGTSTEPSEPGSAGSEPATS GTEPSGSEPATSGTEPSGTSTEPSEPGS AGTSTEPSEPGSAGSEPATSGTEPSGS EPATSGTEPSGTSEPSTSEPGAGSGAS EPTSTEPGTSEPSTSEPGAGSEPATSGT EPSGSEPATSGTEPSGTSTEPSEPGSAG TSTEPSEPGSAGSGASEPTSTEPGSEPA TSGTEPSGSEPATSGTEPSGSEPATSGT EPSGSEPATSGTEPSGTSTEPSEPGSAG SEPATSGTEPSGSGASEPTSTEPGTSTE PSEPGSAGSEPATSGTEPSGSGASEPTS TEPGTSTEPSEPGSAGSGASEPTSTEPG SEPATSGTEPSGSGASEPTSTEPGSEPA TSGTEPSGSGASEPTSTEPGTSTEPSEP GSAGSEPATSGTEPSGSGASEPTSTEP GTSTEPSEPGSAGSEPATSGTEPSGTST EPSEPGSAGSEPATSGTEPSGTSTEPSE PGSAGTSTEPSEPGSAGTSTEPSEPGSA GTSTEPSEPGSAGTSTEPSEPGSAGTST EPSEPGSAGTSEPSTSEPGAGSGASEPT STEPGTSTEPSEPGSAGTSTEPSEPGSA GTSTEPSEPGSAGSEPATSGTEPSGSG ASEPTSTEPGSEPATSGTEPSGSEPATS GTEPSGSEPATSGTEPSGSEPATSGTEP SGTSEPSTSEPGAGSEPATSGTEPSGSG ASEPTSTEPGTSTEPSEPGSAGSEPATS GTEPSGSGASEPTSTEPGTSTEPSEPGS A		Residue totals: H: 0 E: 0 percent: H: 0 E: 0	99.77%

* H: alpha-helix E: beta-sheet

[00670] Example 60: Analysis of polypeptide sequences for repetitiveness

[00671] Polypeptide amino acid sequences can be assessed for repetitiveness by quantifying the number of times a shorter subsequence appears within the overall polypeptide. For example, a polypeptide of 200 amino acid residues has 192 overlapping 9-amino acid subsequences (or 9-mer "frames"), but the number of unique 9-mer subsequences will depend on the amount of repetitiveness within the sequence. In the present analysis, different sequences were assessed for repetitiveness by summing the occurrence of all unique 3-mer subsequences for each 3-amino acid frame across the first 200 amino acids of the polymer portion divided by the absolute number of unique 3-mer subsequences within the 200 amino acid sequence. The resulting subsequence score is a reflection of the degree of repetitiveness within the polypeptide.

[00672] The results, shown in Table 46, indicate that the unstructured polypeptides consisting of 2 or 3 amino acid types have high subsequence scores, while those of consisting of 12 amino acids motifs of the six amino acids G, S, T, E, P, and A with a low degree of internal

repetitiveness, have subsequence scores of less than 10, and in some cases, less than 5. For example, the L288 sequence has two amino acid types and has short, highly repetitive sequences, resulting in a subsequence score of 50.0. The polypeptide J288 has three amino acid types but also has short, repetitive sequences, resulting in a subsequence score of 33.3. Y576 also has three amino acid types, but is not made of internal repeats, reflected in the subsequence score of 15.7 over the first 200 amino acids. W576 consists of four types of amino acids, but has a higher degree of internal repetitiveness, e.g., "GGSG", resulting in a subsequence score of 23.4. The AD576 consists of four types of 12 amino acid motifs, each consisting of four types of amino acids. Because of the low degree of internal repetitiveness of the individual motifs, the overall subsequence score over the first 200 amino acids is 13.6. In contrast, XTEN's consisting of four motifs contains six types of amino acids, each with a low degree of internal repetitiveness have lower subsequence scores; i.e., AE864 (6.1), AF864 (7.5), and AM875 (4.5).

[00673] Conclusions: The results indicate that the combination of 12 amino acid subsequence motifs, each consisting of four to six amino acid types that are essentially non-repetitive, into a longer XTEN polypeptide results in an overall sequence that is non-repetitive. This is despite the fact that each subsequence motif may be used multiple times across the sequence. In contrast, polymers created from smaller numbers of amino acid types resulted in higher subsequence scores, although the actual sequence can be tailored to reduce the degree of repetitiveness to result in lower subsequence scores.

Table 46: Subsequence score calculations of polypeptide sequences

Seq Name	Amino Acid Sequence	Score
J288	GSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGS GGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGG EGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGG GSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGS GGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGS EGGSGGEGGSGGEGGSGGEGGSGGEGGSGGEGGSGGG	33.3
K288	GEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGE GGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGE GGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEG EGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGG EGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGE GEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEGGEGEGGGEG	46.9
L288	SSESSESSSSESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSSESSESSSSE SSSESSESSSSESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSSESSESSSS ESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSSESSESSS SESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSSESSESS SSESSSESSESSSSESSSESSESSSSESSSESSESSSSESSSESSESSSSES	50.0
Y288	GEGSGEGSEGEGSEGSGEGEGSEGSGEGEGGSEGSEGEGGSEGSEGEGGSEG SEGEGSGEGSEGEGGSEGSEGEGSGEGSEGEGSEGGSEGEGGSEGSEGEGSG EGSEGEGGEGGSEGEGSEGSGEGEGSGEGSEGEGSEGSGEGEGSGEGSEGEG SEGSGEGEGSEGSGEGEGGSEGSEGEGSEGSGEGEGGEGSGEGEGSGEGSEG EGGGEGSEGEGSGEGGEGEGSEGGSEGEGGSEGGEGEGSEGSGEGEGSEGG SEGEGSEGGSEGEGSEGSGEGEGSEGSGE	26.8
Q576	GGKPGEGGKPEGGGGKPGGKPEGEGEGKPGGKPEGGGKPGGGEGGKPEGG	18.5

Seq Name	Amino Acid Sequence	Score
	KPEGEGKPGGGEGKPGGKPEGGGGKPEGEGKPGGGGGKPGGKPEGEGKPG GGEGGKPEGKPGEGGEGKPGGKPEGGGEGKPGGGKPGEGGKPGEGKPGGG EGGKPEGGKPEGEGKPGGGEGKPGGKPGEGGKPEGGGEGKPGGKPGEGGE GKPGGGKPEGEGKPGGGKPGGGEGGKPEGEGKPGGKPEGGGEGKPGGKPE GGGKPEGGGEGKPGGGKPGEGGKPGEGEGKPGGKPEGEGKPGGEGGGKPE GKPGGGEGGKPEGGKPGEGGKPEGGKPGEGGEGKPGGGKPGEGGKPEGGG KPEGEGKPGGGGKPGEGGKPEGGKPEGGGEGKPGGGKPEGEGKPGGGEGK PGGKPEGGGGKPGEGGKPEGGKPGGEGGGKPEGEGKPGGKPGEGGGGKPG GKPEGEGKPGEGGEGKPGGKPEGGGEGKPGGKPEGGGEGKPGGGKPGEGG KPEGGGKPGEGGKPGEGGKPEGEGKPGGGEGKPGGKPGEGGKPEGGGEGK PGGKPGGEGGGKPEGGKPGEGGKPEG	
U576	GEGKPGGKPGSGGGKPGEGGKPGSGEGKPGGKPGSGGSGKPGGKPGEGGK PEGGSGGKPGGGGKPGGKPGGEGSGKPGGKPEGGGKPEGGSGGKPGGKPE GGSGGKPGGKPGSGEGGKPGGGKPGGEGKPGSGKPGGEGSGKPGGKPEGG SGGKPGGKPEGGSGGKPGGSGKPGGKPGEGGKPEGGSGGKPGGSGKPGGK PEGGGSGKPGGKPGEGGKPGSGEGGKPGGGKPGGEGKPGSGKPGGEGSGK PGGKPGSGGEGKPGGKPEGGSGGKPGGGKPGGEGKPGSGGKPGEGGKPGS GGGKPGGKPGGEGEGKPGGKPGEGGKPGGEGSGKPGGGGKPGGKPGGEG GKPEGSGKPGGGSGKPGGKPEGGGGKPEGSGKPGGGGKPEGSGKPGGGKP EGGSGGKPGGSGKPGGKPGEGGGKPEGSGKPGGGSGKPGGKPEGGGKPEG GSGGKPGGKPEGGSGGKPGGKPGGEGSGKPGGKPGSGEGGKPGGKPGEGS GGKPGGKPEGGSGGKPGGSGKPGGKPEGGGSGKPGGKPGEGGKPGGEGSG KPGGSGKPG	
W576	GGSGKPGKPGGSGSGKPGSGKPGGGSGKPGSGKPGGGSGKPGSGKPGGGSG KPGSGKPGGGGKPGSGSGKPGGGKPGGSGGKPGGGSGKPGKPGSGGSGKP GSGKPGGGSGGKPGKPGSGGSGGKPGKPGSGGGSGKPGKPGSGGSGGKPG KPGSGGSGGKPGKPGSGGSGKPGSGKPGGGSGKPGSGKPGSGGSGKPGKPG SGGSGKPGSGKPGSGSGKPGSGKPGGGSGKPGSGKPGSGGSGKPGKPGSGG GKPGSGSGKPGGGKPGSGSGKPGGGKPGGSGGKPGGSGGKPGKPGSGGGS GKPGKPGSGGGSGKPGKPGGSGSGKPGSGKPGGGSGKPGSGKPGSGGSGKP GKPGSGGSGGKPGKPGSGGGKPGSGSGKPGGGKPGSGSGKPGGGKPGSGSG KPGGGKPGSGSGKPGGSGKPGSGKPGGGSGGKPGKPGSGGSGKPGSGKPGS GGSGKPGKPGGSGSGKPGSGKPGGGSGKPGSGKPGGGSGKPGSGKPGGGSG KPGSGKPGGGGKPGSGSGKPGGSGGKPGKPGSGGSGGKPGKPGSGGSGKPG SGKPGGGSGGKPGKPGSGG	23.4
Y576	GEGSGEGSEGEGSEGSGEGEGSEGSGEGEGGSEGSEGEGSEGSGEGEGGEGS GEGEGSGEGSEGEGGGEGSEGEGSGEGGEGEGSEGGSEGEGGSEGGEGEGS EGSGEGEGSEGGSEGEGSEGGSEGEGSEGSGEGEGSEGSGEGEGSEGSGEGE GSEGSGEGEGSEGGSEGEGGSEGSEGEGSGEGSEGEGGSEGSEGEGGGEGSE GEGSGEGSEGEGGSEGSEGEGGSEGSEGEGGEGSGEGEGSEGSGEGEGSGEG SEGEGSEGSGEGEGSEGSGEGEGGSEGSEGEGSGEGSEGEGSEGSGEGEGSE GSGEGEGGSEGSEGEGGSEGSEGEGGSEGSEGEGGEGSGEGEGSEGSGEGEG SGEGSEGEGSEGSGEGEGSEGSGEGEGGSEGSEGEGSEGSGEGEGGEGSGEG EGSGEGSEGEGGGEGSEGEGSEGSGEGEGSEGSGEGEGSEGGSEGEGGSEGS EGEGSEGGSEGEGSEGGSEGEGSEGSGEGEGSEGSGEGEGSGEGSEGEGGSE GGEGEGSEGGSEGEGSEGGSEGEGGEGSGEGEGGGEGSEGEGSEGSGEGEG SGEGSE	15.7
AD576	GSSESGSSEGGPGSGGEPSESGSSGSSESGSSEGGPGSSESGSSEGGPGSSESG SSEGGPGSSESGSSEGGPGSSESGSSEGGPGESPGGSSGSESGSEGSSGPGESS GSSESGSSEGGPGSSESGSSEGGPGSSESGSSEGGPGSGGEPSESGSSGESPGG SSGSESGESPGGSSGSESGSGGEPSESGSSGSSESGSSEGGPGSGGEPSESGSS GSGGEPSESGSSGSEGSSGPGESSGESPGGSSGSESGSGGEPSESGSSGSGGEP SESGSSGSGGEPSESGSSGSSESGSSEGGPGESPGGSSGSESGESPGGSSGSES GESPGGSSGSESGESPGGSSGSESGESPGGSSGSESGSSESGSSEGGPGSGGEP SESGSSGSEGSSGPGESSGSSESGSSEGGPGSGGEPSESGSSGSSESGSSEGGP GSGGEPSESGSSGESPGGSSGSESGESPGGSSGSESGSSESGSSEGGPGSGGEP SESGSSGSSESGSSEGGPGSGGEPSESGSSGSGGEPSESGSSGESPGGSSGSES	13.6

Seq Name	Amino Acid Sequence	Score
	GSEGSSGPGESSGSSESGSSEGGPGSEGSSGPGESS	
AE576	AGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEP SEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPG SPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPT STEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPES GPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESAT PESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGT STEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAP	6.1
AF540	GSTSSTAESPGPGSTSSTAESPGPGSTSESPSGTAPGSTSSTAESPGPGSTSSTA ESPGPGTSTPESGSASPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGS TSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESS TAPGSTSESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTS ESPSGTAPGTSTPESGSASPGSTSSTAESPGPGSTSSTAESPGPGTSTPESGSAS PGTSTPESGSASPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGSTSES PSGTAPGSTSESPSGTAPGSTSESPSGTAPGSTSSTAESPGPGTSTPESGSASPG TSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPS GTAPGSTSESPSGTAPGTSTPESGSASPGTSPSGESSTAPGSTSSTAESPGPGTS PSGESSTAPGSTSSTAESPGPGTSTPESGSASPGSTSESPSGTAP	8.8
AF504	GASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPS GATGSPGSNPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSP GTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPS GATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSNPSASTGTGP GSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGASPGT SSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSP GASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGASPGT SSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSP GTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSP	7.0
AE864	GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPS EGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGS PAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTS TEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSE SATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESG PGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESA TPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPG TSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTST EEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSES ATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSP TSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGS EPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAP	6.1
AF864	GSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPES GSASPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGS TSESPSGTAPGTSPSGESSTAPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESS TAPGTSPSGESSTAPGSTSSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTS ESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSSTAESPGPGTSTPESGSAS PGSTSESPSGTAPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSTPE SGSASPGSTSSTAESPGPGSTSSTAESPGPGSTSSTAESPGPGTSSTAESPGPG TSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGPXXXGASASGA PSTXXXXSESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGST SESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSPSGESSTAPGTSPSGESST	7.5

Seq Name	Amino Acid Sequence	Score
	APGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSASPGSTSESPSGTAPGSTSE SPSGTAPGTSPSGESSTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASP GSTSESPSGTAPGTSTPESGSASPGSTSSTAESPGPGSTSESPSGTAPGSTSESP SGTAPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSASPGT SPSGESSTAPGTSPSGESSTAPGTSPSGESSTAPGSTSSTAESPGPGSTSSTAES PGPGTSPSGESSTAPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSP	
AG868	GGSPGASPGTSSTGSPGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGS STPSGATGSPGSNPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGA TGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGS STPSGATGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSNPSAST GTGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGA SPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSST GSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGSPGAS PGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSST GSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSP SASTGTGPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTG SPGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTP SGATGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGS PGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGS GTASSSPGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGS PGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSPGSSPSA STGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSP	7.5
AM875	GTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPES GSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGS EPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTST EPSEGSAPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTEPSEGSAPGTSTEPSEGSAP GSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGASASG APSTGGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSTSSTAESPGPGS TSESPSGTAPGTSPSGESSTAPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTG TGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGSTSSTAESPGPGSTS STAESPGPGTSPSGESSTAPGSEPATSGSETPGSEPATSGSETPGTSTEPSEGSA PGSTSSTAESPGPGTSTPESGSASPGSTSESPSGTAPGTSTEPSEGSAPGTSTEP SEGSAPGTSTEPSEGSAPGSSTPSGATGSPGSSPSASTGTGPGASPGTSSTGSP GSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSSTPSGATGSPGSSPSAS TGTGPGASPGTSSTGSPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAP	4.5
AM1318	GTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSTSSTAESPGPGTSTPES GSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGTSTPESGSASPGS EPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPE SGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTST EPSEGSAPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGTSTEPSEGSAPGSEPATSGSETPGSPAGSPTSTEEGSSTPS GATGSPGTPGSGTASSSPGSSTPSGATGSPGTSTEPSEGSAPGTSTEPSEGSAP GSEPATSGSETPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGPEPTGP APSGGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGSPAGSPTSTEEGSPAGSPTST EEGSTSSTAESPGPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSE SPSGTAPGTSPSGESSTAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSESATPESGPGTSTEPSEGSAPGTSESAT PESGPGTSTEPSEGSAPGTSPSGESSTAPGTSPSGESSTAPGTSPSGESSTAPGT STEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGSSPSASTGTGPGSSTPSGAT GSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGSPGAS ASGAPSTGGTSPSGESSTAPGSTSSTAESPGPGTSPSGESSTAPGTSESATPESG PGTSTEPSEGSAPGTSTEPSEGSAPGSSPSASTGTGPGSSTPSGATGSPGASPG TSSTGSPGTSTPESGSASPGTSPSGESSTAPGTSPSGESSTAPGTSESATPESGP	4.5

Seq Name	Amino Acid Sequence	Score
	GSEPATSGSETPGTSTEPSEGSAPGSTSESPSGTAPGSTSESPSGTAPGTSTPES GSASPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGT SESATPESGPGSEPATSGSETPGSSTPSGATGSPGASPGTSSTGSPGSSTPSGAT GSPGSTSESPSGTAPGTSPSGESSTAPGSTSSTAESPGPGSSTPSGATGSPGASP GTSSTGSPGTPGSGTASSSPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSA P	

[00674] Example 61: Calculation of TEPITOPE scores

[00675] TEPITOPE scores of 9mer peptide sequence can be calculated by adding pocket potentials as described by Sturniolo [Sturniolo, T., et al. (1999) Nat Biotechnol, 17: 555]. In the present Example, separate Tepitope scores were calculated for individual HLA alleles. Table 47 shows as an example the pocket potentials for HLA*0101B, which occurs in high frequency in the Caucasian population. To calculate the TEPITOPE score of a peptide with sequence P1-P2-P3-P4-P5-P6-P7-P8-P9, the corresponding individual pocket potentials in Table 47 were added. The HLA*0101B score of a 9mer peptide with the sequence FDKLPRTSG is the sum of 0, -1.3, 0, 0.9, 0, -1.8, 0.09, 0, 0.

[00676] To evaluate the TEPITOPE scores for long peptides one can repeat the process for all 9mer subsequences of the sequences. This process can be repeated for the proteins encoded by other HLA alleles. Tables 48-51 give pocket potentials for the protein products of HLA alleles that occur with high frequency in the Caucasian population.

[00677] TEPITOPE scores calculated by this method range from approximately -10 to +10. However, 9mer peptides that lack a hydrophobic amino acid (FKLMVWY) in P1 position have calculated TEPITOPE scores in the range of -1009 to -989. This value is biologically meaningless and reflects the fact that a hydrophobic amino acid serves as an anchor residue for HLA binding and peptides lacking a hydrophobic residue in P1 are considered non binders to HLA. Because most XTEN sequences lack hydrophobic residues, all combinations of 9mer subsequences will have TEPITOPEs in the range in the range of -1009 to -989. This method confirms that XTEN polypeptides may have few or no predicted T-cell epitopes.

Table 47: Pocket potential for HLA*0101B allele.

Amino Acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
A	-999	0	0	0	-	0	0	-	0
C	-999	0	0	0	-	0	0	-	0
D	-999	-1.3	-1.3	-2.4	-	-2.7	-2	-	-1.9
E	-999	0.1	-1.2	-0.4	-	-2.4	-0.6	-	-1.9
F	0	0.8	0.8	0.08	-	-2.1	0.3	-	-0.4
G	-999	0.5	0.2	-0.7	-	-0.3	-1.1	-	-0.8
H	-999	0.8	0.2	-0.7	-	-2.2	0.1	-	-1.1
I	-1	1.1	1.5	0.5	-	-1.9	0.6	-	0.7

Amino Acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
K	-999	1.1	0	-2.1	-	-2	-0.2	-	-1.7
L	-1	1	1	0.9	-	-2	0.3	-	0.5
M	-1	1.1	1.4	0.8	-	-1.8	0.09	-	0.08
N	-999	0.8	0.5	0.04	-	-1.1	0.1	-	-1.2
P	-999	-0.5	0.3	-1.9	-	-0.2	0.07	-	-1.1
Q	-999	1.2	0	0.1	-	-1.8	0.2	-	-1.6
R	-999	2.2	0.7	-2.1	-	-1.8	0.09	-	-1
S	-999	-0.3	0.2	-0.7	-	-0.6	-0.2	-	-0.3
T	-999	0	0	-1	-	-1.2	0.09	-	-0.2
V	-1	2.1	0.5	-0.1	-	-1.1	0.7	-	0.3
W	0	-0.1	0	-1.8	-	-2.4	-0.1	-	-1.4
Y	0	0.9	0.8	-1.1	-	-2	0.5	-	-0.9

Table 48: Pocket potential for HLA*0301B allele.

Amino acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
A	-999	0	0	0	-	0	0	-	0
C	-999	0	0	0	-	0	0	-	0
D	-999	-1.3	-1.3	2.3	-	-2.4	-0.6	-	-0.6
E	-999	0.1	-1.2	-1	-	-1.4	-0.2	-	-0.3
F	-1	0.8	0.8	-1	-	-1.4	0.5	-	0.9
G	-999	0.5	0.2	0.5	-	-0.7	0.1	-	0.4
H	-999	0.8	0.2	0	-	-0.1	-0.8	-	-0.5
I	0	1.1	1.5	0.5	-	0.7	0.4	-	0.6
K	-999	1.1	0	-1	-	1.3	-0.9	-	-0.2
L	0	1	1	0	-	0.2	0.2	-	-0
M	0	1.1	1.4	0	-	-0.9	1.1	-	1.1
N	-999	0.8	0.5	0.2	-	-0.6	-0.1	-	-0.6
P	-999	-0.5	0.3	-1	-	0.5	0.7	-	-0.3
Q	-999	1.2	0	0	-	-0.3	-0.1	-	-0.2
R	-999	2.2	0.7	-1	-	1	-0.9	-	0.5
S	-999	-0.3	0.2	0.7	-	-0.1	0.07	-	1.1
T	-999	0	0	-1	-	0.8	-0.1	-	-0.5
V	0	2.1	0.5	0	-	1.2	0.2	-	0.3
W	-1	-0.1	0	-1	-	-1.4	-0.6	-	-1
Y	-1	0.9	0.8	-1	-	-1.4	-0.1	-	0.3

Table 49: Pocket potential for HLA*0401B allele.

Amino acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
A	-999	0	0	0	-	0	0	-	0
C	-999	0	0	0	-	0	0	-	0
D	-999	-1.3	-1.3	1.4	-	-1.1	-0.3	-	-1.7

Amino acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
E	-999	0.1	-1.2	1.5	-	-2.4	0.2	-	-1.7
F	0	0.8	0.8	-0.9	-	-1.1	-1	-	-1
G	-999	0.5	0.2	-1.6	-	-1.5	-1.3	-	-1
H	-999	0.8	0.2	1.1	-	-1.4	0	-	0.08
I	-1	1.1	1.5	0.8	-	-0.1	0.08	-	-0.3
K	-999	1.1	0	-1.7	-	-2.4	-0.3	-	-0.3
L	-1	1	1	0.8	-	-1.1	0.7	-	-1
M	-1	1.1	1.4	0.9	-	-1.1	0.8	-	-0.4
N	-999	0.8	0.5	0.9	-	1.3	0.6	-	-1.4
P	-999	-0.5	0.3	-1.6	-	0	-0.7	-	-1.3
Q	-999	1.2	0	0.8	-	-1.5	0	-	0.5
R	-999	2.2	0.7	-1.9	-	-2.4	-1.2	-	-1
S	-999	-0.3	0.2	0.8	-	1	-0.2	-	0.7
T	-999	0	0	0.7	-	1.9	-0.1	-	-1.2
V	-1	2.1	0.5	-0.9	-	0.9	0.08	-	-0.7
W	0	-0.1	0	-1.2	-	-1	-1.4	-	-1
Y	0	0.9	0.8	-1.6	-	-1.5	-1.2	-	-1

Table 50: Pocket potential for HLA*0701B allele.

Amino acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
A	-999	0	0	0	-	0	0	-	0
C	-999	0	0	0	-	0	0	-	0
D	-999	-1.3	-1.3	-1.6	-	-2.5	-1.3	-	-1.2
E	-999	0.1	-1.2	-1.4	-	-2.5	0.9	-	-0.3
F	0	0.8	0.8	0.2	-	-0.8	2.1	-	2.1
G	-999	0.5	0.2	-1.1	-	-0.6	0	-	-0.6
H	-999	0.8	0.2	0.1	-	-0.8	0.9	-	-0.2
I	-1	1.1	1.5	1.1	-	-0.5	2.4	-	3.4
K	-999	1.1	0	-1.3	-	-1.1	0.5	-	-1.1
L	-1	1	1	-0.8	-	-0.9	2.2	-	3.4
M	-1	1.1	1.4	-0.4	-	-0.8	1.8	-	2
N	-999	0.8	0.5	-1.1	-	-0.6	1.4	-	-0.5
P	-999	-0.5	0.3	-1.2	-	-0.5	-0.2	-	-0.6
Q	-999	1.2	0	-1.5	-	-1.1	1.1	-	-0.9
R	-999	2.2	0.7	-1.1	-	-1.1	0.7	-	-0.8
S	-999	-0.3	0.2	1.5	-	0.6	0.4	-	-0.3
T	-999	0	0	1.4	-	-0.1	0.9	-	0.4
V	-1	2.1	0.5	0.9	-	0.1	1.6	-	2
W	0	-0.1	0	-1.1	-	-0.9	1.4	-	0.8
Y	0	0.9	0.8	-0.9	-	-1	1.7	-	1.1

Table 51: Pocket potential for HLA*1501B allele.

Amino acid	P1	P2	P3	P4	P5	P6	P7	P8	P9
A	-999	0	0	0	-	0	0	-	0
C	-999	0	0	0	-	0	0	-	0
D	-999	-1.3	-1.3	-0.4	-	-0.4	-0.7	-	-1.9
E	-999	0.1	-1.2	-0.6	-	-1	-0.7	-	-1.9
F	-1	0.8	0.8	2.4	-	-0.3	1.4	-	-0.4
G	-999	0.5	0.2	0	-	0.5	0	-	-0.8
H	-999	0.8	0.2	1.1	-	-0.5	0.6	-	-1.1
I	0	1.1	1.5	0.6	-	0.05	1.5	-	0.7
K	-999	1.1	0	-0.7	-	-0.3	-0.3	-	-1.7
L	0	1	1	0.5	-	0.2	1.9	-	0.5
M	0	1.1	1.4	1	-	0.1	1.7	-	0.08
N	-999	0.8	0.5	-0.2	-	0.7	0.7	-	-1.2
P	-999	-0.5	0.3	-0.3	-	-0.2	0.3	-	-1.1
Q	-999	1.2	0	-0.8	-	-0.8	-0.3	-	-1.6
R	-999	2.2	0.7	0.2	-	1	-0.5	-	-1
S	-999	-0.3	0.2	-0.3	-	0.6	0.3	-	-0.3
T	-999	0	0	-0.3	-	-0	0.2	-	-0.2
V	0	2.1	0.5	0.2	-	-0.3	0.3	-	0.3
W	-1	-0.1	0	0.4	-	-0.4	0.6	-	-1.4
Y	-1	0.9	0.8	2.5	-	0.4	0.7	-	-0.9

[00678] Example 62: GPCR Ca2+ mobilization activity assay

[00679] Recombinant GLP2-2G-XTEN was prepared as described in Alters, S. et al. (2012) GLP2-2G-XTEN: a pharmaceutical protein with improved serum half-life and efficacy in a rat Crohn's disease model. PLoS One; 7(11): e50630. The conjugate GLP2-2G-XTEN was prepared as described in Example 26 (FIG. 68) and purified by preparative RP-HPLC (FIG. 70). A GPCR Ca2+ flux mobilization activity assay was performed using an EMD Millipore ChemiSCREEN human recombinant GLP-2 glucagon family receptor calcium-optimized stable cell line, used according to manufacturer's instructions, with results presented in FIG. 110. Both the recombinant and conjugated GLP2-2G-XTEN were profiled as an eight-point, three-fold serial dilution dose response curve. Dose response curves were fitted using a 4PL-regression plot with respective Y-axis RFU, with data expressed as a percentage of absolute maximum RFU against concentration on the X-axis. Both recombinant GLP2-2G-XTEN and conjugate GLP2-2G-XTEN exhibited dose-dependent agonist activity with predicted EC50 potency values of 423 nM and 529 nM, respectively.

[00680] Example 63: In vitro plasma stability assay of conjugate GLP2-2G-XTEN

[00681] Equal concentrations of recombinant GLP2-2G-XTEN and conjugate GLP2-2G-XTEN were independently spiked into respective rat, cynomolgus monkey and human plasma. Samples

were incubated at 37°C for up to 10 days with an aliquot removed at appropriate time interval and stored at -80°C until analysis. The plasma stability of conjugated GLP2-2G-XTEN in the various species was compared to that of recombinant GLP2-2G-XTEN on an anti-XTEN/GLP2 ELISA performed in the respective plasma matrices. The anti-XTEN/GLP2 ELISA comprised of the anti-XTEN mouse antibody as a capture antibody and a biotinylated anti-human GLP2 antibody as a detection antibody. As shown in FIG. 111, the in vitro stability in human plasma of conjugate GLP2-2G-XTEN is comparable to that of recombinant GLP2-2G-XTEN having an calculated stability half-life of >240 h. Similar in vitro stability was also observed with the two GLP2-2G-XTEN proteins in rat and cynomolgus monkey plasma (data not shown).

[00682] Example 64: Pharmacokinetics of conjugate GLP2-2G-XTEN in rats

[00683] Female SD strain rats (200-220 g) were randomly assigned into groups of 3 animals each. Recombinant GLP-2G-XTEN and conjugate GLP2-2G-XTEN were administered by subcutaneous injection at 2 mg/kg into each animal. Blood samples (0.2 ml) were collected in pre-chilled heparinized microtainer tubes at pre-dose, 0.08, 4, 8, 24, 48, 72, 96, 120 and 168 hours after test compound administration. The blood was then processed to plasma and stored immediately at -80°C until analysis. Plasma samples were analyzed using an anti-XTEN/GLP2 ELISA that uses the mouse anti-XTEN antibody as a capture antibody and a biotinylated anti-human GLP2 antibody as a detection antibody. The ELISA was performed using relevant recombinant GLP2-2G-XTEN or conjugate GLP2-2G-XTEN as the respective ELISA calibration standards (FIG. 112). The calculated half-life of recombinant GLP2-2G-XTEN (36 (±7) h) and conjugate GLP2-2G-XTEN (37 (±7) h) was found to be similar.

[00684] Example 65: Trimeric XTEN conjugate linked via C-terminal Cysteines

[00685] A trimeric XTEN conjugate was prepared by the following procedure. An aliquot of the XTEN protein 1xAmino,1xThiol-XTEN432 (XTEN_AE432(Am1,C422)), with one internal cysteine residue, was prepared as a 587 μM (23.23 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. Tris-[2-maleimidoethyl]amine (TMEA, Thermo Scientific, cat. # 33043) was dissolved in anhydrous DMF to a final concentration 10 mM. TMEA was added to the protein solution to link to the thiol group of the XTEN (5x molar excess of protein over linker). The reaction mixture was incubated for 2 hrs at 25°C and the products of the reaction were analyzed by SEC-HPLC (Phenomenex BioSep-SEC-s4000 600 x 7.80mm, buffer: 50 mM Sodium Phosphate pH 6.5, 300mM NaCl, flow rate 0.5 ml/min, isocratic elution for 70 min). Linear XTEN_432, XTEN_864 and XTEN_1296 (having 432, 864, and 1296 amino acids, respectively) were analyzed under the same conditions to identify reaction products (FIG. 113). Peak 1 eluted at 28 min, the same time as XTEN_1296 and was identified as a trimer of XTEN_432. Peak 2 eluted at 30.5 min, the same time as XTEN_864 and was identified as a dimer of XTEN_432. Peak 3 eluted at 35 min, the same time as XTEN_432 and was identified as XTEN_432

precursor. The yields of trimeric XTEN conjugate and dimeric XTEN conjugate were 19% and 36%, respectively. Essentially identical retention times for the trimeric conjugate 3xXTEN_432 and the linear molecule XTEN_1296 suggest that the apparent molecular weight and hydrodynamic radius of an XTEN protein is not dependent on its geometric configuration.

[00686] Example 66: Trimeric XTEN conjugates linked via N-terminal α-amino groups

[00687] A trimeric XTEN conjugate was prepared by the following procedure.

[00688] 1. Synthesis of 1xDBCO-XTEN288

[00689] An aliquot of the protein 1xAmino-XTEN288 (XTEN_AE288(Am1)) was prepared as a 758 µM (20 mg/ml) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. 2 ml of protein was mixed with 0.1 ml 1M HEPES pH 8.0 and 0.152 ml of 50 mM DBCO-Sulfo-NHS (Click Chemistry Tools, cat. # A124) dissolved in anhydrous DMF to link the DBCO group to the N-terminal amino group of the XTEN. The reaction mixture was incubated for 2 hours at 25°C and analyzed by analytical RP-HPLC (FIG. 114A). The reaction mixture was diluted to 15 mL with 0.01% TFA and pH adjusted to ~3 using 10% TFA solution. The protein solution was divided into two equal parts and each fraction was loaded on a preparative C4 RP-HPLC column Vydac C4 250 x 10 mm (Grace Davison Discovery Sciences, cat. # 214TP510). The protein was eluted with a 180 ml linear 5-50% gradient of acetonitrile in 0.01% TFA at 2 ml/min flow rate. Fractions containing 1xDBCO-XTEN288 were adjusted to pH ~ 7 with 1 M HEPES pH 8 and were concentrated by vacuum evaporation.

[00690] 2. Synthesis of 3xAzide-PEG4-TAEA

[00691] Tris(2-aminoethyl)amine (TAEA, Sigma Aldrich, cat. # 225630) was diluted in anhydrous DMF to the final concentration 200 mM. Azido-PEG4-NHS ester (Click Chemistry Tools, cat. # AZ103) was dissolved in anhydrous DMF to the final concentration 1 M. Azido-PEG4-NHS was mixed in 5-fold molar excess with Tris(2-aminoethyl)amine and incubated at 25°C for 1 hour. 3xAzide-PEG4-TAEA was purified using C18 RP-HPLC using Phenomenex Jupiter C18 5u 300Å 150 x 4.60mm column, buffer A 0.1% TFA in water, buffer B 0.1% TFA in acetonitrile, flow rate 1ml/min, gradient 5 to 50%B in 45min. Chromatographic peaks were collected and analyzed by MALDI-TOF MS and ESI-MS to detect the product with MW of 966 Da. 3xAzide-PEG4-TAEA was identified as a peak with retention time 33 min (FIG. 114B). The fraction was neutralized using 1M HEPES pH 8.0 and concentrated by vacuum evaporation.

[00692] 3. Synthesis of the trimeric XTEN conjugate

[00693] 1xDBCO-XTEN288 was prepared as a 7.85 mg/ml (293 uM) solution in 20 mM HEPES, pH 7.0, 50 mM NaCl. 3xAzide-PEG4-TAEA was RP-HPLC purified and formulated in the same buffer. A concentration of the synthesized linker was not determined, and 1xDBCO-XTEN288 and 3xAzide-PEG4-TAEA were mixed empirically in various ratios and incubated at 25°C for 4 hours. Conjugation products were analyzed using SEC-HPLC (Phenomenex BioSep-

SEC-s4000 600 x 7.80mm, buffer: 50mM Sodium Phosphate pH 6.5, 300mM NaCl, flow rate 0.5 ml/min, isocratic elution for 70 min). Linear XTEN_288, XTEN_576 and XTEN_864 were analyzed under the same conditions to identify reaction products (FIG. 115). Peak 1 eluted at 30.5 min, the same time as XTEN_864 and was identified as a trimer of XTEN288. Peak 2 eluted at 34 min, the same time as XTEN_576 and was identified as a dimer of XTEN_288. Peak 3 eluted at 39 min, the same time as XTEN_288 and was identified as XTEN_288 precursor. Peak 4 corresponded to low molecular weight compounds and was not included into quantitation of XTEN species. The yield of the trimeric XTEN conjugate under the optimized protein/linker ratio was 57%. Essentially identical retention times for trimeric conjugate 3xXTEN_288 and linear molecule XTEN_864 confirms the earlier observation that the apparent molecular weight and hydrodynamic radius of an XTEN protein is not dependent on its geometric configuration.

[00694] Example 67: Selective cytotoxicity of 3xFA(γ),3xMMAE-XTEN on KB cells

[00695] The ability to selectively target and kill cells bearing folate receptors was evaluated. Test articles of free MMAE, a non-targeting 3xMMAE-XTEN conjugate (XTEN linked to toxin) and the folate receptor-targeted 3xFA(γ),3xMMAE-XTEN conjugate were evaluated in a CellTiter-Glo anti-proliferation assay using the folate receptor-positive KB cell line. As culture media contain high folic acid content, KB cells were grown in folic acid-free media containing 10% heat-inactivated fetal calf serum at 37°C, 5% CO2 for at least 7 days prior to the commencement of the cell viability experiment, This medium was also utilized for the execution of the experiment. In brief, KB cells were plated at 10,000 cells per well onto a 96-well microtiter assay plate. KB cells were allowed to adhere to the plate by an overnight incubation at 37°C, 5% CO2. The spent media was then removed and wells designated to contain folic acid competitor received assay medium containing folic acid, while wells not designated to have folic acid competitor received assay medium only. The plate was incubated for 30 min at 37°C, 5% CO2 before the assay media was aspirated and plate washed with assay media. Free MMAE, 3xMMAE-XTEN and 3xFA(γ),3xMMAE-XTEN in the presence or absence of folic acid competitor was then added at an appropriate range of doses. The plate was then further incubated for 2- 4 h at 37°C, 5% CO2. Media was then removed, the plate washed and fresh media introduced and the plate was allowed to incubate for an additional 48-72h. After the appropriate incubation period, CellTiter-Glo reagent was added and the plate was read on a luminometer. The IC50 of each test article was determined using a 4 parameter logistic curve fit using GraphPad Prism.

[00696] Results: As shown in FIG. 116, free MMAE drug moiety shows highly potent killing of KB cells, with an IC50 of 0.8nM, while 3 copies of MMAE conjugated to non-targeting XTEN resulted in at least a 3 log reduction in cell killing (IC50 >1,000nM). Significantly, the addition of 3 copies of folate targeting domains to the 3xMMAE-XTEN conjugate restored the cell

killing, with an IC 50 of 4.2 nM; a level of activity close to that observed for free MMAE. Of equal importance, the introduction of folic acid as a competitor to the targeted conjugate impaired the observed cell killing activity of 3xFA(γ),3xMMAE-XTEN on the KB cell line. This reduction from potent cell killing of the folate-XTEN drug conjugate (from 4.2 nM to >1,000nM) supports the conclusion that the detected cell toxicity was, under the experimental conditions, facilitated by use of the folate as the targeting mechanism for the drug conjugate against the KB cell line.

[00697] Example 68: In vitro cell-based screening of folate-XTEN-drug conjugates for activity and specificity

[00698] The ability to selectively target and kill cells bearing folate receptors using targeted folate-XTEN-drug conjugates is evaluated using an in vitro-based screening and selectivity assay.

[00699] Each folate-XTEN-drug conjugate, its corresponding non-targeting XTEN-drug molecule and respective free drug control will be tested in a CellTiter-Glo anti-proliferation assay against a panel of folate receptor positive and negative cell lines. Choice of cell lines is based on relevance to proposed clinical application and includes KB, IGROV, SK-OV-3, HeLa, LoVo, SW620, Madison 109, A549, A375, LS-174T, HT-29, 4T1, SK-BR-3. As culture media contain high folic acid content, cells will be grown and assay performed in folic acid free-media containing 5-10% heat-inactivated fetal calf serum (FCS) at 37°C, 5% CO_2. Heat-inactivated FCS contains endogenous level of folic acid sufficient for folate receptor expressing cells to survive and proliferate. Appropriate assay conditions including optimal cell density and incubation time are pre-determined in folate-free media containing 5-10% FCS using the respective free drug as control. Folate-XTEN-drug conjugates are then tested as follows: cells in log-phase are collected, counted and plated at pre-determined cell density onto each well of a 96-well microtiter assay plate. Adherent cells are allowed to attach to the plate by an overnight incubation at 37°C, 5% CO_2. Folate-XTEN-drug conjugates and corresponding controls are introduced in a dose range in duplicates and plate incubated for an additional 2 to 5 days. Alternatively, cells can also be pulsed with folate-XTEN-drug conjugates and corresponding controls for 2-6 h, washed, fresh media introduced and allowed to incubate for an additional 48-72 h. After the appropriate incubation period, CellTiter-Glo reagent is added to each well, mixed for 2 minute on an orbital shaker. Plate is then centrifuged at 90g and incubated at room temperature for an additional 10 minutes to stabilize the luminescent signal. Luminescence signals are then read on a luminometer & IC_{50}s (half maximal inhibitory concentration) calculated with GraphPad Prism or equivalent software. Quantitative comparisons of IC_{50}s will enable ranking of the compounds' activity for inhibition of cell growth and selectivity against folate receptor positive versus negative cell lines.

[00700] It is expected that the results would support the finding that the folate-XTEN-drug conjugates will show highly selective potent killing on folate receptor positive cells but not on folate receptor negative cells. This will be in contrast to the free drug moiety whereby no discrimination in the strong cytotoxicity is expected between folate receptor positive and negative cell lines. The XTEN-drug control is expected to yield poor cytotoxic activity. The folate-XTEN-drug conjugate with the most favorable activity and cell line selectivity relative to controls will be further verified for folate receptor association by the addition of free competitive folic acid in the assay and demonstrating impaired folate-XTEN-drug cytotoxicity.

[00701] Example 69: In vitro cell-based screening of LHRH-XTEN-drug conjugates for activity and specificity

[00702] The ability to selectively target and kill cells bearing LHRH receptors using targeted LHRH-XTEN-drug conjugates is evaluated using an in vitro-based screening and selectivity assay. Each LHRH-XTEN-drug conjugate, its corresponding non-targeting XTEN-drug molecule and respective free drug control are tested in a CellTiter-Glo anti-proliferation assay against a panel of LHRH receptor positive and negative cell lines. Choice of cell lines is based on relevance to proposed clinical application and includes MCF-7, MDA-MB-231, HCC1806, HCC1937, OV-1063, EFO-21, EFO-27, NIH:OVCAR-3, BG-1, HEC-1A, HEC-1B, Ishikawa, KLE, AN-3-CA, MiaPaCa, Panc-1, rat Dunning R-3327-H, PC-82, MDA-PCa-2b, C4-2 (derivative of LNCaP), A549, A2780, UCI-107, SK-OV-3, SW 626, MFE-296. Appropriate assay conditions, including optimal cell density and incubation time, are pre-determined using the respective free drug as control. LHRH-XTEN-drug conjugates are tested as follows: cells in log-phase are collected, counted and plated at pre-determined cell density onto each well of a 96-well microtiter assay plate. Adherent cells are allowed to attach to the plate by an overnight incubation at 37°C, 5% CO2. LHRH-XTEN-drug conjugates and corresponding controls are introduced in a dose range in duplicates and plate incubated for an additional 2 to 5 days depending on cell lines used. After the appropriate incubation period, CellTiter-Glo reagent is added to each well, mixed for 2 minute on an orbital shaker. Plate is then centrifuged at 90 x g and incubated at room temperature for an additional 10 minutes to stabilize the luminescent signal. Luminescence signals are then read on a luminometer & IC50s (half maximal inhibitory concentration) are calculated with GraphPad Prism or equivalent software. Quantitative comparisons of IC50s will enable ranking of the compounds' activity for inhibition of cell growth and selectivity against LHRH receptor positive versus negative cell lines.

[00703] It is expected that the results would support the finding that the LHRH-XTEN-drug conjugates will show highly-selective and potent killing of LHRH receptor positive cells but not on LHRH receptor-negative cells. This will be in contrast to the free drug moiety whereby no discrimination in the strong cytotoxicity is expected between LHRH receptor positive and

negative cell lines. The XTEN-drug control without the LHRH targeting moiety is expected to yield poor cytotoxic activity. The LHRH-XTEN-drug conjugate with the most favorable activity and cell line selectivity relative to controls are further verified for LHRH receptor association by the addition of free competitive LHRH peptide in the assay and demonstrating impaired LHRH-XTEN-drug cytotoxicity.

[00704] Example 69: In vitro serum stability of LHRH-XTEN-drug conjugates

[00705] As a measure of drug linkage stability, LHRH-XTEN-drug conjugates are incubated independently in normal human, cynomolgus monkey and rodent plasma at 37°C for up to 2 weeks with an aliquot removed at periodic interval and stored at -80°C till analysis. The stability of LHRH-XTEN-drug conjugate can be assessed either by the amount of free drug released or the integrity of the LHRH-XTEN-drug conjugate over time. Free drug is quantitated with RP-HPLC and/or LC-MS/MS whereas the amount of intact LHRH-XTEN-drug conjugate is determined by a XTEN/drug and/or LHRH/drug ELISA. For RP- HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug. For example, doxorubicin is detected at 480 nm. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are treated in parallel with experimental samples. For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs are determined experimentally for each drug. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and is treated in parallel with experimental samples. For quantitative ELISA, optimal concentrations of antibodies for LHRH-XTEN-drug conjugate in the ELISAs are determined using criss-cross serial dilution analysis. An appropriate capture antibody recognizing one component of the conjugate is coated onto a 96-well microtiter plate by an overnight incubation at 4°C. The wells are blocked, washed and serum stability samples added to the wells, each at varying dilutions to allow optimal capture of the LHRH-XTEN-drug conjugate by the coated antibody. After washing, detection antibody recognizing another component of the conjugate is added and allowed to bind to the conjugate captured on the plate. Wells are then washed again and either streptavidin-horseradish peroxidase (complementary to biotinylated version of detection antibody) or an appropriate secondary antibody-horseradish peroxidase (complementary to non-biotinylated version of detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and plate read at 450 nM. Concentrations of

intact conjugate are then calculated for each time point by comparing the colorimetric response to a calibration curve prepared with LHRH-XTEN-drug in the relevant plasma type. The *t*1/2 of the conjugate in human, cyno and mouse serum is then defined using linear regression analysis of the log concentrations vs. time.

[00706] Example 70: In vitro serum stability of folate-XTEN-drug conjugates

[00707] As a measure of drug linkage stability, folate-XTEN-drug conjugates are incubated independently in normal human, cynomolgus monkey and rodent plasma at 37°C for up to 2 weeks with an aliquot removed at periodic interval and stored at -80°C till analysis. The stability of folate-XTEN-drug conjugate can be assessed either by the amount of free drug or the integrity of the folate-XTEN-drug conjugate over time. Presence of free drug is quantitated with HPLC, LC-MS/MS and/or with the anti-proliferation assay as described in the relevant section above. The amount of intact folate-XTEN-drug conjugate is determined by a XTEN/drug and/or folate/drug ELISA. For RP- HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug. For example, doxorubicin is detected at 480 nm. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and is treated in parallel with experimental samples. For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs are determined experimentally for each drug. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and is treated in parallel with experimental samples. When using the anti-proliferation assay as a detection method for the presence of de-conjugated free drug, folate receptor positive or negative cell line could be employed. Folic acid inhibitor is added when assessment is performed in receptor positive cell line and not required when done in receptor negative cell line. In either receptor cell type, increasing concentration of de-conjugated free drug contributes to increased cell toxicity. For quantitative ELISA, optimal concentrations of antibodies for folate-XTEN-drug conjugate in the ELISAs are determined using criss-cross serial dilution analysis. An appropriate capture antibody recognizing one component of the conjugate is coated onto a 96-well microtiter plate by an overnight incubation at 4°C. The wells are blocked, washed and serum stability samples added to the wells, each at varying dilutions to allow optimal capture of the folate-XTEN-drug conjugate by the coated antibody. After washing, detection antibody recognizing another component of the conjugate is added and allowed to bind to the conjugate captured on the plate. Wells are then washed again and either

streptavidin-horseradish peroxidase (complementary to biotinylated version of detection antibody) or an appropriate secondary antibody-horseradish peroxidase (complementary to non-biotinylated version of detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and plate read at 450 nM. Concentrations of intact conjugate are then calculated for each time point by comparing the colorimetric response to a calibration curve prepared with folate-XTEN-drug in the relevant plasma type. The *t*1/2 of the conjugate in human, cyno and mouse serum is then defined using linear regression analysis of the log concentrations vs. time.

[00708] Example 71: In Vivo and ex vivo imaging of LHRH-XTEN-Cy5.5 conjugate

[00709] A Cy5.5 fluorescent tagged LHRH-XTEN conjugate molecule is used as a surrogate to investigate the targeting and biodistribution efficiency of LHRH-XTEN-drug conjugates. Experiments are carried out in nude mice bearing subcutaneous grown xenografts of LHRH receptor positive tumor cells using *in vivo*, followed by *ex vivo*, fluorescence imaging with IVIS 50 optical imaging system (Caliper Life Sciences, Hopkinton, MA). In brief, female nu/nu mice bearing LHRH receptor positive tumor cells are given a single intravenously injection of high or low dose LHRH-XTEN-Cy5.5 and corresponding doses of non-targeting Cy5.5 tagged XTEN control. Whole body scans are acquired pre-injection and then at approximately 8, 24, 48 and 72 hours post-injection on live anesthetized animals using the IVIS 50 optical imaging system. After measuring the distribution of fluorescence in the entire animal at the last time point of 72h, tumor and healthy organs including liver, lung, heart, spleen and kidneys are excised and their fluorescence registered and processed by the imaging system. Cy5.5 excitation (615-665 nm) and emission (695-770 nm) filters are selected to match the fluorescence agents' wavelengths. Small and medium binning of the CCD chip is used and the exposure time optimized to obtain at least several thousand counts from the signals that were observable in each mouse in the image and to avoid saturation of the CCD chip. To normalize images for quantification, a background fluorescence image is acquired using background excitation and emission filters for the Cy5.5 spectral region. The intensity of fluorescence is expressed by different colors with blue color reflecting the lowest intensity and red is indicative of the highest intensity.

[00710] Example 72: In Vivo and ex vivo imaging of folate-XTEN-Cy5.5 conjugates

[00711] A Cy5.5 fluorescent tagged folate-XTEN molecule is used as a surrogate to investigate the targeting and biodistribution efficiency of folate-XTEN-drug conjugates. Experiments are carried out in nude mice bearing subcutaneous grown xenografts of folate receptor positive tumor cells using *in vivo*, followed by *ex vivo*, fluorescence imaging with IVIS 50 optical imaging system (Caliper Life Sciences, Hopkinton, MA). As culture media contain high folate content, folate receptor positive tumor cells to be transplanted onto these mice are grown in folate-free cell culture media containing 5-10% heat-inactivated FCS with no antibiotics.

Similarly, normal rodent chow contains a high concentration of folic acid; nude mice used in this study are maintained on folate-free diet 2 weeks prior to tumor implantation and for the duration of the imaging analysis to reduce serum folate concentration. Female nu/nu mice bearing folate receptor positive tumor cells are given a single intravenously injection of high or low dose folate-XTEN-Cy5.5 and corresponding doses of non-targeting Cy5.5 tagged XTEN control. Whole body scans are acquired pre-injection and then at approximately 8, 24, 48 and 72 hours post-injection on live anesthetized animals using the IVIS 50 optical imaging system. After measuring the distribution of fluorescence in the entire animal at the last time point of 72h, tumor and healthy organs including liver, lung, heart, spleen and kidneys are excised and their fluorescence registered and processed by the imaging system. Cy5.5 excitation (615-665 nm) and emission (695-770 nm) filters are selected to match the fluorescence agents' wavelengths. Small and medium binning of the CCD chip is used and the exposure time optimized to obtain at least several thousand counts from the signals that were observable in each mouse in the image and to avoid saturation of the CCD chip. To normalize images for quantification, a background fluorescence image is acquired using background excitation and emission filters for the Cy5.5 spectral region. The intensity of fluorescence is expressed by different colors with blue color reflecting the lowest intensity and red is indicative of the highest intensity.

[00712] Example 73:Pharmacokinetic analysis of LHRH-XTEN-drug conjugates

[00713] The *in vivo* pharmacokinetics of LHRH-XTEN-drug constructs is assessed using standard methods for protein compositions. Pharmacokinetics are assessed in multiple species, however mice, rats, cynomolgus monkeys, and dogs are preferred due to their common usage in predicting human pharmacokinetics. Compositions of LHRH-XTEN-drug constructs are provided in an aqueous buffer compatible with in vivo administration (for example: phosphate-buffered saline, Tris-buffered saline or Hepes-buffered saline). The compositions are administered at appropriate doses and via multiple routes: most preferably via intravenous or subcutaneous routes. Blood samples are collected at appropriate time points ranging from 0.08 to 504 hours, and processed into plasma. Plasma samples will then be analyzed for concentration of LHRH-XTEN-drug conjugates by one of a variety of methods including ELISA, HPLC and/or LC-MS/MS. ELISA analysis will be performed using a sandwich ELISA format that can recognize 2 components of the LHRH-XTEN-drug conjugate, for instance, XTEN/LHRH, XTEN/drug moiety, LHRH/drug moiety and/or XTEN/XTEN combinations. Typically antibody recognizing one component of the LHRH-XTEN-drug conjugate is coated onto wells of a 96-well microtiter plate. The wells are blocked, washed and plasma samples that have been collected at different time points are then added to the wells, each at varying dilutions, to allow capture of the conjugate by the coated antibody. Wells are then washed extensively, and bound protein detected using either a biotinylated antibody or an appropriate secondary antibody against the

second LHRH-XTEN-drug conjugate component. Wells are then washed again and streptavidin-horseradish peroxidase (complementary to the biotinylated detection antibody) or a secondary antibody-horseradish peroxidase (complementary to a non biotinylated detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and plate read at 450nM. Concentrations of conjugate are then calculated for each time point by comparing the colorimetric response to a LHRH-XTEN-drug calibration curve. Pharmacokinetic parameters are calculated using the WinNonLin software package. For RP- HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug. For example, doxorubicin is detected at 480 nm. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are treated in parallel with experimental samples. For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs are determined experimentally for each drug. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are treated in parallel with experimental samples. It is expected that the results would support the finding that addition of an XTEN to LHRH and drug moiety as a conjugate preparation will greatly increase the terminal half-life and enhance pharmacokinetic properties compared to targeting peptides and drug moiety not linked to XTEN. This in turn will translate into a less frequent, more convenient dosing regimen for such conjugates.

[00714] Example 74: Pharmacokinetic analysis of folate-XTEN-drug conjugates

[00715] The *in vivo* pharmacokinetics of folate-XTEN-drug constructs are assessed using standard methods for protein compositions. Pharmacokinetics are assessed in multiple species, however mice, rats, cynomolgus monkeys, and dogs are preferred due to their common usage in predicting human pharmacokinetics. As normal feed contains a high concentration of folic acid (example 6mg/kg mouse chow), animals to be used in pharmacokinetic studies of folate conjugates are maintained on folate-free diet for 2 weeks prior to study initiation and for the duration of the study. Compositions of folate-XTEN-drug constructs are typically provided in an aqueous buffer compatible with in vivo administration (for example: phosphate-buffered saline, Tris-buffered saline or Hepes-buffered saline). The compositions would be administered at appropriate doses and via multiple routes: most preferably via intravenous or subcutaneous routes. Blood samples would be collected at appropriate time points ranging from 0.08 to 504 hours, and processed into plasma. Plasma samples will then be analyzed for concentration of

folate-XTEN-drug conjugates by a variety of methods including ELISA, HPLC and/or LC-MS/MS. ELISA analysis are performed using a sandwich ELISA format that can recognize 2 components of the folate-XTEN-drug conjugate, for instance, XTEN/folate, XTEN/drug moiety, folate/drug moiety and/or XTEN/XTEN combinations. Typically antibody recognizing one component of the folate-XTEN-drug conjugate is coated onto wells of a 96-well microtiter plate. The wells are blocked, washed and plasma samples that have been collected at different time points are then added to the wells, each at varying dilutions, to allow capture of the conjugate by the coated antibody. Wells are then washed extensively, and bound protein detected using either a biotinylated antibody or an appropriate secondary antibody against the second LHRH-XTEN-drug conjugate component. Wells are then washed again and streptavidin-horseradish peroxidase (complementary to the biotinylated detection antibody) or a secondary antibody-horseradish peroxidase (complementary to a non biotinylated detection antibody) is then added. After appropriate incubation and a final wash step, tetramethylbenzidine (TMB) substrate is added and plate read at 450nM. Concentrations of conjugate are then calculated for each time point by comparing the colorimetric response to a folate-XTEN-drug calibration curve. Pharmacokinetic parameters are calculated using the WinNonLin software package. For RP- HPLC analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are detected by UV absorption at wavelength specific for a particular drug. For example, doxorubicin is detected at 480 nm. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are treated in parallel with experimental samples. For LC-MS/MS analysis, plasma samples are treated with organic solvents such as acetonitrile or acetone to precipitate proteins. Soluble fractions are evaporated in vacuum, redissolved in loading solutions and analyzed by RP-HPLC. Analytes are in-line detected and quantitated by triple quadrupole tandem mass spectrometry. Parental ion–daughter ion pairs are determined experimentally for each drug. Calibration standards are prepared by adding known amounts of free drug to corresponding plasma type and are treated in parallel with experimental samples. It is expected that the results would support the finding that addition of an XTEN to folate and drug moiety as a conjugate preparation will greatly increase the terminal half-life and enhance pharmacokinetic properties compared to targeting peptides and drug moiety not linked to XTEN. This in turn will translate into a less frequent, more convenient dosing regimen for such conjugates.

[00716] Example 75: In vivo efficacy and toxicity analysis of LHRH-XTEN-drug conjugates

[00717] LHRH-XTEN-drug conjugate is intended for targeted delivery of highly potent toxin to LHRH receptor positive tumor cells. As such, the *in vivo* pharmacologic activity of LHRH-

XTEN-drug constructs can be assessed using human tumor cell expressing LHRH receptor transplanted onto nude mice. Prior to beginning the efficacy study, an initial assessment in nude mice is carried out to establish the maximum tolerated dose (MTD) of the LHRH-XTEN-drug candidates. The MTD, the highest dose that is tolerated by the animal for the study duration, will then be used to calculate the dose range for the efficacy and toxicity study in the standard xenograft model. Briefly, the MTD experiment are carried out with 5 mice per group evaluating the intravenous administration of LHRH-XTEN-drug conjugates at various dose level, interval and duration. The starting MTD dose and number of dose groups required are based on scientific literature, knowledge of the targeting LHRH moiety, the nature of the drug moiety conjugated, toxicological properties of closely related compounds, and data from the initial pharmacokinetic studies (see section above). Standard MTD parameters such as reduction in body weight, food and water consumption and signs of piloerection, hunched, behavior patterns, respiratory pattern, tremors, convulsions, prostration and self-mutilation is carefully monitored on a daily basis. The highest dose of LHRH-XTEN-drug that does not cause unacceptable toxicity is assigned as the MTD. The tumor xenograft study will include 3 to 4 dosing levels of LHRH-XTEN-drug conjugate and will depend on the results from the MTD study; with other parameters depending on the tumor cell line chosen. Example 69 describes examples of tumor lines that can be used in the xenograft study. Thus an appropriate number of LHRH receptor positive cells from the relevant human tumor line are injected subcutaneously and allowed to form tumors, the size of which is measured with calipers and the volume calculated as $0.5 \times L \times W^2$, where L=measurement of longest axis in millimeters and W=measurement of axis perpendicular to L in millimeters. Following randomization of mice containing tumor volume in the desired size range into groups of 8-10 animals, vehicle control, free drug control and LHRH-XTEN-drug conjugate are administered intravenously at the chosen doses and interval. Cessation or regression of tumor growth is determined through measuring the tumor size and hence volume at selected time points with calipers. Body weights and food consumption are measured every 1to 2 days to assess gross toxicity. Survival of animals is monitored daily. At the end of the study, all animals are sacrificed and clinical pathology and histopathology on major organs are performed. Targeted cytotoxins are among the most promising strategies for the selective elimination of malignant cells. It is anticipated that the results would support the finding that the LHRH-XTEN-drug conjugate will produce an excellent therapeutic index as exhibited by potent efficacy and low systemic toxicity. In contrast, the non-LHRH targeted free drug dosed at equimolar doses will not only be less potent but more highly toxic. The vehicle control is expected to display uncontrolled tumor growth and severe toxicity.

[00718] Example 76: In vivo efficacy and toxicity analysis of folate-XTEN-drug conjugates

[00719] Folate-XTEN-drug conjugate is intended for targeted delivery of highly potent toxin to folate receptor positive tumor cells. As such, the *in vivo* pharmacologic activity of folate-XTEN-drug constructs can be assessed using human tumor cell expressing folate receptor xenograft onto nude mice. Prior to beginning the efficacy study, an initial assessment in nude mice are carried out to establish the maximum tolerated dose (MTD) of the folate-XTEN-drug candidates. The MTD, the highest dose that is tolerated by the animal for the study duration, will then be used to calculate the dose range for the efficacy and toxicity study in the standard xenograft model. As normal rodent chow contains a high concentration of folic acid (6mg/kg chow), mice to be used in these studies are maintained on folate-free diet for 2 weeks prior to study initiation and for the duration of the study. The MTD experiment is carried out with 5 mice per group evaluating the intravenous administration of folate-XTEN-drug conjugates at various dose level, interval and duration. The starting MTD dose and number of dose groups required is based on scientific literature, knowledge of the targeting folate moiety, the nature of the drug moiety conjugated, toxicological properties of closely related compounds, and data from the initial pharmacokinetic studies (see section above). Standard MTD parameters such as reduction in body weight, food and water consumption and signs of piloerection, hunched, behavior patterns, respiratory pattern, tremors, convulsions, prostration and self-mutilation is carefully monitored on a daily basis. The highest dose of folate-XTEN-drug that does not cause unacceptable toxicity is assigned as the MTD. The tumor xenograft study will include 3 to 4 dosing levels of folate-XTEN-drug and will depend on the results from the MTD; with other parameters depending on the tumor cell line chosen. Example 69 describes examples of tumor lines that can be used in the xenograft study. To reduce folate content, folate receptor positive tumor cells to be transplanted onto nude mice are grown in folate-free cell culture media containing 5-10% heat-inactivated fetal calf serum with no antibiotics. Similarly, to reduce serum folate concentration, mice used in the xenograft studies are maintained on folate-free diet 2 weeks prior to tumor implantation and for the duration of the study. Thus an appropriate number of folate receptor positive cells from the relevant line are injected subcutaneously and allowed to form tumors, the size of which is measured with calipers and the volume calculated as $0.5 \times L \times W^2$, where L=measurement of longest axis in millimeters and W=measurement of axis perpendicular to L in millimeters. Following randomization of mice containing tumor volume in the desired size range into groups of 8-10 animals, vehicle control, free drug control and folate-XTEN-drug are administered intravenously at the chosen doses and interval. Cessation or regression of tumor growth is determined through measuring the tumor size and hence volume at selected time points with calipers. Body weights and food consumption are measured every 1to 2 days to assess gross toxicity. Survival of animals is monitored daily. At the end of study, all animals are sacrificed and clinical pathology and histopathology on major organs are performed. Targeted cytotoxins

are among the most promising strategies for the selective elimination of malignant cells. It is anticipated that targeted chemotherapeutic folate-XTEN-drug conjugate will be more effective and less toxic than free cytotoxic drug alone on folate receptor positive tumors.

[00720] Example 76: Clinical applications of LHRH-XTEN-drug conjugates

[00721] Targeted chemotherapy is a modern approach aimed at increasing the efficacy of systemic chemotherapy and reducing its side effects. Brentuximab vedotin (Adcentris), approved for Hodgkin lymphoma and systemic anaplastic large cell lymphoma is a leading example of effective toxin-targeted therapy. LHRH is a peptide that functions in reproductive organs. Because its receptors are particularly concentrated on certain tumors but are not expressed in most normal tissue, LHRH receptor is an ideal target for selective destruction of malignant tumors. Indeed, ~52% of breast, ~80% of ovarian and endometrial, and ~85% of prostate cancer specimens is targetable via the LHRH receptor. Of note, LHRH-dependent therapies would be especially useful for triple negative breast tumors, which do not overexpress estrogen or progesterone receptors or HER2 and are therefore unsuitable for treatment with many available targeted drugs. Patients with advanced endometrial, ovarian, or prostate cancer often have particularly poor outcomes, as these malignancies can be prone to recurrence and/or resistant to current treatments. In support of this, clinical studies with AEZS-108, a targeted doxorubicin analog of LHRH, indicate that each of these cancer types is susceptible to LHRH-based therapies. Fusion of a XTEN carrying ≥1 copy of LHRH to a XTEN bearing ≥ 3 drug molecules to create a targeted peptide-drug conjugate is expected to have vastly improved therapeutic index and half-life that will enable dosing at levels way below MTD, reduce dosing frequency and cost (reduced drug required per dose).

[00722] Clinical evaluation of LHRH-XTEN-drug composition are conducted in patients suffering from advanced breast, endometrial, ovarian, and prostate or bladder cancers. Clinical trials are designed such that the efficacy and advantages of the LHRH-XTEN-drug conjugate can be verified in humans. Such studies in patients would comprise three phases. First, a Phase I safety and pharmacokinetics study is conducted to determine the maximum tolerated dose (MTD) and to characterize the dose-limiting toxicity, pharmacokinetics and preliminary pharmacodynamics in humans. These initial studies are performed in patients with metastatic or unresectable cancers and for which standard curative or palliative measures could not be used or were no longer effective or tolerated. To enhance treatment efficacy, LHRH receptor positive status would be an enrollment criteria; determined by immunohistochemistry of primary tumors or metastatic specimens and/or by LHRH-targeted molecular imaging agent. The scheme of the phase I study is to use single escalating doses of LHRH-XTEN-drug conjugate and measure the biochemical, PK, and clinical parameters. This would permit the determination of the MTD and establish the threshold and maximum concentrations in dosage and in circulating drug that

constitute the therapeutic window to be used in subsequent Phase II and Phase III trials. It also defines potential toxicities and adverse events to be tracked in future studies.

[00723] Phase II clinical studies of human patients are independently conducted in LHRH receptor positive advanced (stage 3 or 4) or recurrent breast, endometrial, ovarian, and prostate or bladder cancer patients. The trial evaluates the efficacy and safety of LHRH-XTEN-drug conjugate alone and in combination with a current chemotherapy employed in that specific indication. Patients receive intravenously administered LHRH-XTEN-drug clinical candidate at a dose level and regimen pre-determined in Phase I with or without the standard chemo-agent. A control arm comprising of the chemo-agent plus placebo is included. The primary endpoint is response rate as defined by the Response Evaluation Criteria in Solid Tumors (RECIST). Secondary endpoints include safety and tolerability, time-to-progression and overall survival.

[00724] A phase III efficacy and safety study is structured to replicate or modify the phase II trial design in LHRH receptor positive advanced (resistant, recurrent) breast, endometrial, ovarian, and prostate or bladder cancer patients depending on the phase II clinical observations. Refinement of patient enrollment criteria, further patient stratification (example LHRH receptor expression level), dosage, regimen, status of standard chemo-agent etc. could be further adjusted. The primary endpoint is progression-free-survival, as measured by RECIST, in patients defined as LHRH receptor positive. The trial is statistically powered for overall survival as a secondary endpoint with projected enrollment in excess of 400 patients. Incidence of adverse events, serious adverse event and deaths is assessed.

[00725] It is anticipated that LHRH-XTEN-drug candidate will demonstrate anticancer activity without cardiotoxicity even in these highly-pretreated patient populations.

[00726] Example 76: Clinical applications of folate-XTEN-drug conjugates

[00727] Targeted chemotherapy is a modern approach aimed at increasing the efficacy of systemic chemotherapy and reducing its side effects. Brentuximab vedotin (Adcentris), approved for Hodgkin lymphoma and systemic anaplastic large cell lymphoma is a leading example of effective toxin targeted therapy. Folate, also known as folic acid, vitamin B_9, is a vital nutrient required by all living cells for nucleotide biosynthesis and function as cofactor in certain biological pathways. It is especially important in aiding rapid cell division and growth. As such, the folate receptor is a focus for the development of therapies to treat fast dividing malignancy in particular ovarian cancer and non-small cell lung carcinoma. Some ovarian tumor type is likely to recur after initial successes with surgery and platinum-based chemotherapy, to which the regrowth can become resistant to available therapies. While folate receptor expression is negligible in normal ovary, ~90% of epithelial ovarian cancers overexpress the folate receptor, as do many lung adenocarinomas, thereby opening the possibility of directed therapies. In support of this, clinical studies with EC-145, a targeted vinca alkaloid analog of folate, indicated

that platinum-resistant ovarian cancer and non-small cell lung carcinoma are susceptible to folate-based therapies. Fusion of a XTEN carrying ≥1 copy of folate to a XTEN bearing ≥ 3 drug molecules to create a targeted peptide-drug conjugate is expected to have vastly improved therapeutic index and half-life that will enable dosing at levels way below maximum tolerated dose (MTD), reduce dosing frequency and cost (reduced drug required per dose).

[00728] Clinical evaluation of folate-XTEN-drug composition is conducted in patients with relapsed or refractory advanced tumors or specifically in patients suffering from platinum-resistant ovarian cancer and non-small cell lung carcinoma who have failed numerous chemotherapies. Clinical trials are designed such that the efficacy and advantages of the folate-XTEN-drug conjugate can be verified in humans. Such studies in patients would comprise three phases. First, a Phase I safety and pharmacokinetics study is conducted to determine the MTD and to characterize the dose-limiting toxicity, pharmacokinetics and preliminary pharmacodynamics in humans. These initial studies are performed in patients with relapsed or refractory advanced tumors and for which standard curative or palliative measures could not be used or were no longer effective or tolerated. To enhance treatment efficacy, folate receptor positive status is an enrollment criteria, determined by immunohistochemistry of primary tumors or metastatic specimens and/or by folate-targeted molecular imaging agent. The scheme of the phase I study is to use single escalating doses of folate-XTEN-drug conjugate and measure the biochemical, PK, and clinical parameters. This would permit the determination of the MTD and establish the threshold and maximum concentrations in dosage and in circulating drug that constitute the therapeutic window to be used in subsequent Phase II and Phase III trials. It also defines potential toxicities and adverse events to be tracked in future studies.

[00729] Phase II clinical studies of human patients are independently conducted in folate receptor positive platinum-resistant ovarian cancer patient population; non-small cell lung carcinoma patients having failed numerous chemotherapies; and patients suffering from relapsed or refractory advanced tumors. The trial evaluates the efficacy and safety of folate-XTEN-drug conjugate alone and in combination with a current chemotherapy employed in the specific indication. Patients receive intravenously administered folate-XTEN-drug conjugate at a dose level and regimen pre-determined in Phase I with or without the standard chemo-agent. A control arm comprising of the chemo-agent plus placebo is included. The primary endpoint is response rate as defined by the Response Evaluation Criteria in Solid Tumors (RECIST). Secondary endpoints would include safety and tolerability, time-to-progression and overall survival.

[00730] A phase III efficacy and safety study is structured to replicate or modify the phase II trial design in folate receptor positive platinum-resistant ovarian cancer patients; non-small cell lung carcinoma patients; and advanced tumor relapsed or refractory patients depending on the phase II clinical observations. Refinement of patient enrollment criteria, further patient

stratification (example folate receptor expression level), dosage, regimen, status of standard chemo-agent etc., is further adjusted. The primary endpoint is progression-free-survival, as measured by RECIST, in patients defined as folate receptor positive. The trial will also be statistically powered for overall survival as a secondary endpoint with projected enrollment in excess of 400 patients. Incidence of adverse events, serious adverse event and deaths is also assessed.

[00731] It is anticipated that folate-XTEN-drug candidate will demonstrate anticancer activity without severe toxicity even in these highly pretreated patient populations.

Table 52: XTEN-cleavage sequence-affinity tag Polypeptide Sequences

Construct	Amino Acid Sequence
AC710	APTTAGAGRPRPRPRPRPRPRPRPRPRPGRGSPGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAP GTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGP GSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGP GTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEE GTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAP GRHHHHHHHHH
AC698	ANTPVSGNLKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKD QTFWADHAAIIGSNGSYNGITSNVKGTFVKMSSSTNNADTYLEISFTGGTLEPGAHV QIQGRFAKNDWSNYTQSNDYSFKSASQFVEWDQVTAYLNGVLVWGKEPGGSVVGS GSGSGRGSPGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSP AGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTS TEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEP ATSGSETPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPA GSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTE PSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAG SPTSTEEGTSTEPSEGSAPTAEAAGKPGTAEAAGTSESATPESGPGSEPATSGSETPGT SESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTS ESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTS TEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSP AGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTS ESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTS TEPSEGSAPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGKATHHHHHHHH
AC815	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTAEAAGCGTA EAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTE EGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE

Construct	Amino Acid Sequence
	GTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEE GSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEE GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEE GTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETP GSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETP GTSESATPESGPGTSTEPSEGSAPSASRSAHHHHHHHHH
AC816	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTAEAAGCGTA EAAGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEG SAPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGS APGTSTEPSEGSAPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSE TPGTSTEPSEGSAPGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTE EGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSA PGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEE GTSTEPSEGSAPTAEAAGCGTAEAAGTSESATPESGPGSEPATSGSETPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGSPAGSPTSTEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTST EEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPES GPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGS APGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPTAEAAGCGTAEAASASRSAH HHHHHHHH
AC763	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTAEAAGCGTA EAAGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPE SGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSG SETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPE SGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTS TEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAEAASASRSAH HHHHHHHH
AC767	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGPGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTS TEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTS TEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSAPSASRSAHHHHHHHHH
AC769	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTAEAAGCGTA EAAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTAEAAGCGTAEAASTEPS EGSAPGTSESATPESGPGSPAGSPTSTEEGSPATAEAAGCGTAEAASPTSTEEGTSESA TPESGPGTSTEPSEGSAPGTSESATTAEAAGCGTAEAASETPGTSESATPESGPGSEPA TSGSETPGTSESATPESGTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEP ATSGSETPGTTAEAAGCGTAEAAAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTS ESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGTAEAA GCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAE AASASRSAHHHHHHHHH
AC771	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP TAEAAGCGTAEAAPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTAEAAGC GTAEAASTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPATAEAAGCGTAEAASP

Construct	Amino Acid Sequence
	TSTEEGTSESATPESGPGTSTEPSEGSAPGTSESATTAEAAGCGTAEAASETPGTSESA TPESGPGSEPATSGSETPGTSESATPESGTAEAAGCGTAEAAGSPAGSPTSTEEGTSES ATPESGPGSEPATSGSETPGTTAEAAGCGTAEAAAGSPTSTEEGSPAGSPTSTEEGTST EPSEGSAPGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSE PATSGTAEAAGCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTA EAAGCGTAEAASASRSAHHHHHHHHH
AC817	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGP GTESASRSAHHHHHHHHH
AC818	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTESASRSAHHH HHHHH
AC780	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTEEGTSESATP ESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSE GSAPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSE GSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATP ESGPGTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPT STEEGTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPE SGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGS APGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSE TPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPSASRSAHHHHHHHHH
AC785	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTEGTSTEPSEG SAPGTSESTAEAAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSG TAEAAGCGTAEAATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAG CGTAEAASASRSAHHHHHHHHH
AC765	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPES GPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESATPES GPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTST EEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAEAASASRSAHH HHHHHH
AC766	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGSEPATSGSE TPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSESATPES GPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPESGPGTSTEPSEGS APGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPES GPGTSTEPSEGSAPTAEAAGCGTAEAAGSPAGSPTSTEEGTSESATPESGPGSEPATSG SETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESTAE AAGCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSP TSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAEAASASRS AHHHHHHHHH
AC768	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTPGTSESATPES GPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGS APGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEEGTSESATPES GPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGPGSEPATSGSE TPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAPGTSESTAEAA

Construct	Amino Acid Sequence
	GCGTAEAATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGTAEAAGCGTAEA ATEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPTAEAAGCGTAEAASASRSA HHHHHHHHH
AC786	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAP GTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGP GTESASRSAHHHHHHHHH
AC792	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSTSSTAESPG PGSTSSTAESPGPGCTSESPSGTAPGSTSSTAESPGPGSTSSTAESPGPGTSTPESGSASP GSTSCSPSGEAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPETSPSGESCTAPG STSASRSAHHHHHHHHH
AC793	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGTPGSGTASSS PGSSTPSGATGSPGCAGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGS PGSSTCSGATGSPGSSPSASTGTGPGSSPSASTGTGPGASPGTSSTGSPGTPGSGTACSS PGSSSASRSAHHHHHHHHH
AC798	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSPAGSPTSTE EGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSA PGTSESATPESGPGSEPATSGSETPGSEPATSGSETPGSPAGSPTSTEEGTSESATPESGP GTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAP GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSTEPSEGSAP GTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAP GTSTEPSEGSAPGTSTEPSEGSAPGTSTEPSEGSAPGSPAGSPTSTEEGTSTEPSEGSAP GTSESATPESGPGSEPATSGSETPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GTSTEPSEGSAPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGSPAGSPTSTEE GTSESATPESGPGTSTEPSEGSAPGTSESATPESGPGSEPATSGSETPGTSESATPESGP GSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTSTEEGTSESATPESGP GSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTSTEEGTSTEPSEGSAP GTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGSETPGSEPATSGSETP GSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGSETPGTSESATPESGP GTESASKSAHHHHHHHHH
AC809	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGPGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTS TEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTS TEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTACSEGSAPSASRSAHHHHHHHHH
AC810	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGPGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTS TEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTS TEEGTSTEPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSEGSCASASRSAHHHHHHHHH
AC831	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSTSSTAESPG PGSTSSTAESPGPGSTSESPSGTAPGSTSSTAESPGPGSTSSTAESPGPGTSTPESGSASP GSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPG

Construct	Amino Acid Sequence
	STSESPSGTAPGSTSESPSGTAPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTAPGS TSESPSGTAPGTSTPESGSASPGSTSESPSGTAPGTSTPESGSASPGSTSSTAESPGPGST SSTAESPGPGTSTPESGSASPGTSTPESGSASPGSTSESPSGTAPGTSTPESGSASPGTST PESGSASPGSTSESPSGTAPGSTSESPSGTAPGSTSESPSGTAPGSTSSTAESPGPGTSTP ESGSASPGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSES PSGTAPGSTSESPSGTAPGTSTPESGSASPGTSPSGESSTAPGSTSSTAESPGPGTSPSGE SSTAPGSTSSTAESPGPGTSTPESGSASPGSTSESPSGTAPGSTSSTAESPGPGTSTPESG SASPGTSTPESGSASPGSTSSTAESPGPGTSPSGESSTAPGTSTPESGSASPGSTSESPSG TAPGSTSESPSGTAPGTSTPESGSASPGTSPSGESSTAPGSTSSTAESPGPGTSPSGESST APGSTSSTAESPGPGSTSSTAESPGPGTSPSGESSTAPGSTSESPSGTAPGSTSESPSGTA PGTSTPESGSASPGSTSESPSGTAPGSTSESPSGTAPGTSTPESGSASPGSTSESPSGTAP GSTSESPSGTAPGSTSESPSGTAPGSTSSTAESPGPGTSPSGESSTAPGTSSASRSAHHH HHHHH
AC832	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGASPGTSSTGS PGSSPSASTGTGPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTG PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSSPGASPGTSSTGS PGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGASPGTSSTGSPGTPGSGTASSS PGSSTPSGATGSPGSSPSASTGTGPGSSPSASTGTGPGSSTPSGATGSPGSSTPSGATGS PGASPGTSSTGSPGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGS PGASPGTSSTGSPGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGASPGTSSTGS PGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSTPSGATGSPGASPGTSSTGS PGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTG PGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGASPGTSSTGSPGASPGTSSTGS PGASPGTSSTGSPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGTPGSGTASSS PGSSTPSGATGSPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGSPGSSPSASTGTG PGSSPSASTGTGPGASPGTSSTGSPGTPGSGTASSSPGSSTPSGATGSPGSSPSASTGTG PGSSPSASTGTGPGASPGTSSTGSPGASPGTSSTGSPGSSTPSGATGSPGSSPSASTGTG PGASPGTSSTGSPGSSPSASTGTGPGTPGSGTASSSPGSSTPSGATGSPGSSTPSGATGS PGASSASRSAHHHHHHHHH
AC819	KKQEQEEKKAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPGSCAGSPTSTE EGTSESACPESGPGTSTEPSEGSCPGSPAGSPTSTEEGTCTEPSEGSAPGTSTEPCSGSA PGTSESATPESCPGSEPATSGSETPGSCPATSGSETPGSPAGSCTSTEEGTSESATPESC PGTESASRSAHHHHHHHHH
AC820	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGCGSEPATSG SETPGTSESATPESGPGSEPATSGSETPGTSESATPESGPGTSTEPSEGSAPGSPAGSPTS TEEGTSESATPESGPGSEPATSGSETPGTSESATPESGPGSPAGSPTSTEEGSPAGSPTS TEEGTSCTPSEGSAPGTSESATPESGPGTSESATPESGPGTSESATPESGPGSEPATSGS ETPGSEPATSGSETPGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGSAPGSEPATSGS ETPGTSESATPESGPGTSTEPSCGSAPSASRSAHHHHHHHHH
AC821	KNPEQAEEQAEEQREETRPRPRPRPRPRPRPRPRPRPSASRSAGSPTGCGSEPATSG SETPGTSESATPESGPGSEPATSGSCTPGTSESATPESGPGTSTEPSEGSAPGSPAGSPC STEEGTSESATPESGPGSEPATSGSETPGTSESCTPESGPGSPAGSPTSTEEGSPAGSPTS TEEGTSCTPSEGSAPGTSESATPESGPGTSESATPESGPGCSESATPESGPGSEPATSGS ETPGSEPATSGSETCGSPAGSPTSTEEGTSTEPSEGSAPGTSTEPSEGCAPGSEPATSGS ETPGTSESATPESGPGTSTEPSCGSAPSASRSAHHHHHHHHH

CLAIMS

1. A method of producing a composition comprising a substantially homogenous population of XTEN sequences, the method comprising:

a. providing a polypeptide composition comprising at least one polypeptide having an amino acid sequence selected from the group of sequences set forth in Table 6, wherein the amino acid sequence comprises at least one cleavage sequence,

b. treating said polypeptide composition with trypsin under conditions effective to cleave the cleavage sequence; and

wherein at least 95%, 96%, 97%, 98%, or 99% of individual sequences in the resulting substantially homogeneous population of XTEN sequences have an identical sequence length.

2. The method of claim 1, further comprising:

a. adsorbing the XTEN sequences onto a chromatography substrate under conditions effective to capture the XTEN sequences but not the protease;

b. eluting the XTEN sequences; and

c. recovering the XTEN sequences wherein at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of individual molecules of the population have an identical sequence length.

3. The method of claim 2, wherein the chromatography substrate is an anion exchange substrate.

4. The method of claim 3, wherein the anion exchange substrate is selected from the group consisting of macrocap Q, capto Q, superQ-650M, and poros D.

5. The method of any one of claims 1-4, wherein the XTEN sequence has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a sequence selected from the group of amino acid sequences set forth in Table 6.

6. The method of any one of claims 1-5, wherein the XTEN sequence has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to a sequence selected from the group of amino acid sequences set forth in Tables 2 or 3.

7. A composition produced by the method of any one of claims 1-6.

8. A composition comprising a substantially homogenous population of polypeptides comprising an extended recombinant polypeptide (XTEN), and wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of individual polypeptide molecules in said population have an identical sequence length.

9. The composition of claim 8, wherein the XTEN is characterized in that:

a. the XTEN comprises about 36 to about 3000 amino acid residues;

b. the sum of glycine (G), alanine (A), serine (S), threonine (T), glutamate (E) and proline (P) residues constitutes more than about 90% of the total amino acid residues of the XTEN;

c. the XTEN sequence is substantially non-repetitive such that (i) the XTEN sequence contains no three contiguous amino acids that are identical unless the amino acids are serine, (ii) at least about 80% of the XTEN sequence consists of non-overlapping sequence motifs, each of the sequence motifs comprising about 9 to about 14 amino acid residues, wherein any two contiguous amino acid residues does not occur more than twice in each of the sequence motifs; or (iii) the XTEN sequence has a subsequence score of less than 10;

d. the XTEN sequence has greater than 90% random coil formation as determined by GOR algorithm;

e. the XTEN sequence has less than 2% alpha helices and 2% beta-sheets as determined by Chou-Fasman algorithm; and

f. the XTEN sequence lacks a predicted T-cell epitope when analyzed by TEPITOPE algorithm, wherein the TEPITOPE algorithm prediction for epitopes within the XTEN sequence is based on a score of –9.

10. The composition of claim 8, wherein the XTEN comprises a sequence having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 2, Table 3, Table 4 and Tables 22-25.

11. The composition of claim 8, further comprising a first affinity tag.

12. The composition of claim 11, wherein the first affinity tag has binding affinity for a chromatography substrate selected from the group consisting of hydrophobic interaction chromatography (HIC) substrate, cation exchange substrate, anion exchange substrate, immobilized metal ion affinity chromatography (IMAC) substrate, and immobilized antibody substrate.

13. The composition of claim 11, wherein the first affinity tag is selected from the group consisting of the sequences set forth in Table 7.

14. The composition of any one of claims 11-13, further comprising a helper sequence.

15. The composition of claim 14, wherein the helper sequence comprises a sequence having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of the sequences set forth in Table 10.

16. The composition of claim 14, wherein the helper sequence is selected from the group consisting of

a. KNPEQAEEQX1EET wherein X1 is independently S or R;

b. ANPEQAEEQX1EET wherein X1 is independently S or R;

c. KNPEQAEEQAEEQX1EET wherein X1 is independently S or R;

d. KX2X3EQAEEQAEEQX1EET wherein X1 is independently S or R, X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

e. KX2(X3)10QX1EET wherein X1 is independently S or R, X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

f. KX2(X3)7AEEQX1EET wherein X1 is independently S or R, X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

g. KX2X3EQE(X3)3AEEQREET wherein X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

h. KX2X3EQE(X3)3AEE(X3)5 wherein X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

i. KKQEQEKEQAEEQ(X4X5)2REET wherein X4 is independently A or S and X5 is independently K, Q, or E; KKQEQEKEQAEEQ(X4X5)4REET wherein X4 is independently A or S and X5 is independently K, Q, or E;

j. KKQEQEKEQAEEQ(Z)4REET, wherein Z is any naturally-occurring L-amino acid;

k. KX2(X3)n, wherein n is an integer from 10-40 and X2 is independently K or N, and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

l. (X3)n wherein n is an integer from10-50 and X3 is independently K, N, T, Q, H, P, E, D, A, R, or S;

m. KX2QEQEKEQAEEQ(X4X5)nX1EET wherein n is zero or an integer from 1-10 and X1 is independently S or R, X2 is independently K or N, X4 is independently A or S, and X5 is independently K, Q, or E;

n. KX2(X3)n(X4X5)mX1EET, wherein n is an integer from 5-20, m is zero or an integer from 1-10, X1 is independently S or R, X2 is independently K or N, X3 is independently K, N, T, Q, H, P, E, D, A, R, or S, X4 is independently A or S, and X5 is independently K, Q, or E; and

o. KX2(X3)n(Z)mX1EET, wherein n is an integer from 5-20, m is zero or an integer from 1-10, X1 is independently S or R, X2 is independently K or N, X3 is independently K, N, T, Q, H, P, E, D, A, R, or S, and Z is any naturally-occurring L-amino acid.

17. The composition of any one of claims 11-16, further comprising a first cleavage sequence, wherein the first cleavage sequence is selected from the group consisting of the sequences set forth in Table 8 and Table 9.

18. The composition of claim 17, wherein the composition has the configuration of formula I:

(HS)-(AT1)-(CS1)-(XTEN) I

wherein

a. HS is the helper sequence;

b. AT1 is the first affinity tag;

c. CS1 is the first cleavage sequence; and

d. XTEN is the extended recombinant polypeptide.

19. The composition of claim 17, further comprising a second cleavage sequence wherein the first and the second cleavage sequences are capable of being cleaved by the same protease, and wherein the composition has the configuration of formula II:

(HS)-(CS1)-(XTEN)-(CS2)-(AT1) II

wherein

a. HS is a helper sequence;

b. AT1 is the first affinity tag;

c. CS1 is the first cleavage sequence;

d. CS2 is the second cleavage sequence; and

e. XTEN is the extended recombinant polypeptide.

20. The composition of claim 18 or claim 19, wherein the first affinity tag comprises the sequence RPRPRPRPRPRPR or HHHHHH.

21. The composition of any one of claims 11-17, further comprising a second affinity tag and a second cleavage sequence, wherein the second affinity tag has binding affinity to a different chromatography substrate than the first affinity tag, wherein the chromatography substrate is selected from the group consisting of a HIC substrate, cation exchange substrate, anion exchange substrate, IMAC substrate, and immobilized antibody substrate, and wherein the first and the second cleavage sequences are capable of being cleaved by the same protease.

22. The composition of claim 21, wherein the second affinity tag is different from the first affinity tag and is the second affinity tag is selected from the group of sequences set forth in Table 7.

23. The composition of claim 21 or claim 22, wherein the composition has the configuration of formula III:

(HS)-(AT1)-(CS1)-(XTEN)-(CS2)-(AT2) III

wherein

a. HS is the helper sequence;

b. AT1 is the first affinity tag;

c. CS1 is the first cleavage sequence;

d. CS2 is the second cleavage sequence;

e. XTEN is the extended recombinant polypeptide; and

f. AT2 is the second affinity tag.

24. The composition of claim 23, wherein the first affinity tag comprises the sequence RPRPRPRPRPRPR and the second affinity tag comprises the sequence HHHHHH.

25. The composition of claim 23, wherein the first affinity tag comprises the sequence HHHHHH and the second affinity tag comprises the sequence RPRPRPRPRPRPR.

26. A composition comprising a substantially homogenous population of a polypeptide obtained by the process comprising:

a. culturing a host cell that comprises a vector encoding the polypeptide in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product of the host cell, wherein the encoded polypeptide comprises an XTEN, a first cleavage sequence and a first affinity tag;

b. adsorbing the polypeptide of the crude expression product onto a first chromatography substrate under conditions effective to capture the first affinity tag onto the first chromatography substrate;

c. eluting the polypeptide; and

d. recovering the polypeptide wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides of the population have an identical sequence length.

27. The composition of claim 26, wherein the first chromatography substrate is selected from the group consisting of a HIC substrate, cation exchange substrate, anion exchange substrate, and IMAC substrate.

28. The composition of claim 26, wherein the affinity tag is selected from the group consisting of the affinity tags of Table 7.

29. The composition of claim 27, wherein the first chromatography substrate is cation exchange and the first affinity tag comprises the sequence RPRPRPRPRPRPR.

30. The composition of claim 27, wherein the first chromatography substrate is IMAC and the first affinity tag comprises the sequence HHHHHHHH.

31. The composition of claim 26, wherein the vector encodes the polypeptide of any one of claims 11-19.

32. The composition of any one of claims 26-28, wherein the vector further encodes a second cleavage sequence and a second affinity tag wherein the first and the second cleavage sequences are capable of being cleaved by the same protease and wherein the second affinity tag has binding affinity to a second, different chromatography substrate than the first affinity tag, and wherein the composition is obtained by the process further comprising:

a. adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag onto the second chromatography substrate;

b. eluting the polypeptide; and

c. recovering the polypeptide wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides of the population have an identical sequence length.

33. The composition of claim 32, wherein the vector encodes the polypeptide of claim 23.

34. The composition of claim 32, wherein first chromatography substrate is different from the second chromatography substrate and each of the first and the second chromatography substrate are independently selected from the group consisting of HIC, cation exchange, anion exchange, and IMAC.

35. The composition of claim 32, wherein the first chromatography substrate is cation exchange and the first affinity tag comprises the sequence RPRPRPRPRPRPR and the second chromatography substrate is IMAC and the first affinity tag comprises the sequence HHHHHHHH.

36. The composition of claim 32, wherein the first chromatography substrate is IMAC and the first affinity tag comprises the sequence HHHHHHHH and the second chromatography substrate is cation exchange and the first affinity tag comprises the sequence RPRPRPRPRPRPR.

37. The composition of any one of claims 23-28 or 32-34, the process further comprising:

a. treating the composition with a protease under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the affinity tag(s);

b. adsorbing the XTEN onto a chromatography substrate under conditions effective to capture the XTEN but not the affinity tag(s) or the protease;

c. eluting the XTEN; and

d. recovering the XTEN wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of XTEN have an identical sequence length.

38. The composition of claim 37, wherein the cleavage sequence(s) are capable of being cleaved by a protease selected from the group consisting of the proteases of Table 9.

39. The composition of claim 38, wherein the cleavage sequence(s) are capable of being cleaved by trypsin wherein the sequence is selected from the group consisting of the sequences set forth in Table 8, and wherein the protease is trypsin.

40. The composition of claims 37 or 38, wherein the chromatography substrate is anion exchange.

41. The composition of claim 40, wherein the anion exchange chromatography substrate is selected from the group consisting of macrocap Q, capto Q, superQ-650M, and poros D.

42. The composition of any one of claims 23-28 or 32-34, the process further comprising:

a. treating the composition with a protease under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the affinity tag(s);

b. adsorbing the protease onto a chromatography substrate under conditions effective to capture the protease but not the XTEN; and

c. recovering the XTEN from the eluate wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the individual molecules of XTEN have an identical sequence length.

43. The composition of claim 42, wherein the cleavage sequence(s) are capable of being cleaved by a protease selected from the group consisting of the proteases of Table 9.

44. The composition of claim 42 or claim 43, wherein the cleavage sequence(s) are capable of being cleaved by trypsin wherein the sequence is selected from the group consisting of the sequences set forth in Table 8, and wherein the protease is trypsin.

45. The composition of any one of claims 42-44, wherein the chromatography substrate is one or more of cation exchange substrate, HIC substrate or IMAC substrate.

46. A composition comprising an XTEN sequence, wherein the XTEN sequence further comprises one or more cleavage sequences capable of being cleaved by trypsin and wherein treatment with trypsin under conditions effective to cleave all the cleavage sequences results in a preparation of XTEN fragments wherein each XTEN fragment has at least about 95%, 96%, 97%, 98%, or 99% sequence identity to every other fragment in the preparation.

47. The composition of claim 46, wherein the cleavage sequence has at least 86% sequence identity to or is identical to the sequence SASRSA or SASKSA.

48. The composition of claim 46, wherein the cleavage sequence comprises the sequence RX or KX, wherein X is any L-amino acid other than proline.

49. The composition of claim 46, wherein the composition has at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the sequences selected from the group of sequences set forth in Table 6.

50. A method for producing an XTEN sequence in a host cell, the method comprising culturing a host cell that comprises a vector encoding a polypeptide comprising a) the XTEN sequence and b) a helper sequence, in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product at a concentration of more than about 2 grams/liter (g/L), or about 3 g/L, or about 4 g/L, or about 5 g/L, or about 6 g/L, or about 7 g/L of said polypeptide.

51. A method for producing an XTEN sequence in a host cell, the method comprising culturing a host cell that comprises a vector encoding a polypeptide comprising a) the XTEN sequence and b) a helper sequence, in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product at a concentration of more than about 10 milligrams/gram of dry weight host cell (mg/g), or at least about 15 mg/g, or at least about 20 mg/g, or at least about 25 mg/g, or at least about 30 mg/g, or at least about 40 mg/g, or at least about 50 mg/g of said polypeptide.

52. A method for producing an XTEN sequence in a host cell, the method comprising culturing a host cell that comprises a vector encoding a polypeptide comprising a) the XTEN sequence and b) a helper sequence, in a fermentation reaction under conditions effective to express the polypeptide as a component of a crude expression product at a concentration of more than about 10 milligrams/gram of dry weight host cell (mg/g), or at least about 250 micromoles/L, or about 300 micromoles/L, or about 350 micromoles/L, or about 400 micromoles/L, or about 450 micromoles/L, or about 500 micromoles/L of said polypeptide.

53. The method of any one of claims 50-52, wherein the concentration is measured when the fermentation reaction reaches an optical density of at least 130 at a wavelength of 600 nm.

54. The method of any one of claims 50-52, wherein the helper sequence of the expressed polypeptide is at the N-terminus of the polypeptide and wherein the helper sequence has at least about 90%, 91%, 92%, 93%, 94%, or 95% sequence identity or is identical to a sequence selected from the group consisting of the sequences set forth in Table 10.

55. The method of claim 54, wherein the vector encodes the polypeptide of any one of claims 14-17.

56. The method of claim 55, further comprising

a. recovering the crude expression product of the host cell fermentation reaction mixture;

b. adsorbing the polypeptide of the crude expression product onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate, wherein the first chromatography substrate is selected from the group consisting of a HIC substrate, a cation exchange substrate, an anion exchange substrate, and an IMAC substrate;

c. eluting and recovering the XTEN sequence wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides have an identical sequence length.

57. The method of any one of claims 50-52, wherein the vector encodes the polypeptide of any one of claims 21-23.

58. The method of claim 57, further comprising:

a. recovering the crude expression product of the host cell fermentation reaction mixture;

b. adsorbing the polypeptide onto a first chromatography substrate under conditions effective to capture the first affinity tag of the polypeptide onto the chromatography substrate wherein the first chromatography substrate is selected from the group consisting of a HIC substrate, a cation exchange substrate, an anion exchange substrate, and an IMAC substrate;

c. eluting the polypeptide;

d. adsorbing the polypeptide onto a second chromatography substrate under conditions effective to capture the second affinity tag of the polypeptide onto the chromatography substrate

wherein the second chromatography substrate is selected from the group consisting of a HIC substrate, a cation exchange substrate, an anion exchange substrate, and an IMAC substrate;

e. eluting the polypeptide; and

f. recovering the XTEN sequence wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the polypeptides have an identical sequence length.

59. The method of claim 56 or claim 58, the method further comprising:

a. treating the polypeptide with a protease under conditions effective to cleave the cleavage sequence, thereby releasing the XTEN from the polypeptide;

b. adsorbing the XTEN onto an anion chromatography substrate under conditions effective to capture the XTEN;

c. eluting the XTEN; and

d. recovering the XTEN wherein at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95% of the individual XTEN molecules have an identical sequence length.

60. The method of claim 59, wherein the anion chromatography substrate is selected from the group consisting of macrocap Q, capto Q, superQ-650M, and poros D.

61. The method of claim 59 or claim 60, wherein the protease is trypsin and wherein the sequence is selected from the group consisting of the sequences set forth in Table 8.

62. The method of claim 56 or claim 58, the method further comprising:

a. treating the polypeptide with a protease under conditions effective to cleave the cleavage sequence(s), thereby releasing the XTEN from the polypeptide;

b. adsorbing the protease onto a chromatography substrate under conditions effective to capture the protease but not the XTEN; and

c. recovering the XTEN in the eluate wherein at least 90%, 91%, 92%, 93%, 94%, or 95% of the XTEN have an identical sequence length.

63. The method of claim 62, wherein the protease is trypsin, and wherein the sequence is selected from the group consisting of the sequences set forth in Table 8.

64. The method of claim 62 or claim 63, wherein the chromatography substrate is one or more of a HIC substrate, a cation exchange substrate, and an IMAC substrate.

65. A solid support comprising immobilized thereon a population of substantially identical polypeptides, wherein the solid support comprises a chromatography substrate, and the immobilized polypeptides each comprise an XTEN, a first affinity tag, and a second affinity tag, wherein:

a. the first affinity tag is joined to the XTEN by a cleavage sequence at the N-terminus of the XTEN;

b. the second affinity tag is joined to the XTEN by a cleavage sequence at the C-terminus of the XTEN;

c. the second affinity tag is different from the first affinity tag;

d. the chromatography substrate is capable of binding to either said first or said second affinity tag but not both; and

e. at least 90%, 91%, 92%, 93%, 94%, or 95% of the immobilized polypeptide molecules have an identical sequence length.

66. The solid support of claim 65, wherein the immobilized polypeptide molecules comprise the polypeptides any one of claims 21-25.

67. The solid support of claim 65 or claim 66, wherein the cleavage sequence has at least about 86% sequence identity to or is identical to the sequence SASRSA or SASKSA.

68. The solid support of claim 65 or claim 66, wherein the cleavage sequence comprises the sequence RX or KX, wherein X is any L-amino acid other than proline.

69. The solid support of any one of claims 65-68, wherein the solid support is selected from the group consisting of HIC chromatography resin, cation exchange chromatography resin, anion exchange chromatography resin, and IMAC chromatography resin.

70. The composition of claim 69, wherein the first affinity tag comprises the sequence RPRPRPRPRPRPR and the second affinity tag comprises the sequence HHHHHH.

71. The composition of claim 69, wherein the first affinity tag comprises the sequence HHHHHH and the second affinity tag comprises the sequence RPRPRPRPRPRPR.

72. A conjugate composition comprising an XTEN covalently linked to one or more molecules of at least a first cross-linker, wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13, the alkyne reactants set forth in Table 15, and the azide reactants set forth in Table 15, and the XTEN is selected from the group consisting of the XTEN of claim 37, the XTEN of claim 42, the XTEN of claim 7, the sequences set forth in Table 2, and the sequences set forth in Table 3.

73. The conjugate composition of claim 72, wherein the first cross-linker is conjugated to the at least first XTEN at a location selected from the group consisting of:

a. an alpha-amino group of an N-terminal amino acid residue of the XTEN;

b. an epsilon amino group of each lysine residue of the XTEN; and

c. a thiol group of each cysteine residue of the XTEN.

74. The conjugate composition of claim 72 or claim 73, wherein the XTEN has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 2 and Table 3.

75. The conjugate composition of claim 74, wherein the XTEN is selected from the group consisting of AE144, AE288, AE432, AE576, AE864, Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199, and the cross-linker is conjugated to the alpha amino-group of the N-terminal amino acid of the XTEN.

76. The conjugate composition of claim 74, wherein the XTEN is selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3, and the cross-linker is conjugated to the thiol group of each cysteine residue of the XTEN.

77. The conjugate of any one of claims 72-76, wherein the first cross-linker is selected from the group consisting of an N-maleimide, an iodoacetyl reagent, a pyridyl disulfide reagent, a vinyl sulfone reagent, 3-propargyloxypropanoic acid, (oxyethyl)n-acetylene where n is 1-10, dibenzylcyclooctyne (DBCO), cyclooctyne (COT), 3-azide-propionic acid, 6-azide-hexanoic acid, and (oxyethyl)n-azide where n is 1-10.

78. The conjugate composition of claim 76, wherein the first cross-linker is conjugated to the thiol group of each cysteine residue of the XTEN, and the conjugate further comprises a second cross-linker conjugated to the alpha amino-group of the N-terminal amino acid of the XTEN wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13, the alkyne reactants of Table 15, and the azide reactants of Table 15.

79. The conjugate composition of claim 78, having the configuration of formula V:
wherein independently for each occurrence;

a. CL1 is the first cross-linker conjugated to cysteine residues of the XTEN;

b. CL2 is the second cross-linker conjugated to XTEN at the N-terminus;

c. x is an integer of 1 to about 10;

d. y is an integer of 1 with the proviso that x + y is > 2;

e. XTEN is a cysteine engineered XTEN comprising x number of cysteine residues.

80. The conjugate composition of any one of claims 72-77, further comprising a single atom residue of a first payload conjugated to each first cross-linker wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

81. The conjugate composition of claim 80, wherein the first payload of the single atom residue is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21.

82. The conjugate composition of any one of claims 72-77, further comprising a payload selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21 conjugated to each first cross-linker.

83. The conjugate composition of claim 78 or claim 79, further comprising a single atom residue of a first payload conjugated to each of the first cross-linkers wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur, and a single atom residue of a second payload conjugated to the second cross-linker wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

84. The conjugate composition of claim 83, wherein the first payload of the single atom residue is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21 and the second payload of the single atom residue is a different payload from the first payload and is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21.

85. The conjugate composition of claim 78 or claim 79, further comprising a first payload conjugated to each of the first cross-linkers wherein the payload is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21, and a second payload different from the first payload conjugated to the second cross-linker wherein the second payload is selected from the group consisting of payloads set forth in Tables 6, 7, 18, and 21.

86. The conjugate composition of claim 78 or claim 79, further comprising a first payload conjugated to each of the first cross-linkers wherein the payload is selected from the group consisting drug moieties of Table 21, and a second payload different from the first payload conjugated to the second cross-linker wherein the second payload is selected from the group consisting of targeting moieties of Table 21.

87. The conjugate composition of claim 85 or claim 86, wherein the second payload is linked to the N-terminus of the XTEN by the second cross-linker conjugated by reaction of an alkyne reactant and an azide reactant selected from the group consisting of the reactants of Table 15.

88. A conjugate composition comprising at least a first and a second XTEN, wherein the XTEN are the same or are different and each is selected from the group consisting of the XTEN of claim 37, the XTEN of claim 42, the XTEN of claim 7, and the sequences set forth in Table 3, and in which the first and the second XTEN are conjugated to each other by the N-termini of the first and the second XTEN with a cross-linker created by reaction of an alkyne reactant and an azide reactant selected from the group consisting of the reactants of Table 15.

89. The conjugate composition of claim 88, wherein the first XTEN and the second XTEN are different and each independently has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 3.

90. The conjugate composition of claim 89, wherein the first XTEN has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at

least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3 and the second XTEN has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a different sequence selected from the group of sequences consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3.

91. The conjugate composition of claim 88, wherein the first XTEN and the second XTEN are the same are each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 3.

92. The conjugate composition of claim 91, wherein the first XTEN and the second XTEN each have at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3.

93. The conjugate composition of any one of claims 88-92, wherein the first and the second XTEN each comprises one or more cysteine residues, and further comprises a first cross-linker conjugated to each cysteine residue of the first XTEN and a second cross-linker conjugated to each cysteine residue of the second XTEN, wherein the first and the second cross-linkers are independently selected from the group consisting of the cross-linkers set forth in Table 13.

94. The conjugate composition of any one of claims 88-92, wherein the first and the second XTEN each comprises one or more lysine residues, and further comprises a cross-linker conjugated to each lysine residue of the first and/or the second XTEN of the conjugate, wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13.

95. The conjugate composition of claim 93 or claim 94, further comprising a single atom residue of a first payload conjugated to each cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur, and further comprises a single atom residue of a second payload conjugated to each cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

96. The conjugate composition of claim 95, wherein the first payload of the single atom residue is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21, and the second payload of the single atom residue is a different payload from the first payload and is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21.

97. The conjugate composition of claim 93 or claim 94, further comprising a first payload conjugated to each cross-linker of the first XTEN wherein the first payload is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21, and further comprises a second payload different from the first payload wherein the second payload is conjugated to each cross-linker of the second XEN wherein the second payload is selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21.

98. The conjugate composition of claim 93 or claim 94, further comprising a first payload conjugated to each cross-linker of the first XTEN wherein the first payload is selected from the group consisting of the targeting moieties set forth in Table 18, and further comprises a second payload different from the first payload wherein the second payload is conjugated to each cross-linker of the second XTEN wherein the second payload is selected from the group of toxins set forth in Table 18.

99. The conjugate composition of claim 93 or claim 94, further comprising a first payload conjugated to each cross-linker of the first XTEN wherein the first payload is selected from the group consisting of the targeting moieties set forth in Table 21, and further comprises a second payload different from the first payload wherein the second payload is conjugated to each cross-linker of the second XTEN wherein the second payload is selected from the group of toxins set forth in Table 21.

100. The conjugate composition of claim 99, wherein the first XTEN is Seg 176 of Table 3 and the second XTEN is selected from the group consisting of Seg 176 and Seg 177 set forth in Table 3.

101. A conjugate composition comprising at least a first XTEN, a second XTEN, and a third XTEN wherein the XTEN are each independently selected from the group consisting of the XTEN of claim 37, the XTEN of claim 42, the XTEN of claim 7, and the sequences set forth in Table 3, wherein the the first and the second and the third XTEN are conjugated to each other at the N-termini using a trivalent cross-linker selected from the group consisting of the trivalent cross-linkers set for in Table 13 or Table 14.

102. The conjugate composition of claim 100, wherein the trivalent cross-linker is selected from the group consisting of Tris-(2-Maleimidoethyl)amine (TMEA) and amine-reactive Tris-(succimimidyl aminotricetate) (TSAT).

103. The conjugate composition of any one of claims 100-102, wherein the first, the second, and the third XTEN are the same and each has at least about 90%, or at least about 91%, or at

least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3.

104. The conjugate composition of any one of claims 100-102, wherein the first and the second XTEN are the same and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3, and the third XTEN is different from the first and the second XTEN and has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3.

105. The conjugate composition of claim 103 or claim 104, wherein the conjugate further comprises a first cross-linker conjugated to each cysteine residue of the first XTEN, a second cross-linker conjugated to each cysteine residue of the second XTEN, and a third cross-linker conjugated to each cysteine residue of the third XTEN, wherein the cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13.

106. The conjugate composition of claim 105, having the configuration of formula XII:

```
(CL1)x-(XTEN1)-3xCL-(XTEN2)-(CL2)y
                 |
            (XTEN3)-(CL3)z              XII
```

wherein independently for each occurrence;

a. 3xCL is the trivalent cross-linker;

b. CL1 is the first cross-linker conjugated to XTEN1;

c. CL2 is the second cross-linker conjugated to XTEN2;

d. CL3 is the third cross-linker conjugated to XTEN3;

e. x is an integer of 1 to about 10;

f. y is an integer of 1 to about 10;

g. z is an integer of 1 to about 10 with the proviso that $x + y + z$ is > 3;

h. XTEN1 is the first XTEN;

i. XTEN2 is the second XTEN; and

j. XTEN3 is the third XTEN.

107. The conjugate composition of claim 105 or claim 106, further comprising

a. a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur;

b. a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and

c. a single atom residue of a third payload conjugated to each third cross-linker of the third XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

108. The conjugate composition of claim 105 or claim 106, further comprising

a. a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21;

b. a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21, wherein the payload is the same or is different from the first payload; and

c. a third payload conjugated to each third cross-linker of the third XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21, wherein the third payload is the same or is different from the first or the second payload.

109. The conjugate composition of claim 108, wherein the first payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and the second and the third payloads are a drug, which may be the same or may be different and wherein the drug is selected from the group consisting of the drugs set forth in Table 6, Table 18, and Table 21.

110. The conjugate composition of claim 109, wherein the targeting moiety is selected from the group consisting of LHRH and folate, and wherein the drug is selected from the group consisting of doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin.

111. The conjugate composition of claim 108, wherein the targeting moiety, and the drug moiety correspond to any one of conjugates 1-290 set forth in Table 21.

112. The conjugate composition of claim 111, wherein the conjugate has the XTEN, the targeting moiety, and the drug moiety corresponding to conjugate 71 of Table 21.

113. A conjugate composition comprising at least a first and a second and a third and a fourth XTEN, wherein the XTEN are selected from the group consisting of the XTEN of claim 37, the XTEN of claim 42, the XTEN of claim 7, and the sequences set forth in Table 3, wherein the XTEN may be the same or different, and in which the first and the second and the third and the fourth XTEN are conjugated to each other by the N-terminus using a tetravalent cross-linker wherein the tetravalent cross-linker is a tetravalent maleimide cluster.

114. The conjugate composition of claim 113, wherein the first, the second, the third, and the fourth XTEN are the same and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3.

115. The conjugate composition of claim 113, wherein the first and the second XTEN are the same and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3, and the third and the fourth XTEN are the same but are different from the first and the second XTEN and each has at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group consisting of Seg 174, Seg 175, Seg 176, Seg 177, Seg 186, Seg 187, Seg 188, Seg 189, Seg 190, Seg 191, Seg 192, Seg 193, Seg 194, Seg 195, Seg 196, Seg 197, Seg 198, and Seg 199 set forth in Table 3.

116. The conjugate composition of claim 114 or claim 115, wherein the conjugate further comprises a first cross-linker conjugated to each cysteine residue of the first XTEN, a second cross-linker conjugated to each cysteine residue of the second XTEN, a third cross-linker conjugated to each cysteine residue of the third XTEN, and a fourth cross-linker conjugated to each cysteine residue of the fourth XTEN, wherein each cross-linker is selected from the group consisting of the cross-linkers set forth in Table 13.

117. The conjugate composition of any one of claim 116, having the configuration of formula XIV

(CL1)v-(XTEN1)-4xCL-(XTEN2)-(CL2)x

/\

(CL3)y-(XTEN3) (XTEN4)-(CL4)z XIV

wherein independently for each occurrence:

a. 4xCL is the tretravalent cross-linker;

b. CL1 is the first cross-linker conjugated to XTEN1;

c. CL2 is the second cross-linker conjugated to XTEN2;

d. CL3 is the third cross-linker conjugated to XTEN3;

e. CL4 is the fourth cross-linker conjugated to XTEN4;

f. v is an integer of 1 to about 10;

g. x is an integer of 1 to about 10;

h. y is an integer of 1 to about 10;

i. z is an integer of 1 to about 10 with the proviso that x + y + z is > 4;

j. XTEN1 is the first XTEN;

k. XTEN2 is the second XTEN;

l. XTEN3 is the third XTEN; and

m. XTEN4 is the fourth XTEN.

118. The conjugate composition of claim 116 or claim 117, further comprising

a. a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur;

b. a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur;

c. a single atom residue of a third payload conjugated to each third cross-linker of the third XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and

d. a single atom residue of a fourth payload conjugated to each fourth cross-linker of the fourth XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur..

119. The conjugate composition of claim 116 or claim 117, further comprising

a. a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21;

b. a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21, wherein the payload is the same or is different from the first payload;

c. a third payload conjugated to each third cross-linker of the third XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21, wherein the payload is the same or is different from the first or the second payload; and

d. a fourth payload conjugated to each fourth cross-linker of the fourth XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18, and 21, wherein the payload is the same or is different from the first or the second or the third payload.

120. The conjugate composition of claim 119, wherein the first payload is a targeting moiety with specific binding affinity to a target wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and at least one other of the second, third, and fourth payloads is a drug wherein the drug is selected from the group consisting of the drugs set forth in Tables 6, 18 and 21.

121. The conjugate composition of claim 120, wherein the targeting moiety is selected from the group consisting of LHRH and folate, and the drug is selected from the group consisting of doxorubicin, paclitaxel, auristatin, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, Il-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin.

122. The conjugate composition of claim 119, wherein the first payload is a targeting moiety with specific binding affinity to a target wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and at least one other of the second, third, and fourth payloads is a drug wherein the drug is selected from the group consisting of the drugs set forth in Tables 6, 18 and 21, and wherein the XTEN, the targeting moiety, and the drug moiety correspond to any one of conjugates 1-290 set forth in Table 21.

123. The conjugate composition of claim 101, having the configuration of formula XVI:

(CL1)x-(XTEN1)-3xCL-(XTEN2)-(CL2)y

|

(XTEN3) XVI

wherein independently for each occurrence;

a. 3xCL is the trivalent cross-linker;

b. CL1 is the first cross-linker conjugated to XTEN1;

c. CL2 is the second cross-linker conjugated to XTEN2;

d. x is an integer of 1 to about 10;

e. y is an integer of 1 to about 10 with the proviso that x + y is > 2;

f. XTEN1 is the first XTEN;

g. XTEN2 is the second XTEN; and

h. XTEN3 is the third XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2.

124. The conjugate composition of claim 123, further comprising

a. a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur; and

b. a single atom residue of a second payload conjugated to each second cross-linker of the second XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

125. The conjugate composition of claim 123, further comprising:

a. a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21; and

b. a second payload conjugated to each second cross-linker of the second XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21, wherein the payload is the same or is different from the first payload.

126. The conjugate composition of claim 125, wherein the first payload is a targeting moiety with specific binding affinity to a target, wherein the targeting moiety is selected from the group consisting of the targeting moieties set forth in Tables 17-19 and 21, and the second payload is a drug, which may be the same or may be different and wherein the drug is selected from the group consisting of the drugs set forth in Table 6, Table 18, and Table 21.

127. The conjugate composition of claim 126, wherein the targeting moiety is selected from the group consisting of LHRH and folate, and wherein the drug is selected from the group consisting of doxorubicin, paclitaxel, auristatin, monomethyl auristatin E (MMAE), monomethyl auristatin F, maytansine, dolastatin, calicheamicin, vinca alkaloid, camptothecin, mitomycin C, epothilone, hTNF, II-12, bortezomib, ranpirnase, pseudomonas exotoxin, SN-38, and rachelmycin.

128. The conjugate composition of claim 125, wherein the first payload is selected from the group consisting of the drugs of Table 11 and the proteins of Table 12 and the second payload is different from the first payload and is selected from the group consisting of the drugs of Table 11 and the proteins of Table 12.

129. The conjugate composition of claim 125, wherein the first payload and the second payload are identical and are selected from the group consisting of the drugs of Table 11 and the proteins of Table 12.

130. The conjugate composition of claim 101, having the configuration of formula XVII:

(CL1)x-(XTEN1)-3xCL-(XTEN2)
|
(XTEN3) XVII

wherein independently for each occurrence;

a. 3xCL is the trivalent cross-linker;

b. CL1 is the first cross-linker conjugated to XTEN1;

c. x is an integer of 1 to about 10;

d. XTEN1 is the first XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 3;

e. XTEN2 is the second XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2; and

f. XTEN3 is the third XTEN wherein the XTEN is selected from the group consisting of the sequences set forth in Table 2.

131. The conjugate composition of claim 130, further comprising a single atom residue of a first payload conjugated to each first cross-linker of the first XTEN wherein the residue is selected from the group consisting of carbon, nitrogen, oxygen and sulfur.

132. The conjugate composition of claim 130, further comprising a first payload conjugated to each first cross-linker of the first XTEN selected from the group consisting of the payloads set forth in Tables 6, 7, 18 and 21.

133. A composition comprising multimeric branched XTEN molecules, wherein a solution of the composition has a viscosity that is less than a solution comprising a corresponding linear XTEN having the same number of amino acids and the same molar concentration.

134. The composition of claim 133, wherein the XTEN molecules have a trimeric, tetrameric, or pentameric configuration.

135. The composition of claim 133, wherein the XTEN molecules are selected from the group consisting of the sequences set forth in Table 2 and Table 3.

136. The composition of any one of claims 133-135, wherein the viscosity of the solution is reduced by at least 5, 6, 7, 8, 9 or 10 cP in a solution containing ≧100 mg/ml of the multimeric XTEN compared to a solution containing ≧100 mg/ml of the corresponding linear XTEN of equal molar concentration.

137. A polypeptide having at least about 90%, or at least about 91%, or at least about 92%, or at least about 93%, or at least about 94%, or at least about 95%, or at least about 96%, or at least about 97%, or at least about 98%, or at least about 99%, or 100% sequence identity to a sequence selected from the group of sequences set forth in Table 52.

138. A pharmaceutical composition, comprising the conjugate of any one of claims 85-87, 97-99, 108-112, 118-122, 125-127, 129 or 132 and a pharmaceutically acceptable carrier.

139. The pharmaceutical composition of claim 138 for treatment of a condition selected from the group of conditions set forth in Table 16.

140. The pharmaceutical composition of claim 138 for use in a pharmaceutical regimen for treatment of a subject, said regimen comprising the pharmaceutical composition.

141. The pharmaceutical composition of claim 140, wherein the pharmaceutical regimen further comprises the step of determining the amount of pharmaceutical composition needed to achieve a beneficial effect in a subject having a condition selected from the group of conditions set forth in Table 16.

142. The pharmaceutical composition of claim 141, wherein the pharmaceutical regimen for treating the subject comprises administering the pharmaceutical composition in two or more successive doses to the subject at an effective amount, wherein the administration results in at least a 10%, or 20%, or 30%, or 40%, or 50%, or 60%, or 70%, or 80%, or 90% greater improvement of at least one, two, or three parameters associated with the condition compared to an untreated subject.

143. A conjugate of any one of claims 85-87, 97-99, 108-112, 118-122, 125-127, 129 or 132 for use in the preparation of a medicament for treatment of a condition selected from the group of conditions set forth in Table 16.

144. A method of selecting a combination of payloads linked to XTEN as a therapeutic agent, the method comprising

a. providing a library of XTENs comprising a plurality of XTEN sequences wherein each of said XTEN sequences is conjugated to at least a first payload and at least a second payload which is different from the first payload;

b. from said library, selecting an XTEN sequence as the therapeutic agent if it exhibits an improved in vitro or in vivo parameter as compared to that of (1) an XTEN sequence conjugated to the first payload alone; and (2) an XTEN sequence conjugated to the second payload alone.

145. The method of claim 144, wherein first payload and second payload are therapeutically effective for ameliorating a common disease.

146. The method of claim 144, wherein the first drug and second drug are therapeutically effective for treating different symptoms of a common disease.

147. The method of claim 145 or claim 146, wherein the common disease is selected from cancer, cancer supportive care, cardiovascular, central nervous system, endocrine disease, gastrointestinal, genitourinary, hematological, HIV infection, hormonal disease, inflammation, autoimmune disease, infectious disease, metabolic disease, musculoskeletal disease, nephrology disorders, ophthalmologic diseases, pain, and respiratory.

148. The method of claim 144, wherein the first payload and second payload mediate their therapeutic effect via a common biological pathway.

149. The method of claim 144, wherein the first payload and second payload are different drugs selected from the group consisting of the drugs set forth in Table 6, Table 18 and Table 21.

150. The method of claim 144, wherein the first payload and second payload are different biologically active proteins selected from the group consisting of the proteins set forth in Table 7, Table 18 and Table 21.

151. The method of claim 144, wherein the first payload is a drug selected from the group consisting of the drugs set forth in Table 6, Table 18 and Table 21 and the second payload is a biologically active protein selected from the group consisting of the proteins set forth in Table 7, Table 18 and Table 21.

152. An isolated polypeptide comprising an extended recombinant polypeptide (XTEN) that is linked to an affinity purification tag via a proteolytic cleavage site having a sequence selected from SASRSA or SASXSA where X is R or K.

153. A polypeptide comprising an extended recombinant polypeptide (XTEN) that is linked at its N-terminus to a first affinity purification tag via a proteolytic cleavage site having a sequence selected from SASRSA or SASXSA where X is R or K, and at its C-terminus to a second affinity purification tag via a proteolytic cleavage site having a sequence selected from SASRSA or SASXSA where X is R or K.

154. A composition having the structure set forth in FIG. 117.